

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

ID AX836857 standard; PRT; 752 AA.

XX

AC AX836857;

XX

SV AX836857.1

XX

DT 15-DEC-2003 (Rel. 78, Created)

DT 15-DEC-2003 (Rel. 78, Last updated, Version 1)

XX

DE Sequence 3981 from Patent EP1347046.

XX

KW

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RA Isogai T., Sugiyama T., Otsuki T., Wakamatsu A., Sato H., Ishii S.,

RA Yamamoto J.I., Isono Y., Hio Y., Otsuka K., Nagai K., Irie R.,

RA Tamechika I., Seki N., Yoshikawa T., Otsuka M., Nagahari K., Masuho Y.,

RT "Full-length cDNA sequences";

RL Patent number EP1347046-A/3981, 24-SEP-2003.

RL Research Association for Biotechnology (JP).

XX

FH Key Location/Qualifiers

FH

FT source 1..752

FT /db_xref="taxon:9606"

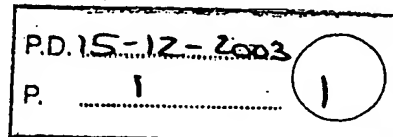
FT /organism="Homo sapiens"

XX

SQ Sequence 752 AA; 83707 MW; 90E70013 CRC32;

MQHSCIPTPP SPFSAPPAFL PVVTRESRRG LSSGGSAGRN AGVTATAAAA DGWKGRLPSP
 LVLLPRASRC QARRRRGGRT SSLLLLPTTP ERALPASPS DPSPRGLGAS SGAAEGAGAG
 LLLGCRASMS DNQSWNSSGS EEDPETESGP PVERCGVLSK WTNYYHGWQD RWVVLKNNAL
 SYYKSEDETE YGCRGSICLS KAVITPHDFD ECRFDISVND SVWYLRAQDP DHRQQWIDAI
 BQHKTESGYG SESSLRRHGS MVSLSVGASG YSATSTSSPK KGHSLREKLA EMETFRDILC
 RQVDTLQKYP DACADAVSKD ELQDKVVED DEDDFPTTRS DGDFLHSTNG NKEKLFPHVT
 PKGINGIDPK GEAITPKATT AGILATLSHC IELMVKREDS WQKRLDKETE KKRRTTEAYK
 NAMTELKKKS HFGGPDYEEG PNSLINEEFP FDAVEAALDR QDKIEEQSQS EKVRLHWPTS
 LPSGDAPSSV GTHRFVQKPY SRSSSMSSID LVSASDDVHR PSSQVEEMVQ NHMTYSLQDV
 GGDANWQLVV EEGEMKVYRR EVEENGIVLD PLKATHAVKG VTGHEVCNYF WNVDVRNDWE
 TTIENTPHVVE TLADNAIIIIY QTHKRVWPAS QRDVLYLSVI RKIPALTEND PETWIVCNFS
 VDHDASAPLNN RCVRAKINVA MICQTLVSPP EGNQEISRDN ILCKITYVAN VNPGGWAPAS
 VLRVAKREY PKFLKRFTSY VQKTAGKPI LF

//



THIS PAGE BLANK (USPTO)

(19)



Europäisches Patentamt

European Patent Office

Office européen des brevets



(11)

EP 1 347 046 A1

(12)

EUROPEAN PATENT APPLICATION

(43) Date of publication:

24.09.2003 Bulletin 2003/39

(51) Int Cl.7: **C12N 15/00, C07K 14/00**

(21) Application number: **02008400.0**

(22) Date of filing: **12.04.2002**

(84) Designated Contracting States:

**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU
MC NL PT SE TR**

Designated Extension States:

AL LT LV MK RO SI

(30) Priority: **22.03.2002 JP 2002137785**

(71) Applicant: **Research Association for
Biotechnology**

Tokyo 105-0003 (JP)

(72) Inventors:

- **Isogai, Takao**
Inashiki-gun, Ibaraki 300-0303 (JP)
- **Sugiyama, Tomoyasu**
Tokyo 130-0003 (JP)
- **Otsuki, Tetsuji**
Kisarazu-shi, Chiba 292-0055 (JP)
- **Wakamatsu, Ai**
Kisarazu-shi, Chiba 292-0014 (JP)
- **Sato, Hiroyuki**
Toyonaka-shi, Osaka 560-0021 (JP)
- **Ishii, Shizuko**
Kisarazu-shi, Chiba 292-0812 (JP)
- **Yamamoto, Jun-ichi**
Kisarazu-shi, Chiba 292-0041 (JP)
- **Isono, Yuuko**
Kisarazu-shi, Chiba 292-0014 (JP)

- **Hio, Yuri**
Kisarazu-shi, Chiba 292-0812 (JP)
- **Otsuka, Kaoru**
Honjo-shi, Saitama 367-0047 (JP)
- **Nagai, Keiichi**
Yamato-shi, Tokyo 207-0022 (JP)
- **Irie, Ryotaro**
Kisarazu-shi, Chiba 292-0801 (JP)
- **Tamechika, Ichiro**
Hirakata-shi, Osaka 573-0034 (JP)
- **Seki, Naohiko**
Chiba-shi, Chiba 261-0001 (JP)
- **Yoshikawa, Tsutomu**
Kisarazu-shi, Chiba 292-0043 (JP)
- **Otsuka, Motoyuki**
Tokyo 125-0062 (JP)
- **Nagahari, Kenji**
Tokyo 167-0053 (JP)
- **Masuhō, Yasuhiko**
Koganei-shi, Tokyo 184-0011 (JP)

(74) Representative: **VOSSIUS & PARTNER**

**Siebertstrasse 4
81675 München (DE)**

Remarks:

The complete document including Reference Tables and the Sequence Listing is available on CD-ROM from the European Patent Office, Vienna sub-office

(54) **Full-length cDNA sequences**

(57) Novel full-length cDNAs are provided.

2443 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide

sequences have been determined. Because the cDNA of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

Description

FIELD OF THE INVENTION

[0001] The present invention relates to polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 40 species of prokaryotes, a lower eukaryote, yeast, a multicellular eukaryote, *C. elegans*, and a higher plants, *arabidopsis*, etc. are already determined. For human genome, presumably having 3 billion base pairs, the analysis was advanced under global cooperative organization, and a draft sequence was disclosed in 2001. Moreover, all the structures are to be clear and to be disclosed in 2002 - 2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence was able to be deduced. On the other hand, the human genome has been estimated to contain about 30 000 - 40 000 genes. Further, 100,000 or more types of mRNAs are said to exist when variants produced by alternative splicing are taken into consideration. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than three million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among human cDNAs, the number of the corresponding mRNAs whose encoding full-length protein sequences are deduced is approximately 13 000.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains atg codon, the translation start site in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene involved in diseases. In addition, genes encoding proteins that are involved in signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly involved in diseases. Thus, identification of the full-length cDNA clones encoding those

proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning, from a cDNA library having very high fullness-ratio, a human full-length cDNA that is predicted to be a full-length cDNA clone, where the cDNA library is synthesized by an improved method (WO 01/04286) of the oligo-capping method (K. Maruyama and S. Sugano, *Gene*, 138: 171-174 (1994); Y. Suzuki et al., *Gene*, 200: 149-156 (1997)). Then, the nucleotide sequences of cDNA clones whose fullness-ratio is high, obtained by this method, were determined mainly from their 5'-ends, and, if required, from 3'-ends.

[0012] Further, representative clones, which were estimated to be novel and full-length, among the clones obtained, were analyzed for their full-length nucleotide sequences. The determined full-length nucleotide sequences were analyzed by BLAST homology search of the databases shown below. Because the homology search of the present invention is carried out based on the information of full-length cDNAs including the entire coding regions, homology to every part of a polypeptide can be analyzed. Thus, in the present invention, the reliability of homology search has been greatly improved.

[1] SwissProt

(http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html),

[2] GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>),

[3] UniGene (Human) (<http://www.ncbi.nlm.nih.gov/UniGene>), and

[4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (<http://www.rcsb.org/pdb/index.html>), PIR (<http://pir.georgetown.edu/pirwww/pirhome.shtml>), and PRF (<http://www.prf.or.jp/en/>); overlapping sequences have been removed.)

[0013] Further, the gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. In addition to the analysis for the expression profile by computer, the profiles of gene expression in living cells were also determined by PCR. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

[0014] In the present invention, gene functions were revealed by the analysis of expression profiles *in silico* based on the information of full-length nucleotide sequences. The expression profiles used in the expression frequency analysis were studied based on the database containing sufficient amount of fragment sequence data. The expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of many cDNA clones obtained in the present invention. Thus, a highly reliable analysis can be achieved by referring to the full-length nucleotide sequences of a wide variety of genes for the sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect the gene expression frequency in tissues and cells from which a certain cDNA library was derived. In other words, the information of full-length cDNA nucleotide sequence of the present invention made it possible to achieve the highly reliable expression frequency analysis.

[0015] The full-length cDNA clones of this invention were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the high fullness ratio by oligo-capping, and [2] assembling 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction). However, the uses of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable readily obtaining full-length cDNAs without such a special technique. The primer, which is designed to be used for obtaining cDNAs capable of being expressed, is not limited to the 5'- and 3'-end sequences of polynucleotide.

[0016] Specifically, the present invention relates to a polynucleotide selected from the group consisting of the following (a) to (g):

(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs shown in Table 1;

(b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1;

(c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1, wherein, in said amino acid sequence, one or more amino

acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;

(d) a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs shown in Table 1, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of (a); and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of (a).

[0017] The present invention also relates to a polypeptide encoded by the above-mentioned polynucleotide or a partial peptide thereof, an antibody binding to the polypeptide or the peptide, and a method for immunologically assaying the polypeptide or the peptide, which comprises the steps of contacting the polypeptide or the peptide with the antibody, and observing the binding between the two.

[0018] Furthermore, the present invention features a vector comprising the above-mentioned polynucleotide, a transformant carrying the polynucleotide or the vector, a transformant carrying the polynucleotide or the vector in an expressible manner, and a method for producing the polypeptide or the peptide, which comprises the steps of culturing the transformant and recovering an expression product.

[0019] Another feature of the present invention is an oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443 or to a complementary strand thereof. This oligonucleotide can be used as a primer for synthesizing the above-mentioned polynucleotide or used as a probe for detecting the polynucleotide. The present invention includes an antisense polynucleotide against the polynucleotide or a part thereof, and a method for detecting the polynucleotide, which comprises the following steps of:

- a) incubating a target polynucleotide with the oligonucleotide under hybridizable conditions, and
- b) detecting hybridization of the target polynucleotide with the oligonucleotide.

[0020] Still another feature of the present invention is a database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 2443 and/or on at least one of the amino acid sequences of SEQ ID NOs: 2444 to 4886.

[0021] Herein, "polynucleotide" is defined as a molecule, such as DNA and RNA, in which multiple nucleotides are polymerized. There are no limitations on the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template polynucleotide by an enzymatic reaction such as PCR. Furthermore, the polynucleotide of the present invention may be modified chemically. Moreover, not only a single-strand polynucleotide but also a double-strand polynucleotide is included in the present invention. In this specification, especially in claims, when the polynucleotide is described merely as "polynucleotide", it means not only a single-strand polynucleotide but also a double-strand polynucleotide. When it means double-strand polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the complementary strand thereof is essentially determined.

[0022] As used herein, an "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0023] The term "substantially pure" as used herein in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any

appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0024] All the cDNAs provided by the present invention are full-length cDNAs. The "full-length cDNA" herein means that the cDNA contains the ATG codon, which is the start point of translation therein. The untranslated regions upstream and downstream of the protein-coding region, both of which are naturally contained in natural mRNAs, are not indispensable. It is preferable that the full-length cDNAs of the present invention contain the stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] Figure 1 shows the restriction map of the vector pME18SFL3.

DETAILED DESCRIPTION OF THE INVENTION

[0026] All the clones (2443 clones) of the present invention are novel and encode the full-length polypeptides. Further, all the clones are cDNAs with the high fullness ratio, which were obtained by oligo-capping method, and also clones which are not identical to any of known human mRNAs (namely, novel clones) selected by searching, for the 5'-end sequences. mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases by using the BLAST homology search [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]; they are also clones that were assumed to have higher fullness ratio among the members in the cluster formed by assembling. Most of the clones assessed to have high fullness ratio in the cluster had the nucleotide sequences longer in the 5'-end direction.

[0027] All the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on the 5'-end and 3'-end sequences or using primer sets of primers designed based on the 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of full-length cDNA of 2443 clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rule of "DDBJ/EMBL/GenBank Feature Table Definition" (<http://www.ncbi.nlm.nih.gov/collab/FT/index.html>). The start position number corresponds to the first letter of "ATG" that is the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated being flanked with the mark "...". However, with respect to the clones having no stop codon, the termination position is indicated by the mark ">" according to the above rule.

Table 1

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
3NB6910001910	1	30..1661	2444
3NB6920014080	2	80..922	2445
3NB6920014590	3	1..693	2446
ADIPS10000640	4	127..1098	2447
ADIPS20004250	5	170..2212	2448
ADRGL10001470	6	368..829	2449
ADRGL20000640	7	599..1345	2450
ADRGL20011190	8	61..>2254	2451
ADRGL20012870	9	827..1300	2452
ADRGL20013010	10	1127..1444	2453
ADRGL20013520	11	226..837	2454
ADRGL20018300	12	320..2233	2455
ADRGL20018540	13	55..363	2456
ADRGL20028570	14	218..976	2457
ADRGL20035850	15	55..522	2458
ADRGL20044590	16	692..1042	2459
ADRGL20048330	17	189..2204	2460
ADRGL20061930	18	293..>1899	2461
ADRGL20067670	19	108..512	2462

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 ADRGL20068170	20	217.. 615	2463
ADRGL20068460	21	576.. 1280	2464
ADRGL20073570	22	556.. 891	2465
ADRGL20076360	23	159.. 515	2466
ADRGL20078100	24	418.. 1563	2467
10 ADRGL20083310	25	871.. 1368	2468
ASTRO10001650	26	369.. 2168	2469
ASTRO20001410	27	319.. 744	2470
ASTRO20005330	28	196.. 642	2471
15 ASTRO20008010	29	735.. 1169	2472
ASTRO20012490	30	286.. 783	2473
ASTRO20027430	31	129.. 848	2474
ASTRO20032120	32	860.. 1189	2475
ASTRO20033160	33	139.. 1014	2476
20 ASTRO20055750	34	16.. 2007	2477
ASTRO20058630	35	28.. 957	2478
ASTRO20064750	36	1381.. >2654	2479
ASTRO20072210	37	274.. >1868	2480
25 ASTRO20084250	38	35.. 1381	2481
ASTRO20100720	39	394.. 714	2482
ASTRO20105820	40	205.. 1368	2483
ASTRO20106150	41	138.. 1811	2484
ASTRO20108190	42	791.. 2539	2485
30 ASTRO20111490	43	517.. 921	2486
ASTRO20114370	44	145.. 1782	2487
ASTRO20114610	45	53.. 433	2488
ASTRO20125520	46	1674.. 2456	2489
35 ASTRO20130500	47	15.. 2417	2490
ASTRO20136710	48	319.. 657	2491
ASTRO20138020	49	285.. 995	2492
ASTRO20141350	50	394.. 1767	2493
ASTRO20143630	51	103.. 1305	2494
40 ASTRO20145760	52	347.. 2008	2495
ASTRO20152140	53	760.. 1233	2496
ASTRO20155290	54	208.. 2298	2497
ASTRO20166810	55	7.. 381	2498
ASTRO20168470	56	334.. 1329	2499
45 ASTRO20173480	57	119.. 724	2500
ASTRO20181690	58	84.. 1967	2501
ASTRO20190390	59	2282.. 2662	2502
BEAST20004540	60	1022.. 1513	2503
50 BGGI110000240	61	123.. 1649	2504
BGGI110001930	62	81.. 1307	2505
BGGI120006160	63	6.. 680	2506
BLADE20003400	64	71.. 1876	2507
BLADE20003890	65	555.. 2405	2508
55 BLADE20004630	66	58.. 405	2509
BNGH420088500	67	2.. 1270	2510
BRACE20003070	68	310.. 1563	2511

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20006400	69	32..364	2512
	BRACE20011070	70	21..1553	2513
	BRACE20019540	71	538..993	2514
	BRACE20027620	72	24..1289	2515
	BRACE20037660	73	143..469	2516
10	BRACE20038000	74	646..2187	2517
	BRACE20038470	75	963..1307	2518
	BRACE20038480	76	1838..2626	2519
	BRACE20038850	77	1099..1413	2520
15	BRACE20039040	78	1273..1671	2521
	BRACE20039440	79	216..797	2522
	BRACE20039540	80	1153..1905	2523
	BRACE20050900	81	115..1788	2524
	BRACE20051380	82	1433..1783	2525
20	BRACE20051690	83	380..742	2526
	BRACE20052160	84	20..1024	2527
	BRACE20053280	85	736..1524	2528
	BRACE20053480	86	24..875	2529
25	BRACE20053630	87	81..950	2530
	BRACE20054500	88	364..669	2531
	BRACE20055180	89	156..656	2532
	BRACE20056810	90	338..940	2533
	BRACE20057190	91	1016..1660	2534
30	BRACE20057420	92	539..856	2535
	BRACE20057620	93	1226..1588	2536
	BRACE20057730	94	819..1592	2537
	BRACE20058580	95	146..1330	2538
35	BRACE20058810	96	40..345	2539
	BRACE20059370	97	192..1574	2540
	BRACE20060550	98	197..1687	2541
	BRACE20060720	99	220..618	2542
	BRACE20060840	100	37..927	2543
40	BRACE20060890	101	170..964	2544
	BRACE20061050	102	1130..1573	2545
	BRACE20061740	103	434..865	2546
	BRACE20062400	104	1310..1732	2547
45	BRACE20062640	105	278..2089	2548
	BRACE20062740	106	753..1151	2549
	BRACE20063630	107	414..800	2550
	BRACE20063780	108	11..892	2551
	BRACE20063800	109	70..435	2552
50	BRACE20063930	110	1795..2433	2553
	BRACE20064880	111	365..1420	2554
	BRACE20067430	112	875..1189	2555
	BRACE20068590	113	260..1759	2556
55	BRACE20069090	114	1484..1960	2557
	BRACE20081720	115	1182..1565	2558
	BRACE20082950	116	1713..2018	2559
	BRACE20090440	117	58..444	2560

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20096200	118	168..1130	2561
	BRACE20096540	119	43..729	2562
	BRACE20097320	120	51..509	2563
	BRACE20099570	121	3..425	2564
	BRACE20101700	122	579..968	2565
10	BRACE20101710	123	187..681	2566
	BRACE20106690	124	335..691	2567
	BRACE20106840	125	19..402	2568
	BRACE20107530	126	437..1063	2569
15	BRACE20108130	127	927..1229	2570
	BRACE20108880	128	417..782	2571
	BRACE20109370	129	1197..1778	2572
	BRACE20109830	130	747..1382	2573
	BRACE20111830	131	366..737	2574
20	BRACE20114780	132	515..886	2575
	BRACE20115450	133	399..764	2576
	BRACE20115920	134	41..937	2577
	BRACE20116110	135	830..1150	2578
25	BRACE20116460	136	84..509	2579
	BRACE20118380	137	657..1421	2580
	BRACE20121850	138	474..857	2581
	BRACE20136240	139	111..518	2582
	BRACE20141080	140	148..534	2583
30	BRACE20142320	141	164..499	2584
	BRACE20142570	142	591..926	2585
	BRACE20147800	143	133..513	2586
	BRACE20148210	144	1101..1541	2587
35	BRACE20148240	145	713..2128	2588
	BRACE20150310	146	94..408	2589
	BRACE20151320	147	137..1189	2590
	BRACE20152870	148	207..653	2591
	BRACE20153680	149	87..956	2592
40	BRACE20154120	150	351..989	2593
	BRACE20163150	151	699..1085	2594
	BRACE20163350	152	443..1597	2595
	BRACE20165830	153	401..709	2596
45	BRACE20171240	154	62..439	2597
	BRACE20172980	155	20..445	2598
	BRACE20175870	156	67..396	2599
	BRACE20177200	157	1178..1675	2600
	BRACE20179340	158	47..1171	2601
50	BRACE20185680	159	880..1341	2602
	BRACE20188470	160	1247..2926	2603
	BRACE20190040	161	6..464	2604
	BRACE20190440	162	382..1287	2605
55	BRACE20192440	163	1199..2062	2606
	BRACE20195100	164	251..736	2607
	BRACE20201570	165	661..1056	2608
	BRACE20210140	166	248..550	2609

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRACE20220300	167	1057..1392	2610
BRACE20223280	168	6..1976	2611
BRACE20223330	169	97..2373	2612
BRACE20224480	170	1568..1924	2613
BRACE20224500	171	1674..2081	2614
BRACE20228480	172	1268..2176	2615
BRACE20229280	173	239..700	2616
BRACE20230700	174	354..752	2617
BRACE20232840	175	79..2019	2618
BRACE20235400	176	213..593	2619
BRACE20237270	177	3..494	2620
BRACE20238000	178	135..437	2621
BRACE20240740	179	83..1546	2622
BRACE20248260	180	682..1533	2623
BRACE20253160	181	26..559	2624
BRACE20253330	182	220..1041	2625
BRACE20257100	183	1638..2021	2626
BRACE20262930	184	256..681	2627
BRACE20262940	185	259..591	2628
BRACE20266750	186	58..1143	2629
BRACE20267250	187	139..612	2630
BRACE20269200	188	4..408	2631
BRACE20269710	189	338..1063	2632
BRACE20273890	190	1365..1766	2633
BRACE20274080	191	350..655	2634
BRACE20276130	192	232..>2028	2635
BRACE20283920	193	717..1025	2636
BRACE20284100	194	1026..1865	2637
BRACE20286360	195	170..727	2638
BRACE20287410	196	603..956	2639
BRALZ20013500	197	215..640	2640
BRALZ20014450	198	6..374	2641
BRALZ20017430	199	232..747	2642
BRALZ20018340	200	879..1481	2643
BRALZ20019660	201	180..773	2644
BRALZ20054710	202	135..1223	2645
BRALZ20058860	203	102..1607	2646
BRALZ20059500	204	722..1081	2647
BRALZ20064740	205	24..350	2648
BRALZ20065600	206	25..624	2649
BRALZ20069760	207	14..319	2650
BRALZ20073760	208	576..1124	2651
BRALZ20075450	209	775..1200	2652
BRALZ20075760	210	148..726	2653
BRALZ20077900	211	1900..2529	2654
BRALZ20077930	212	50..2077	2655
BRALZ20080310	213	1304..2005	2656
BRALZ20088690	214	104..661	2657
BRAMY100C1300	215	2352..2795	2658

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAMY10001570	216	696..1604	2659
	BRAMY20000520	217	329..1204	2660
	BRAMY20000860	218	246..548	2661
	BRAMY200027	219	76.. 447	2662
	BRAMY20004110	220	145.. 540	2663
10	BRAMY20011140	221	2661.. 3011	2664
	BRAMY20025840	222	1058.. 2002	2665
	BRAMY20039260	223	101.. 424	2666
	BRAMY20045240	224	662.. 1792	2667
15	BRAMY20054880	225	508.. 981	2668
	BRAMY20060920	226	110.. 439	2669
	BRAMY20063970	227	246.. 551	2670
	BRAMY20071850	228	178.. 705	2671
	BRAMY20102080	229	513..1136	2672
20	BRAMY20103570	230	114..1001	2673
	BRAMY20104640	231	334..1410	2674
	BRAMY20110640	232	1400..1735	2675
	BRAMY20111960	233	534..854	2676
25	BRAMY20112800	234	31..606	2677
	BRAMY20116790	235	2348.. 2794	2678
	BRAMY20120910	236	182.. 976	2679
	BRAMY20121190	237	81.. 398	2680
	BRAMY20121620	238	51.. 1688	2681
30	BRAMY20124260	239	95.. 1759	2682
	BRAMY20134140	240	1.. 510	2683
	BRAMY20135900	241	4.. 1053	2684
	BRAMY20136210	242	1810.. 2145	2685
35	BRAMY20137560	243	2220.. 2795	2686
	BRAMY20144620	244	892..1326	2687
	BRAMY20147540	245	147..611	2688
	BRAMY20148130	246	204..2138	2689
	BRAMY20152110	247	1257..1580	2690
40	BRAMY20153110	248	11..763	2691
	BRAMY20157820	249	94..1740	2692
	BRAMY20160700	250	1686..2015	2693
	BRAMY20162510	251	186..1757	2694
45	BRAMY20163250	252	96..719	2695
	BRAMY20163270	253	531..1010	2696
	BRAMY20167060	254	347..865	2697
	BRAMY20167710	255	900.. 1532	2698
	BRAMY20168920	256	91.. 1275	2699
50	BRAMY20170140	257	115.. 681	2700
	BRAMY20174550	258	74.. 2179	2701
	BRAMY20178640	259	226.. 2025	2702
	BRAMY20181220	260	678.. 980	2703
	BRAMY20182730	261	208.. 738	2704
55	BRAMY20183080	262	213.. 653	2705
	BRAMY20184670	263	871.. 1548	2706
	BRAMY20195090	264	2087.. 2476	2707

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRAMY20196000	265	50..439	2708
BRAMY20204450	266	34..462	2709
BRAMY20205740	267	177..554	2710
BRAMY20210400	268	131..703	2711
BRAMY20211390	269	1407..2303	2712
BRAMY20211420	270	131..2407	2713
BRAMY20213100	271	245..2026	2714
BRAMY20215230	272	207..515	2715
BRAMY20217460	273	612..1217	2716
BRAMY20218250	274	161..2167	2717
BRAMY20218670	275	338..652	2718
BRAMY20229800	276	1270..1662	2719
BRAMY20229840	277	1022..1678	2720
BRAMY20230600	278	614..1840	2721
BRAMY20231720	279	429..773	2722
BRAMY20240040	280	693..2660	2723
BRAMY20242470	281	1527..2243	2724
BRAMY20245300	282	59..2482	2725
BRAMY20247110	283	321..1382	2726
BRAMY20247280	284	611..925	2727
BRAMY20248490	285	1723..2079	2728
BRAMY20250240	286	1179..1619	2729
BRAMY20250320	287	18..323	2730
BRAMY20252180	288	1150..1506	2731
BRAMY20252720	289	595..1113	2732
BRAMY20260910	290	67..2646	2733
BRAMY20261680	291	298..1041	2734
BRAMY20266850	292	26..685	2735
BRAMY20267130	293	235..708	2736
BRAMY20268990	294	137..460	2737
BRAMY20270730	295	124..2118	2738
BRAMY20271400	296	177..3011	2739
BRAMY20273960	297	48..1826	2740
BRAMY20277140	298	1135..1485	2741
BRAMY20277170	299	545..2221	2742
BRAMY20280720	300	103..489	2743
BRAMY20284910	301	1059..1415	2744
BRAMY20285160	302	1483..1977	2745
BRAMY20285930	303	811..1143	2746
BRAMY20286820	304	1463..1777	2747
BRAWH10000930	305	843..1454	2748
BRAWH20002320	306	162..716	2749
BRAWH20004600	307	66..1361	2750
BRAWH20011710	308	229..1872	2751
BRAWH20012390	309	71..562	2752
BRAWH20012410	310	291..593	2753
BRAWH20014920	311	353..1378	2754
BRAWH20015350	312	1285..1641	2755
BRAWH20015890	313	806..1837	2756

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAWH20016620	314	1721..2254	2757
	BRAWH20016660	315	51..1205	2758
	BRAWH20016860	316	548..877	2759
	BRAWH20017010	317	155..628	2760
	BRAWH20018730	318	56..1570	2761
10	BRAWH20028110	319	123..1718	2762
	BRAWH20029630	320	929..1276	2763
	BRAWH20030250	321	264..1421	2764
	BRAWH20064050	322	272..1591	2765
15	BRAWH20075700	323	349..1407	2766
	BRAWH20096780	324	272..1840	2767
	BRAWH20100690	325	1430..1849	2768
	BRAWH20101360	326	163..852	2769
	BRAWH20103180	327	1081..1659	2770
20	BRAWH20103290	328	71..2626	2771
	BRAWH20105840	329	139..1083	2772
	BRAWH20106180	330	628..933	2773
	BRAWH20107540	331	1..540	2774
25	BRAWH20110660	332	156..578	2775
	BRAWH20110790	333	1994..2338	2776
	BRAWH20110960	334	74..1210	2777
	BRAWH20111550	335	569..949	2778
	BRAWH20112940	336	850..1968	2779
30	BRAWH20113430	337	135..869	2780
	BRAWH20114000	338	72..1619	2781
	BRAWH20117950	339	465..1568	2782
	BRAWH20118230	340	146..565	2783
35	BRAWH20121640	341	98..1516	2784
	BRAWH20122580	342	104..721	2785
	BRAWH20122770	343	1283..1612	2786
	BRAWH20125380	344	382..918	2787
	BRAWH20126190	345	154..459	2788
40	BRAWH20126980	346	222..686	2789
	BRAWH20128270	347	295..1020	2790
	BRAWH20132190	348	157..561	2791
	BRAWH20137480	349	273..1313	2792
45	BRAWH20138660	350	261..1376	2793
	BRAWH20139410	351	13..354	2794
	BRAWH20142340	352	99..413	2795
	BRAWH20147290	353	460..810	2796
	BRAWH20149340	354	442..1620	2797
50	BRAWH20155950	355	8..2074	2798
	BRAWH20158530	356	138..1136	2799
	BRAWH2016028	357	2093..2587	2800
	BRAWH20162690	358	33..1085	2801
55	BRAWH20164460	359	345..>2067	2802
	BRAWH20166790	360	224..571	2803
	BRAWH20171030	361	152..1996	2804
	BRAWH20173050	362	1272..1604	2805

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 BRAWH20182060	363	118..1740	2806
BRAWH20185060	364	248..607	2807
BRCAN10001490	365	60..452	2808
BRCAN20003460	366	239..1030	2809
BRCAN20006200	367	908..1234	2810
10 BRCAN20006390	368	252..743	2811
BRCAN20054490	369	345..1067	2812
BRCAN20060190	370	206..595	2813
BRCAN20064010	371	134..685	2814
15 BRCAN20071190	372	192..1586	2815
BRCAN20091560	373	190..2004	2816
BRCAN20103740	374	207..530	2817
BRCAN20124080	375	187..2079	2818
BRCAN20126130	376	580..897	2819
20 BRCAN20143700	377	14..817	2820
BRCAN20147880	378	121..519	2821
BRCAN20216690	379	66..383	2822
BRCAN20224720	380	549..1544	2823
25 BRCAN20237240	381	23..796	2824
BRCAN20263400	382	316..729	2825
BRCAN20273100	383	76..468	2826
BRCAN20273340	384	50..352	2827
BRCAN20273550	385	652..1848	2828
30 BRCAN20273640	386	131..1201	2829
BRCAN20275130	387	374..847	2830
BRCAN20279700	388	2372..2839	2831
BRCAN20280210	389	644..1393	2832
35 BRCAN20280360	390	265..1548	2833
BRCAN20280400	391	1280..1618	2834
BRCAN20283190	392	416..1321	2835
BRCAN20283380	393	93..533	2836
BRCAN20284600	394	97..549	2837
40 BRCAN20285450	395	118..567	2838
BRIOC10000870	396	186..602	2839
BRIOC20001860	397	1061..2179	2840
BRIOC20004040	398	383..1171	2841
BRIOC20004870	399	199..765	2842
45 BRIOC20006370	400	21..455	2843
BRIOC20008160	401	166.. >2490	2844
BRIOC20008500	402	151.. >2854	2845
BRIOC20020850	403	1371.. 1820	2846
50 BRIOC20021550	404	1121.. 2110	2847
BRIOC20023230	405	682.. 1500	2848
BRIOC20026640	406	148.. 516	2849
BRIOC20027510	407	369.. 1088	2850
BRIOC20031000	408	207.. 581	2851
55 BRIOC20031250	409	799..1122	2852
BRIOC20031870	410	375..1031	2853
BRIOC20035130	411	171..527	2854

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRCOC20037320	412	547..3384	2855
	BRCOC20037400	413	152..493	2856
	BRCOC20041750	414	230..535	2857
	BRCOC20055420	415	99..1556	2858
	BRCOC20059510	416	199..582	2859
10	BRCOC20074760	417	10..1918	2860
	BRCOC20077690	418	867..1202	2861
	BRCOC20078640	419	849..1208	2862
	BRCOC20090520	420	1157..1663	2863
15	BRCOC20091960	421	1371..1895	2864
	BRCOC20093800	422	204..590	2865
	BRCOC20099370	423	1..1890	2866
	BRCOC20101230	424	94..810	2867
	BRCOC20105100	425	2393..2716	2868
20	BRCOC20107300	426	709..1086	2869
	BRCOC20110100	427	369..713	2870
	BRCOC20114180	428	167..487	2871
	BRCOC20117690	429	152..781	2872
25	BRCOC20119960	430	147..500	2873
	BRCOC20121720	431	26..2983	2874
	BRCOC20122290	432	92..448	2875
	BRCOC20128130	433	150..1364	2876
	BRCOC20134480	434	587..1060	2877
30	BRCOC20135730	435	1603..2064	2878
	BRCOC20136750	436	2876..3229	2879
	BRCOC20144000	437	64..459	2880
	BRCOC20147480	438	228..578	2881
35	BRCOC20148330	439	169..1290	2882
	BRCOC20155970	440	111..632	2883
	BRCOC20158240	441	1357..2178	2884
	BRCOC20176520	442	185..1153	2885
	BRCOC20178270	443	244..1257	2886
40	BRCOC20178560	444	65..1000	2887
	BRHIP10001290	445	838..1731	2888
	BRHIP10001740	446	148..594	2889
	BRHIP20000870	447	1235..1540	2890
45	BRHIP20001630	448	287..1486	2891
	BRHIP20003120	449	170..1951	2892
	BRHIP20005340	450	597..1853	2893
	BRHIP20005530	451	30..1052	2894
	BRHIP20096170	452	119..817	2895
50	BRHIP20096850	453	311..1582	2896
	BRHIP20103090	454	1345..1737	2897
	BRHIP20104440	455	166..576	2898
	BRHIP20105710	456	1056..1466	2899
55	BRHIP20106100	457	314..1060	2900
	BRHIP20107440	458	827..1528	2901
	BRHIP20110800	459	577..1083	2902
	BRHIP20111200	460	261..578	2903

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRHIP20115080	461	762..1751	2904
	BRHIP20115760	462	877..1182	2905
	BRHIP20118380	463	2..316	2906
	BRHIP20118910	464	82..426	2907
	BRHIP20119330	465	420..2564	2908
10	BRHIP20121410	466	68..505	2909
	BRHIP20123140	467	73..432	2910
	BRHIP20129720	468	934..1809	2911
	BRHIP20132860	469	1..897	2912
15	BRHIP20135100	470	423..743	2913
	BRHIP20137230	471	71..1180	2914
	BRHIP20139720	472	33..3254	2915
	BRHIP20140630	473	3521..3922	2916
	BRHIP20142850	474	259..612	2917
20	BRHIP20143730	475	229..1638	2918
	BRHIP20143860	476	1159..1638	2919
	BRHIP20149540	477	155..544	2920
	BRHIP20153560	478	1134..1445	2921
25	BRHIP20153600	479	40..675	2922
	BRHIP20167880	480	183..656	2923
	BRHIP20169680	481	27..347	2924
	BRHIP20169900	482	68..502	2925
	BRHIP20170100	483	166..936	2926
30	BRHIP20173150	484	494..820	2927
	BRHIP20174040	485	71..2923	2928
	BRHIP20175420	486	3..872	2929
	BRHIP20176420	487	914..1756	2930
35	BRHIP20179200	488	2532..2870	2931
	BRHIP20180140	489	1028..1345	2932
	BRHIP20183690	490	148..1620	2933
	BRHIP20186120	491	322..723	2934
	BRHIP20186500	492	3089..3727	2935
40	BRHIP20189980	493	247..1002	2936
	BRHIP20190070	494	65..433	2937
	BRHIP20191490	495	1929..2270	2938
	BRHIP20191770	496	191..502	2939
45	BRHIP20191860	497	282..2084	2940
	BRHIP20194940	498	119..1312	2941
	BRHIP20195890	499	1002..1376	2942
	BRHIP20196410	500	2371..2706	2943
	BRHIP20198190	501	2979..3407	2944
50	BRHIP20205090	502	270..593	2945
	BRHIP20207430	503	370..687	2946
	BRHIP20207990	504	90..1628	2947
	BRHIP20208270	505	967..1353	2948
	BRHIP20208420	506	103..462	2949
55	BRHIP20208590	507	212..607	2950
	BRHIP20214950	508	1637..2020	2951
	BRHIP20217620	509	2731..3087	2952

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRHIP20218580	510	1930..2589	2953
BRHIP20222280	511	269..1768	2954
BRHIP20227080	512	1613..2011	2955
BRHIP20230710	513	198..554	2956
BRHIP20232290	514	110..502	2957
BRHIP20233090	515	1782..2105	2958
BRHIP20234380	516	15..1079	2959
BRHIP20236950	517	29..>2580	2960
BRHIP20238600	518	154..729	2961
BRHIP20238690	519	51..383	2962
BRHIP20238880	520	13..2625	2963
BRHIP20240460	521	2151..2540	2964
BRHIP20243470	522	2929..3579	2965
BRHIP20249110	523	134..2887	2966
BRHIP20252450	524	123..>3738	2967
BRHIP20253660	525	255..1031	2968
BRHIP20254480	526	362..994	2969
BRHIP20277620	527	124..1074	2970
BRHIP20283030	528	219..4088	2971
BRHIP20284800	529	217..606	2972
BRHIP20285830	530	611..1321	2973
BRHIP20285930	531	105..779	2974
BRHIP30001110	532	1740..2294	2975
BRHIP30004570	533	189..1034	2976
BRHIP30004880	534	191..2902	2977
BRSSN10000920	535	1850..2215	2978
BRSSN20003120	536	359..>2933	2979
BRSSN20006340	537	937..1401	2980
BRSSN20013420	538	111..2741	2981
BRSSN20014260	539	167..1069	2982
BRSSN20015030	540	105..458	2983
BRSSN20015790	541	542..1639	2984
BRSSN20018690	542	110..463	2985
BRSSN20021600	543	13..1497	2986
BRSSN20028570	544	424..726	2987
BRSSN20038200	545	86..1555	2988
BRSSN20038410	546	187..852	2989
BRSSN20039370	547	900..1628	2990
BRSSN20043040	548	1959..2342	2991
BRSSN20046570	549	18..368	2992
BRSSN20046790	550	253..1014	2993
BRSSN20046860	551	406..1461	2994
BRSSN20066110	552	725..1165	2995
BRSSN20097020	553	1352..2092	2996
BRSSN20101100	554	1851..2330	2997
BRSSN20105870	555	8..3064	2998
BRSSN20105960	556	183..497	2999
BRSSN20108300	557	92..415	3000
BRSSN20117990	558	733..1428	3001

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
BRSSN20120810	559	770..1687	3002
BRSSN20121030	560	18..890	3003
BRSSN20137020	561	1097..1429	3004
BRSSN20142940	562	1411..1803	3005
BRSSN20146100	563	181..2376	3006
BRSSN20151990	564	15..401	3007
BRSSN20152380	565	17..418	3008
BRSSN20159070	566	393..728	3009
BRSSN20159820	567	867..1661	3010
BRSSN20169050	568	118..636	3011
BRSSN20176820	569	13..1917	3012
BRSSN20177570	570	303..2651	3013
BRSSN20187310	571	163..1332	3014
BRSTN10000830	572	216..959	3015
BRSTN20000580	573	617..1672	3016
BRSTN20002200	574	159..515	3017
BRSTN20005360	575	43..1173	3018
BRTHA20000570	576	641..988	3019
BRTHA20004740	577	192..1082	3020
BRTHA20046290	578	1657..2298	3021
BRTHA20046390	579	191..571	3022
BRTHA20046420	580	446..835	3023
CD34C30001250	581	59..>3188	3024
CD34C30003140	582	458..2803	3025
CD34C30004240	583	430..1290	3026
CD34C30004940	584	970..1299	3027
COLON10001350	585	18..1544	3028
COLON20043180	586	451..867	3029
COLON20093370	587	1261..1779	3030
CTONG10000100	588	90..1118	3031
CTONG10000220	589	191..847	3032
CTONG10000620	590	94..2943	3033
CTONG10000930	591	18..2621	3034
CTONG10000940	592	182..868	3035
CTONG10001650	593	1916..2512	3036
CTONG10002770	594	182..>3049	3037
CTONG20002180	595	90..554	3038
CTONG20004690	596	301..885	3039
CTONG20009770	597	321..3287	3040
CTONG20014280	598	176..1723	3041
CTONG20027090	599	280..2370	3042
CTONG20028410	600	600..2936	3043
CTONG20038890	601	961..1371	3044
CTONG20049410	602	157..669	3045
CTONG20050280	603	157..1944	3046
CTONG20052650	604	1210..1647	3047
CTONG20052900	605	130..1548	3048
CTONG20075860	606	63..1391	3049
CTONG20076130	607	11..994	3050

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	CTONG20077790	608	270.. 635	3051
	CTONG20082690	609	75.. 896	3052
	CTONG20085950	610	905.. 2125	3053
	CTONG20091080	611	166.. 717	3054
	CTONG20091320	612	1223.. 1627	3055
10	CTONG20092570	613	690.. 1601	3056
	CTONG20092580	614	1555.. 1920	3057
	CTONG20092680	615	365.. 823	3058
	CTONG20092700	616	224.. 928	3059
15	CTONG20093950	617	205.. 2388	3060
	CTONG20095270	618	1147.. 1611	3061
	CTONG20095290	619	312.. 749	3062
	CTONG20095340	620	109.. 2631	3063
	CTONG20096430	621	311.. 1384	3064
20	CTONG20096750	622	738.. 1184	3065
	CTONG20097660	623	133.. 876	3066
	CTONG20098440	624	206.. 1132	3067
	CTONG20099380	625	1417.. 1806	3068
25	CTONG20099550	626	74.. 1939	3069
	CTONG20099630	627	99.. 2060	3070
	CTONG20100240	628	620.. 2155	3071
	CTONG20101480	629	13.. 411	3072
	CTONG20103480	630	30.. 356	3073
30	CTONG20105080	631	28.. 1260	3074
	CTONG20105660	632	75.. 674	3075
	CTONG20106230	633	2015.. >3067	3076
	CTONG20106520	634	1693.. 3147	3077
35	CTONG20108210	635	234.. 1319	3078
	CTONG20114290	636	388.. 3225	3079
	CTONG20114740	637	1191.. 1832	3080
	CTONG20118150	638	144.. 2831	3081
	CTONG20118250	639	52.. 840	3082
40	CTONG20119200	640	2128.. 2637	3083
	CTONG20120770	641	2946.. 3341	3084
	CTONG20121010	642	143.. 1732	3085
	CTONG20121580	643	97.. >2930	3086
45	CTONG20124010	644	206.. 1369	3087
	CTONG20124220	645	177.. 2477	3088
	CTONG20124470	646	701.. 1237	3089
	CTONG20124730	647	894.. 1280	3090
	CTONG20125540	648	616.. 1071	3091
50	CTONG20125640	649	756.. 1688	3092
	CTONG20126070	650	42.. 2843	3093
	CTONG20127450	651	2271.. 2642	3094
	CTONG20128430	652	330.. 2180	3095
55	CTONG20128470	653	916.. 1479	3096
	CTONG20129960	654	118.. 3249	3097
	CTONG20131490	655	1191.. 1553	3098
	CTONG20131560	656	242.. >2879	3099

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
CTONG2013220	657	1155..1598	3100
CTONG20133390	658	679..2304	3101
CTONG20133480	659	86..391	3102
CTONG20133520	660	128..2140	3103
CTONG20136300	661	1078..1521	3104
CTONG20138030	662	3061..3396	3105
CTONG20139070	663	2508..2819	3106
CTONG20139340	664	1182..1535	3107
CTONG20139860	665	28..2169	3108
CTONG20140320	666	2454..2786	3109
CTONG20140580	667	74..1180	3110
CTONG20141650	668	190..570	3111
CTONG20143690	669	169..2583	3112
CTONG20146300	670	1195..1674	3113
CTONG20146970	671	1201..1536	3114
CTONG20147050	672	1304..1648	3115
CTONG20149460	673	149..1942	3116
CTONG20149950	674	42..371	3117
CTONG20150910	675	792..1130	3118
CTONG20153300	676	755..2338	3119
CTONG20153580	677	488..1858	3120
CTONG20155180	678	486..>3005	3121
CTONG20155400	679	1940..2458	3122
CTONG20156780	680	33..3104	3123
CTONG20158040	681	152..1297	3124
CTONG20158150	682	66..2057	3125
CTONG20158660	683	171..2258	3126
CTONG20159530	684	231..1094	3127
CTONG20160560	685	79..>2796	3128
CTONG20161850	686	27..734	3129
CTONG20162170	687	156..734	3130
CTONG20163550	688	772..1134	3131
CTONG20164990	689	1343..1753	3132
CTONG20165050	690	1575..2018	3133
CTONG20186320	691	78..1595	3134
CTONG20200310	692	2..2254	3135
CTONG20265130	693	419..892	3136
CTONG20267700	694	2046..2432	3137
CTONG20273610	695	513..923	3138
D3OST10001090	696	50..1462	3139
D3OST10002670	697	77..853	3140
D3OST10002700	698	84..461	3141
D3OST20006180	699	148..2259	3142
D3OST20006540	700	140..442	3143
D3OST20007340	701	369..1220	3144
D3OST20013280	702	756..1118	3145
D3OST20024170	703	1373..1714	3146
D3OST20024360	704	1984..2361	3147
D3OST20024520	705	3..422	3148

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 D3OST20036070	706	122..1039	3149
D3OST20037970	707	256..735	3150
D3OST20038560	708	1976..2350	3151
D3OST30002580	709	1509..2957	3152
D3OST30002910	710	1811..2248	3153
10 D6OST20003580	711	1760..2167	3154
D6OST20004450	712	1513..2547	3155
D6OST20005070	713	2835..3398	3156
D9OST20000310	714	239..637	3157
15 D9OST20002780	715	644..1360	3158
D9OST20015470	716	187..1386	3159
D9OST20023970	717	872..1327	3160
D9OST20026730	718	145..3159	3161
D9OST20031370	719	616..1251	3162
20 D9OST20033970	720	24..1811	3163
D9OST20035800	721	524..1057	3164
D9OST20035940	722	217..867	3165
D9OST20040180	723	189..1127	3166
25 DFNES10000030	724	897..1322	3167
DFNES10001850	725	471..899	3168
DFNES20001530	726	26..382	3169
DFNES20010910	727	159..1136	3170
DFNES20014040	728	148..1272	3171
30 DFNES20025880	729	1080..1415	3172
DFNES20031920	730	631..1104	3173
DFNES20037420	731	186..2090	3174
DFNES20055270	732	159..818	3175
35 DFNES20071130	733	248..1156	3176
DFNES20082800	734	258..698	3177
FCBBF10000240	735	507..2942	3178
FCBBF10000380	736	1024..1344	3179
FCBBF10000630	737	533..1654	3180
40 FCBBF10000770	738	56..1810	3181
FCBBF10001150	739	351..2555	3182
FCBBF10001210	740	38..1066	3183
FCBBF10001550	741	60..653	3184
45 FCBBF10001710	742	322..2133	3185
FCBBF10001820	743	10..1032	3186
FCBBF10002430	744	349..1158	3187
FCBBF10002700	745	189..551	3188
FCBBF10002800	746	485..2818	3189
50 FCBBF10003220	747	479..832	3190
FCBBF10003670	748	139..1266	3191
FCBBF10003740	749	407..2365	3192
FCBBF10003760	750	1044..1358	3193
FCBBF10003770	751	242..>3001	3194
55 FCBBF10004120	752	142..816	3195
FCBBF10004370	753	432..1511	3196
FCBBF10005060	754	1340..2323	3197

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF10005460	755	179..2092	3198
	FCBBF10005500	756	1518..2123	3199
	FCBBF10005740	757	954..1667	3200
	FCBBF20006760	758	356..679	3201
	FCBBF20014270	759	49..315	3202
10	FCBBF20023700	760	251..589	3203
	FCBBF20032970	761	845..1186	3204
	FCBBF20035280	762	13..393	3205
	FCBBF20042170	763	186..1337	3206
15	FCBBF20042560	764	115..576	3207
	FCBBF20049300	765	32..631	3208
	FCBBF20051220	766	523..948	3209
	FCBBF20054260	767	119..535	3210
	FCBBF20056370	768	57..704	3211
20	FCBBF20059090	769	928..1245	3212
	FCBBF20064520	770	368..1243	3213
	FCBBF20067810	771	68..1231	3214
	FCBBF20068820	772	74..712	3215
25	FCBBF20071860	773	384..911	3216
	FCBBF20072650	774	1471..1944	3217
	FCBBF20075560	775	730..1086	3218
	FCBBF20076330	776	684..998	3219
	FCBBF30001840	777	1503..1832	3220
30	FCBBF30007660	778	9..2117	3221
	FCBBF30008470	779	1157..1504	3222
	FCBBF30010810	780	149..1483	3223
	FCBBF30012350	781	419..1507	3224
35	FCBBF30012810	782	372..>2409	3225
	FCBBF30013770	783	375..2795	3226
	FCBBF30015940	784	24..>2507	3227
	FCBBF30016320	785	990..1877	3228
	FCBBF30016570	786	574..999	3229
40	FCBBF30018550	787	231..>3402	3230
	FCBBF30019120	788	54..398	3231
	FCBBF30024750	789	126..560	3232
	FCBBF30025560	790	171..1301	3233
45	FCBBF30028160	791	258..830	3234
	FCBBF30033050	792	7..1089	3235
	FCBBF30039020	793	955..2727	3236
	FCBBF30049550	794	222..>4213	3237
	FCBBF30052160	795	2829..4214	3238
50	FCBBF30054440	796	33..2822	3239
	FCBBF30057290	797	143..2068	3240
	FCBBF30062860	798	1135..>3256	3241
	FCBBF30070770	799	1049..2113	3242
55	FCBBF30071520	800	280..735	3243
	FCBBF30078240	801	280..1875	3244
	FCBBF30083620	802	125..1159	3245
	FCBBF30083820	803	298..774	3246

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF30086440	804	192..863	3247
	FCBBF30090690	805	545..1657	3248
	FCBBF30095260	806	204..686	3249
	FCBBF30123470	807	1084..1614	3250
	FCBBF30129630	808	257..973	3251
10	FCBBF30170590	809	1313..1672	3252
	FCBBF30172550	810	1350..1703	3253
	FCBBF30175310	811	120..1280	3254
	FCBBF30178730	812	348..833	3255
15	FCBBF30189490	813	1935..2468	3256
	FCBBF30190850	814	43..1560	3257
	FCBBF30195640	815	577..>2751	3258
	FCBBF30199610	816	972..1391	3259
	FCBBF30215060	817	42..446	3260
20	FCBBF30225660	818	231..2750	3261
	FCBBF30233680	819	28..>4395	3262
	FCBBF30238870	820	587..2761	3263
	FCBBF30240020	821	248..1747	3264
25	FCBBF30240960	822	465..1520	3265
	FCBBF30242250	823	271..>2723	3266
	FCBBF30243640	824	339..665	3267
	FCBBF30246230	825	1893..2357	3268
	FCBBF30246630	826	19..2070	3269
30	FCBBF30247930	827	558..1187	3270
	FCBBF30250730	828	116..>2647	3271
	FCBBF30251420	829	2590..2904	3272
	FCBBF30252520	830	27..380	3273
35	FCBBF30252800	831	139..1110	3274
	FCBBF30252850	832	45..1022	3275
	FCBBF30262360	833	51..446	3276
	FCBBF30262510	834	36..2327	3277
	FCBBF30266780	835	2080..2382	3278
40	FCBBF30266920	836	5..316	3279
	FCBBF30278630	837	492..821	3280
	FCBBF30279030	838	1653..2447	3281
	FCBBF30281880	839	83..2221	3282
45	FCBBF30284720	840	230..751	3283
	FCBBF30285280	841	185..3043	3284
	FCBBF40001420	842	364..681	3285
	FCBBF40001730	843	105..932	3286
	FCBBF40005480	844	119..589	3287
50	FEBRA10001880	845	494..2236	3288
	FEBRA10001900	846	6..389	3289
	FEBRA20002100	847	375..1064	3290
	FEBRA20003210	848	10..414	3291
55	FEBRA20004620	849	297..1568	3292
	FEBRA20007620	850	61..2400	3293
	FEBRA20009090	851	667..1032	3294
	FEBRA20010120	852	608..1216	3295

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 FEBRA20017050	853	1775..2197	3296
FEBRA20018280	854	16..678	3297
FEBRA20018690	855	664..981	3298
FEBRA20024100	856	68..2659	3299
FEBRA20025270	857	116..>2317	3300
10 FEBRA20025520	858	669..1133	3301
FEBRA20026110	859	233..2692	3302
FEBRA20026280	860	54..623	3303
FEBRA20027810	861	155..2740	3304
15 FEBRA20029860	862	29..757	3305
FEBRA20034360	863	1288..2013	3306
FEBRA20034680	864	240..1955	3307
FEBRA20037260	865	2376..2702	3308
FEBRA20037500	866	10..1308	3309
20 FEBRA20040530	867	76..1407	3310
FEBRA20042190	868	1590..1925	3311
FEBRA20052910	869	1136..1486	3312
FEBRA20060610	870	599..1201	3313
25 FEBRA20072120	871	106..2877	3314
FEBRA20079310	872	2384..2806	3315
FEBRA20080810	873	679..1401	3316
FEBRA20082010	874	106..1779	3317
FEBRA20082100	875	1042..1524	3318
30 FEBRA20086620	876	215..1591	3319
FEBRA20088360	877	2964..3521	3320
FEBRA20090290	878	383..823	3321
FEBRA20092890	879	198..2297	3322
35 FEBRA20093520	880	651..1070	3323
FEBRA20095140	881	264..>2245	3324
FEBRA20095880	882	1872..2186	3325
FEBRA20097310	883	74..2101	3326
FEBRA20098460	884	291..686	3327
40 FEBRA20111460	885	859..1221	3328
FEBRA20113560	886	22..558	3329
FEBRA20125070	887	10..1002	3330
FEBRA20130190	888	131..1192	3331
45 FEBRA20132740	889	770..1111	3332
FEBRA20140100	890	1664..2377	3333
FEBRA20144170	891	342..1976	3334
FEBRA20145780	892	1262..1564	3335
FEBRA20161120	893	173..484	3336
50 FEBRA20166540	894	101..511	3337
FEBRA20167390	895	429..869	3338
FEBRA20171380	896	338..2002	3339
FEBRA20174410	897	125..2029	3340
55 FEBRA20176800	898	1320..1877	3341
FEBRA20184330	899	36..533	3342
FEBRA20192420	900	2120..3799	3343
FEBRA20195820	901	175..678	3344

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FEBRA2C195370	902	353.. 2032	3345
	FEBRA2C195630	903	482.. 2359	3346
	FEBRA2C197110	904	632.. 1222	3347
	FEBRA2C204000	905	1958.. 2482	3348
	FEBRA2C204060	906	366.. 728	3349
10	FEBRA2C211710	907	282.. 929	3350
	FEBRA2C214970	908	620.. 1264	3351
	FFBRA2C215500	909	726.. 1256	3352
	FEBRA2C216360	910	1398.. 1904	3353
15	FEBRA2C222040	911	954.. 1391	3354
	FEBRA2C223220	912	1254.. 1898	3355
	FEBRA2C225040	913	13.. 1692	3356
	FEBRA2C225010	914	1439.. 1933	3357
	FEBRA2C229560	915	37.. 381	3358
20	FEBRA2C229630	916	184.. 987	3359
	FEBRA2C232850	917	774.. 1193	3360
	FEBRA2C233770	918	64.. 636	3361
	FEBRA2C235500	919	1206.. >2520	3362
25	FEBRA2C237640	920	331.. 933	3363
	FEHRT2C003250	921	173.. 1243	3364
	FELNG2C002410	922	1257.. 1577	3365
	HCASM10000500	923	300.. 1754	3366
	HCHON10001760	924	238.. 1182	3367
30	HCHON20000380	925	210.. 644	3368
	HCHON20001560	926	565.. 1611	3369
	HCHON20002260	927	694.. 1389	3370
	HCHON20003220	928	23.. >2278	3371
35	HCHON20003440	929	1982.. >2519	3372
	HCHON20007380	930	163.. 1248	3373
	HCHON20007510	931	189.. 2636	3374
	HCHON20008150	932	204.. >2358	3375
	HCHON20008180	933	671.. 1087	3376
40	HCHON20008320	934	1240.. >2284	3377
	HCHON20008980	935	578.. 904	3378
	HCHON20009350	936	63.. 422	3379
	HCHON20009560	937	1644.. 2489	3380
45	HCHON20010990	938	531.. 1085	3381
	HCHON20011160	939	839.. 1156	3382
	HCHON20014970	940	302.. 2143	3383
	HCHON20015230	941	950.. 1453	3384
	HCHON20015350	942	647.. >2887	3385
50	HCHON20015980	943	100.. 1413	3386
	HCHON20016040	944	3.. 323	3387
	HCHON20016650	945	44.. 3418	3388
	HCHON20022470	946	1526.. 1978	3389
55	HCHON20035130	947	1192.. 1614	3390
	HCHON20036420	948	356.. 811	3391
	HCHON20036760	949	228.. 647	3392
	HCHON20040020	950	257.. 1288	3393

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 HCHON20043590	951	263..712	3394
HCHON20059870	952	198..2297	3395
HCHON20064590	953	66..2063	3396
HCHON20067220	954	313..642	3397
HCHON20067700	955	160..591	3398
10 HCHON20068410	956	116..>2811	3399
HCHON20068710	957	335..688	3400
HCHON20074820	958	19..735	3401
HCHON20076500	959	1778..2473	3402
15 HCHON20086720	960	133..864	3403
HCHON20097490	961	1434..2819	3404
HCHON20100740	962	138..1277	3405
HEART20003060	963	109..1407	3406
HEART20005410	964	302..784	3407
20 HEART20017730	965	19..2064	3408
HEART20021840	966	22..507	3409
HEART20025980	967	293..1180	3410
HEART20034320	968	31..2013	3411
25 HEART20037810	969	803..1108	3412
HEART20043400	970	178..549	3413
HEART20043410	971	44..613	3414
HEART20043800	972	15..509	3415
HEART20061950	973	153..1961	3416
30 HEART20063340	974	220..1281	3417
HEART20067870	975	256..855	3418
HEART20067890	976	3..338	3419
HEART20072310	977	47..1057	3420
35 HEART20074430	978	205..540	3421
HEART20077670	979	90..1223	3422
HEART20083640	980	192..1376	3423
HEART20083440	981	150..1523	3424
HEART20093000	982	197..2116	3425
40 HEART20095990	983	523..1077	3426
HHDPC10000650	984	920..1531	3427
HHDPC10000830	985	110..520	3428
HHDPC20001040	986	2080..2442	3429
45 HHDPC20006920	987	1758..2066	3430
HHDPC20014320	988	5..526	3431
HHDPC20030490	989	71..529	3432
HHDPC20031130	990	369..2249	3433
HHDPC20034390	991	94..705	3434
50 HHDPC20034720	992	167..868	3435
HHDPC20057420	993	44..484	3436
HHDPC20057940	994	1..393	3437
HHDPC20064600	995	231..1493	3438
HHDPC20068620	996	515..1816	3439
55 HHDPC20084140	997	163..2109	3440
HHDPC20091140	998	160..504	3441
HHDPC20091780	999	49..1623	3442

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	HHDPC20092080	1000	133..702	3443
	HHDPC20095280	1001	332..745	3444
	HLUNG10000550	1002	729..1058	3445
	HLUNG20016330	1003	86..>1958	3446
	HLUNG20016770	1004	919..1242	3447
10	HLUNG20017120	1005	644..1144	3448
	HLUNG20023340	1006	228..1181	3449
	HLUNG20033780	1007	156..2285	3450
	HLUNG20084390	1008	542..997	3451
15	IMR3220002430	1009	34..1176	3452
	KIDNE20002520	1010	22..1593	3453
	KIDNE20003940	1011	187..1986	3454
	KIDNE20006780	1012	164..829	3455
	KIDNE20007210	1013	27..350	3456
20	KIDNE20007770	1014	27..1415	3457
	KIDNE20008010	1015	127..>1986	3458
	KIDNE20009470	1016	9..>2664	3459
	KIDNE20011170	1017	347..817	3460
25	KIDNE20011400	1018	1798..2334	3461
	KIDNE20013730	1019	373..777	3462
	KIDNE20017130	1020	226..1740	3463
	KIDNE20018730	1021	35..631	3464
	KIDNE20018970	1022	232..546	3465
30	KIDNE20020150	1023	215..1645	3466
	KIDNE20021680	1024	140..1096	3467
	KIDNE20021910	1025	15..2018	3468
	KIDNE20021980	1026	1578..1910	3469
35	KIDNE20022620	1027	112..2277	3470
	KIDNE20024830	1028	1912..>2715	3471
	KIDNE20027250	1029	359..955	3472
	KIDNE20027950	1030	97..543	3473
	KIDNE20028390	1031	31..519	3474
40	KIDNE20028720	1032	70..1122	3475
	KIDNE20028830	1033	107..1258	3476
	KIDNE20029800	1034	1056..1358	3477
	KIDNE20067330	1035	930..1865	3478
45	KIDNE20079440	1036	192..539	3479
	KIDNE20096280	1037	266..1354	3480
	KIDNE20096470	1038	31..639	3481
	KIDNE20100070	1039	471..2204	3482
	KIDNE20100840	1040	167..778	3483
50	KIDNE20101370	1041	9..503	3484
	KIDNE20101510	1042	62..1795	3485
	KIDNE20102650	1043	322..1614	3486
	KIDNE20102710	1044	791..1501	3487
	KIDNE20104300	1045	188..>1957	3488
55	KIDNE20106740	1046	55..411	3489
	KIDNE20107390	1047	85..399	3490
	KIDNE20107500	1048	180..641	3491

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
KIDNE20107620	1049	222..2213	3492
KIDNE20109730	1050	57..1121	3493
RIDNE20109890	1051	254..>2578	3494
KIDNE20112000	1052	430..750	3495
KIDNE20115080	1053	76..1092	3496
KIDNE20118580	1054	962..1387	3497
KIDNE20120090	1055	1334..1813	3498
KIDNE20121880	1056	192..866	3499
KIDNE20122910	1057	1623..2006	3500
KIDNE20124400	1058	532..2499	3501
KIDNE20125630	1059	67..504	3502
KIDNE20126010	1060	991..1407	3503
KIDNE20126130	1061	285..701	3504
KIDNE20127100	1062	265..1944	3505
KIDNE20127450	1063	570..1088	3506
KIDNE20127750	1064	175..1488	3507
KIDNE20130450	1065	177..512	3508
KIDNE20131580	1066	194..1912	3509
KIDNE20132180	1067	894..1256	3510
KIDNE20137340	1068	889..1710	3511
KIDNE20138010	1069	1564..2046	3512
KIDNE20141190	1070	71..856	3513
KIDNE20144890	1071	385..738	3514
KIDNE20148900	1072	487..981	3515
KIDNE20163880	1073	327..1364	3516
KIDNE20180710	1074	379..855	3517
KIDNE20181660	1075	1109..1564	3518
KIDNE20182690	1076	553..2019	3519
KIDNE20186780	1077	837..1541	3520
KIDNE20190740	1078	321..653	3521
LIVER10001260	1079	1413..1748	3522
LIVER10004790	1080	112..1113	3523
LIVER20002160	1081	79..1944	3524
LIVER20011130	1082	898..1569	3525
LIVER20011910	1083	27..425	3526
LIVER20028420	1084	1305..1724	3527
LIVER20035110	1085	551..940	3528
LIVER20035680	1086	873..1283	3529
LIVER20038540	1087	6..308	3530
LIVER20045650	1088	2359..2886	3531
LIVER20055200	1089	82..618	3532
LIVER20055440	1090	1611..2240	3533
LIVER20059810	1091	1597..1899	3534
LIVER20062510	1092	631..999	3535
LIVER20064100	1093	279..785	3536
LIVER20064690	1094	172..1161	3537
LIVER20075680	1095	2568..2939	3538
LIVER20080530	1096	44..1426	3539
LIVER20084730	1097	240..788	3540

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	LIVER20085800	1098	99..416	3541
	LIVER20087060	1099	140..2056	3542
	LIVER20087510	1100	478..1200	3543
	LIVER20091180	1101	18..374	3544
	MAMGL10000830	1102	40..1551	3545
10	MESAN10001260	1103	80..2137	3546
	MESAN20004570	1104	354..>2589	3547
	MESAN20014500	1105	78..1976	3548
	MESAN20025190	1106	1679..2323	3549
15	MESAN20027090	1107	144..653	3550
	MESAN20029400	1108	210..>2998	3551
	MESAN20031900	1109	138..2348	3552
	MESAN20035290	1110	99..797	3553
	MESAN20036460	1111	1203..1844	3554
20	MESAN20038510	1112	639..1016	3555
	MESAN20089360	1113	386..802	3556
	MESAN20101140	1114	250..504	3557
	MESAN20103120	1115	143..1201	3558
25	MESAN20106640	1116	71..712	3559
	MESAN20115970	1117	234..644	3560
	MESAN20121130	1118	7..942	3561
	MESAN20125860	1119	1396..1875	3562
	MESAN20127350	1120	297..1724	3563
30	MESAN20130220	1121	106..1626	3564
	MESAN20132110	1122	1363..2433	3565
	MESAN20136110	1123	188..1582	3566
	MESAN20138450	1124	249..647	3567
35	MESAN20139360	1125	195..611	3568
	MESAN20141920	1126	250..2724	3569
	MESAN20152770	1127	64..585	3570
	MESAN20153910	1128	141..443	3571
	MESAN20154010	1129	24..620	3572
40	MESAN20157080	1130	1336..1677	3573
	MESAN20161590	1131	767..1081	3574
	MESAN20164090	1132	273..2471	3575
	MESAN20171520	1133	103..774	3576
45	MESAN20174170	1134	1375..1743	3577
	MESAN20182090	1135	5..>2440	3578
	MESAN20186700	1136	1333..>3058	3579
	NESOP10001080	1137	149..1489	3580
	NOVAR10000150	1138	1470..1895	3581
50	NOVAR10000910	1139	247..1482	3582
	NOVAR10001020	1140	136..519	3583
	NOVAR20000380	1141	422..844	3584
	NOVAR20003520	1142	898..1377	3585
55	NT2NE20003740	1143	28..555	3586
	NT2NE20010050	1144	1240..1725	3587
	NT2NE20010210	1145	231..626	3588
	NT2NE20010400	1146	923..1546	3589

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
NT2NE20010490	1147	105..1499	3590
NT2NE20015240	1148	251..646	3591
NT2NE20021620	1149	785..2266	3592
NT2NE20043780	1150	815..1285	3593
NT2NE20053580	1151	9..413	3594
NT2NE20068130	1152	237..1601	3595
NT2NE20072200	1153	94..855	3596
NT2NE20074250	1154	9..377	3597
NT2NE20080170	1155	129..2219	3598
NT2NE20089610	1156	1976..2329	3599
NT2NE20089970	1157	150..488	3600
NT2NE20108540	1158	504..806	3601
NT2NE20110360	1159	44..415	3602
NT2NE20118960	1160	197..2044	3603
NT2NE20122430	1161	1474..2016	3604
NT2NE20124480	1162	135..482	3605
NT2NE20125050	1163	59..1462	3606
NT2NE20130190	1164	728..1438	3607
NT2NE20131890	1165	2276..2611	3608
NT2NE20132170	1166	585..1694	3609
NT2NE20142210	1167	177..2585	3610
NT2NE20146810	1168	387..707	3611
NT2NE20152750	1169	190..726	3612
NT2NE20155110	1170	486..893	3613
NT2NE20156260	1171	286..633	3614
NT2NE20157470	1172	222..1199	3615
NT2NE20158600	1173	348..749	3616
NT2NE20159740	1174	66..664	3617
NT2NE20172590	1175	759..1131	3618
NT2NE20174800	1176	525..860	3619
NT2NE20174920	1177	53..538	3620
NT2NE20177520	1178	636..2108	3621
NT2NE20181650	1179	496..1605	3622
NT2NE20183760	1180	1087..1548	3623
NT2NE20184900	1181	2947..3371	3624
NT2NE20187390	1182	170..580	3625
NT2RI20001330	1183	84..1901	3626
NT2RI20003480	1184	166..1905	3627
NT2RI20005750	1185	66..1088	3628
NT2RI20009870	1186	127..1053	3629
NT2RI20022600	1187	1040..1621	3630
NT2RI20023160	1188	165..947	3631
NT2RI20023590	1189	666..1058	3632
NT2RI20023910	1190	546..2945	3633
NT2RI20025400	1191	315..902	3634
NT2RI20025640	1192	989..1650	3635
NT2RI20028470	1193	140..1297	3636
NT2RI20036670	1194	334..852	3637
NT2RI20040930	1195	362..1075	3638

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RI20040990	1196	124..2169	3639
	NT2RI20041880	1197	79..1368	3640
	NT2RI20046080	1198	36..824	3641
	NT2RI20048840	1199	330..1349	3642
	NT2RI20050960	1200	223..1701	3643
10	NT2RI20054050	1201	172..2154	3644
	NT2RI20055790	1202	489..1178	3645
	NT2RI20056700	1203	115..1491	3646
	NT2RI20069730	1204	607..1209	3647
	NT2RI20076290	1205	145..1197	3648
15	NT2RI20086220	1206	67..1068	3649
	NT2RI20091730	1207	113..2525	3650
	NT2RI20091940	1208	699..1187	3651
	NT2RI20198260	1209	70..372	3652
20	NT2RI20203900	1210	176..487	3653
	NT2RI20207030	1211	33..1181	3654
	NT2RI20216250	1212	812..1312	3655
	NT2RI20240080	1213	176..1090	3656
25	NT2RI20244600	1214	195..1010	3657
	NT2RI20244960	1215	161..595	3658
	NT2RI20250750	1216	263..1186	3659
	NT2RI20252550	1217	927..1622	3660
	NT2RI20273230	1218	40..1215	3661
30	NT2RP60000770	1219	1147..2223	3662
	NT2RP60000850	1220	44..2927	3663
	NT2RP70010740	1221	23..466	3664
	NT2RP70027380	1222	86..3466	3665
35	NT2RP70032610	1223	1048..2514	3666
	NT2RP70036880	1224	105..1491	3667
	NT2RP70037240	1225	221..2002	3668
	NT2RP70043480	1226	134..1912	3669
	NT2RP70044280	1227	91..1506	3670
40	NT2RP70045590	1228	29..877	3671
	NT2RP70056750	1229	177..3578	3672
	NT2RP70062230	1230	310..2748	3673
	NT2RP70063950	1231	499..3750	3674
45	NT2RP70072690	1232	1108..1545	3675
	NT2RP70075240	1233	308..814	3676
	NT2RP70077660	1234	2025..2441	3677
	NT2RP70078420	1235	622..2025	3678
	NT2RP70080850	1236	59..4003	3679
50	NT2RP70081610	1237	41..730	3680
	NT2RP70085440	1238	1856..2317	3681
	NT2RP70102350	1239	225..1043	3682
	NT2RP70105210	1240	132..1880	3683
	NT2RP70110860	1241	803..1129	3684
55	NT2RP70111320	1242	271..627	3685
	NT2RP70122910	1243	789..1112	3686
	NT2RP70125160	1244	10..624	3687

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RP70130020	1245	372..692	3688
	NT2RP70133740	1246	109..972	3689
	NT2RP70134990	1247	24..392	3690
	NT2RP70137290	1248	10..381	3691
	NT2RP70137640	1249	315..>2113	3692
10	NT2RP70143480	1250	482..1177	3693
	NT2RP70147210	1251	258..566	3694
	NT2RP70150800	1252	32..445	3695
	NT2RP70157890	1253	170..1006	3696
15	NT2RP70159960	1254	308..967	3697
	NT2RP70169110	1255	123..485	3698
	NT2RP70175670	1256	89..421	3699
	NT2RP70179710	1257	94..2604	3700
	NT2RP70181970	1258	59..364	3701
20	NT2RP70188020	1259	380..796	3702
	NT2RP70188710	1260	491..1024	3703
	NT2RP70190640	1261	72..1880	3704
	NT2RP70192730	1262	180..1253	3705
25	NT2RP70194450	1263	1074..1901	3706
	NT2RP70195430	1264	201..1256	3707
	NT2RP70198350	1265	131..832	3708
	NT2RP70203790	1266	2156..>2479	3709
	NTONG20009770	1267	124..1947	3710
30	NTONG20013620	1268	1798..2325	3711
	NTONG20015870	1269	65..1627	3712
	NTONG20028070	1270	9..545	3713
	NTONG20029480	1271	318..1898	3714
35	NTONG20029700	1272	242..1693	3715
	NTONG20046140	1273	308..1108	3716
	NTONG20048060	1274	1488..1961	3717
	NTONG20049910	1275	47..679	3718
	NTONG20050620	1276	141..521	3719
40	NTONG20050860	1277	59..877	3720
	NTONG20051530	1278	78..1697	3721
	NTONG20052650	1279	84..>2351	3722
	NTONG20056570	1280	226..1326	3723
45	NTONG20061870	1281	100..996	3724
	NTONG20063010	1282	219..1856	3725
	NTONG20064400	1283	11..1330	3726
	NTONG20064840	1284	1500..2447	3727
	NTONG20065010	1285	156..494	3728
50	NTONG20066460	1286	121..1458	3729
	NTONG20067090	1287	1046..1513	3730
	NTONG20067830	1288	17..1006	3731
	NTONG20070200	1289	318..1418	3732
	NTONG20070340	1290	284..1228	3733
55	NTONG20075220	1291	242..>2591	3734
	NTONG20076930	1292	26..1534	3735
	NTONG20077560	1293	241..567	3736

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NTONG20083650	1294	242..1711	3737
	NTONG20088620	1295	60..>2536	3738
	NTONG20090600	1296	517..1134	3739
	NTONG20090680	1297	673..1389	3740
	NTONG20092290	1298	307..1539	3741
10	NTONG20092330	1299	229..2235	3742
	OCBBF10000540	1300	858..1916	3743
	OCBBF10001750	1301	245..1144	3744
	OCBBF10001850	1302	419..2233	3745
15	OCBBF20005230	1303	56..640	3746
	OCBBF20006770	1304	29..2275	3747
	OCBBF20013890	1305	1978..2289	3748
	OCBBF20019380	1306	69..1364	3749
	OCBBF20019830	1307	325..1536	3750
20	OCBBF20020150	1308	2507..2917	3751
	OCBBF20020830	1309	92..2869	3752
	OCBBF20022900	1310	88..1779	3753
	OCBBF20023570	1311	47..1276	3754
25	OCBBF20026630	1312	18..455	3755
	OCBBF20028050	1313	128..1108	3756
	OCBBF20028650	1314	706..2286	3757
	OCBBF20029800	1315	334..699	3758
	OCBBF20030280	1316	263..898	3759
30	OCBBF20030910	1317	383..1258	3760
	OCBBF20032460	1318	347..805	3761
	OCBBF20035930	1319	65..895	3762
	OCBBF20037440	1320	413..1024	3763
35	OCBBF20039250	1321	24..821	3764
	OCBBF20041680	1322	967..1278	3765
	OCBBF20045330	1323	1407..1886	3766
	OCBBF20046120	1324	82..1641	3767
	OCBBF20046470	1325	400..1137	3768
40	OCBBF20046690	1326	156..1730	3769
	OCBBF20047570	1327	182..577	3770
	OCBBF20048660	1328	292..663	3771
	OCBBF20049300	1329	721..2553	3772
45	OCBBF20049840	1330	246..>2607	3773
	OCBBF20050770	1331	724..>2679	3774
	OCBBF20051610	1332	41..493	3775
	OCBBF20053430	1333	586..2478	3776
	OCBBF20053490	1334	736..1068	3777
50	OCBBF20053730	1335	87..2090	3778
	OCBBP20054200	1336	315..869	3779
	OCBBF20054760	1337	195..1016	3780
	OCBBF20059560	1338	224..>3045	3781
55	OCBBF20060300	1339	1389..2171	3782
	OCBBF20061720	1340	711..1139	3783
	OCBBF20062140	1341	444..749	3784
	OCBBF20062410	1342	1920..2240	3785

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	OC3B ^F 20063320	1343	145..519	3786
	OC3B ^F 20066390	1344	2159..2713	3787
	OC3B ^F 20068490	1345	15..2702	3788
	OC3B ^F 20071210	1346	2029..3486	3789
	OC3B ^F 20071840	1347	45..1670	3790
10	OC3B ^F 20071960	1348	1294..1698	3791
	OC3B ^F 20072240	1349	335..1432	3792
	OC3B ^F 20072320	1350	1749..2087	3793
	OC3B ^F 20073540	1351	56..1132	3794
15	OC3B ^F 20074140	1352	81..>3793	3795
	OC3B ^F 20076220	1353	1552..2013	3796
	OC3B ^F 20078920	1354	849..1340	3797
	OC3B ^F 20079310	1355	240..1349	3798
	OC3B ^F 20079460	1356	12..2099	3799
20	OC3B ^F 20080050	1357	159..2150	3800
	OC3B ^F 20080410	1358	122..1672	3801
	OC3B ^F 20081380	1359	742..1140	3802
	OC3B ^F 20082830	1360	139..1209	3803
25	OC3B ^F 20084660	1361	74..1621	3804
	OC3B ^F 20085200	1362	659..1207	3805
	OC3B ^F 20086400	1363	63..797	3806
	OC3B ^F 20086910	1364	541..2304	3807
	OC3B ^F 20087010	1365	325..633	3808
30	OC3B ^F 20088140	1366	1575..1916	3809
	OC3B ^F 20088220	1367	2505..2915	3810
	OC3B ^F 20091150	1368	256..648	3811
	OC3B ^F 20094240	1369	82..1122	3812
35	OC3B ^F 20097720	1370	471..815	3813
	OC3B ^F 20100400	1371	407..3043	3814
	OC3B ^F 20103130	1372	114..1439	3815
	OC3B ^F 20104040	1373	310..612	3816
	OC3B ^F 20105570	1374	2404..2874	3817
40	OC3B ^F 20107090	1375	127..1935	3818
	OC3B ^F 20107920	1376	1692..2018	3819
	OC3B ^F 20108190	1377	278..1591	3820
	OC3B ^F 20108430	1378	832..1851	3821
45	OC3B ^F 20108580	1379	1152..2354	3822
	OC3B ^F 20108630	1380	249..1133	3823
	OC3B ^F 20109310	1381	34..2355	3824
	OC3B ^F 20111770	1382	291..629	3825
	OC3B ^F 20116850	1383	117..2354	3826
50	OC3B ^F 20118970	1384	361..855	3827
	OC3B ^F 20120390	1385	129..2282	3828
	OC3B ^F 20121390	1386	524..2254	3829
	OC3B ^F 20122620	1387	990..1544	3830
55	OC3B ^F 20124360	1388	1223..1951	3831
	OC3B ^F 20125530	1389	379..2310	3832
	OC3B ^F 20126780	1390	1270..1599	3833
	OC3B ^F 20127040	1391	177..2327	3834

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	OCBBP20127140	1392	1018..1530	3835
	OCBBF20127550	1393	103..>2362	3836
	OCBBF20128120	1394	118..1311	3837
	OCBBF20129360	1395	378..>3283	3838
	OCBBF20130110	1396	132..452	3839
10	OCBBF20130910	1397	2527..2892	3840
	OCBBF20132850	1398	1172..3331	3841
	OCBBF20139260	1399	772..2592	3842
	OCBBF20140640	1400	241..894	3843
15	OCBBF20140890	1401	39..>4369	3844
	OCBBF20145760	1402	894..1757	3845
	OCBBF20148280	1403	87..1787	3846
	OCBBF20148730	1404	50..1855	3847
	OCBBF20149280	1405	1385..2035	3848
20	OCBBF20151150	1406	135..2216	3849
	OCBBF20153340	1407	135..>2621	3850
	OCBBF20153350	1408	1616..1942	3851
	OCBBF20155060	1409	102..3245	3852
25	OCBBF20164050	1410	50..370	3853
	OCBBF20164670	1411	40..1077	3854
	OCBBF20170690	1412	159..503	3855
	OCBBF20173060	1413	63..383	3856
	OCBBF20173250	1414	315..692	3857
30	OCBBF20173980	1415	262..1857	3858
	OCBBF20178150	1416	1245..2231	3859
	OCBBP20178880	1417	2740..3207	3860
	OCBBP20178990	1418	1328..1819	3861
35	OCBBF20180120	1419	218..1780	3862
	OCBBF20180840	1420	1169..1540	3863
	OCBBF20186870	1421	1278..1736	3864
	OCBBF20188730	1422	320..766	3865
	OCBBF20189560	1423	1512..2165	3866
40	PANCR10000910	1424	1219..>1943	3867
	PEBLM10000240	1425	306..674	3868
	PEBLM10000710	1426	1719..1940	3869
	PEBLM20013120	1427	26..952	3870
45	PEBLM20024320	1428	612..1406	3871
	PEBLM20024550	1429	1179..1499	3872
	PEBLM20040150	1430	1731..2165	3873
	PEBLM20042900	1431	226..>2439	3874
	PEBLM20044520	1432	922..1974	3875
50	PEBLM20052820	1433	411..782	3876
	PEBLM20060310	1434	1731..>2083	3877
	PEBLM20060360	1435	58..330	3878
	PEBLM20060490	1436	431..892	3879
55	PEBLM20071880	1437	497..814	3880
	PEBLM20072960	1438	128..1093	3881
	PEBLM20074370	1439	60..458	3882
	PEBLM20075980	1440	53..1153	3883

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
PEBLM20078320	1441	5..1672	3884
PEBLM20085760	1442	122..763	3885
PERIC10000250	1443	689..1516	3886
PERIC20002140	1444	151..1239	3887
PERIC20003860	1445	33..359	3888
PERIC20003870	1446	40..2817	3889
PERIC20004220	1447	130..1935	3890
PERIC20004780	1448	132..956	3891
PLACE50000660	1449	329..2527	3892
PLACE60003480	1450	35..877	3893
PLACE60004630	1451	216..533	3894
PLACE60060420	1452	34..246	3895
PLACE60079250	1453	336..>3307	3896
PLACE60086400	1454	279..764	3897
PLACE60119750	1455	28..570	3898
PLACE60121080	1456	769..1182	3899
PLACE60136500	1457	1900..2241	3900
PLACE60136720	1458	78..2519	3901
PLACE60138830	1459	750..1202	3902
PLACE60153220	1460	247..561	3903
PLACE60155130	1461	833..1171	3904
PLACE60161600	1462	77..1099	3905
PLACE60169420	1463	165..1097	3906
PLACE60177140	1464	1321..2190	3907
PLACE60181070	1465	1355..1708	3908
PLACE60187690	1466	1606..1941	3909
PLACE60188340	1467	430..1224	3910
PROST10003220	1468	187..933	3911
PROST10004800	1469	87..419	3912
PROST20005050	1470	673..1164	3913
PROST20005670	1471	1132..>2293	3914
PROST20021010	1472	612..926	3915
PROST20024890	1473	14..514	3916
PROST20029270	1474	1016..1363	3917
PROST20047270	1475	1300..2250	3918
PROST20047390	1476	163..2283	3919
PROST20050670	1477	1622..2074	3920
PROST20052280	1478	326..634	3921
PROST20057930	1479	237..>2116	3922
PROST20059040	1480	1047..1355	3923
PROST20066880	1481	1937..2521	3924
PROST20079500	1482	863..1957	3925
PROST20083600	1483	209..1087	3926
PROST20087700	1484	481..1287	3927
PROST20097950	1485	91..405	3928
PROST20100460	1486	63..1796	3929
PROST20104000	1487	1059..2012	3930
PROST20107820	1488	304..1524	3931
PROST20111050	1489	772..1281	3932

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PROST20112970	1490	66..671	3933
	PROST20114390	1491	1291..1749	3934
	PROST20115600	1492	4..339	3935
	PROST20120050	1493	176..589	3936
	PROST20120160	1494	283..597	3937
10	PROST20121900	1495	68..385	3938
	PROST20123530	1496	1619..2044	3939
	PROST20127400	1497	1156..1524	3940
	PROST20127800	1498	942..2120	3941
15	PROST20130530	1499	416..1588	3942
	PROST20132600	1500	1447..2040	3943
	PROST20133270	1501	2..529	3944
	PROST20144220	1502	1011..1367	3945
	PROST20146010	1503	298..1953	3946
20	PROST20149160	1504	1677..1991	3947
	PROST20149250	1505	635..1201	3948
	PROST20151240	1506	300..938	3949
	PROST20152460	1507	1542..2084	3950
25	PROST20153320	1508	184..540	3951
	PROST20159240	1509	286..612	3952
	PROST20161950	1510	90..716	3953
	PROST20164440	1511	2570..3004	3954
	PROST20166680	1512	53..874	3955
30	PROST20168290	1513	1757..2143	3956
	PROST20169800	1514	168..1763	3957
	PROST20170980	1515	28..1245	3958
	PROST20171280	1516	306..1493	3959
35	PROST20175290	1517	1538..2323	3960
	PROST20176170	1518	998..2053	3961
	PROST20178360	1519	72..566	3962
	PROST20185830	1520	1200..2015	3963
	PROST20189770	1521	219..2018	3964
40	PROST20191640	1522	318..1229	3965
	PUAEN10000850	1523	121..2040	3966
	PUAEN20003740	1524	104..409	3967
	PUAEN20011880	1525	28..2028	3968
45	PUAEN20015260	1526	141..881	3969
	PUAEN20015860	1527	71..1846	3970
	PUAEN20018820	1528	41..1870	3971
	PUAFN20025680	1529	667..1584	3972
	PUAEN20027580	1530	36..512	3973
50	PUAEN20030180	1531	127..978	3974
	PUAEN20040670	1532	326..2644	3975
	PUAEN20044000	1533	541..957	3976
	PUAEN20045110	1534	335..886	3977
	PUAEN20045250	1535	335..1054	3978
55	PUAEN20051100	1536	228..1319	3979
	PUAEN20052470	1537	1699..2046	3980
	PUAEN20055020	1538	295..2553	3981

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
PUAEN20078980	1539	6..989	3982
PUAEN20081230	1540	62..469	3983
PUAEN20083140	1541	104..1687	3984
PUAEN20085150	1542	167..502	3985
PUAEN20108240	1543	2..1993	3986
RECTM10001410	1544	426..1631	3987
RECTM20003490	1545	876..1193	3988
RECTM20005100	1546	149..1273	3989
SALGL10001710	1547	271..1722	3990
SKMUS20001980	1548	75..1034	3991
SKMUS20003610	1549	86..910	3992
SKMUS20007010	1550	24..977	3993
SKMUS20007800	1551	708..>1835	3994
SKMUS20011640	1552	16..408	3995
SKMUS20012010	1553	300..1019	3996
SKMUS20016220	1554	80..1267	3997
SKMUS20018230	1555	98..442	3998
SKMUS20018500	1556	273..1172	3999
SKMUS20020840	1557	79..1014	4000
SKMUS20021530	1558	432..2135	4001
SKMUS20024750	1559	201..1208	4002
SKMUS20028210	1560	358..753	4003
SKMUS20028400	1561	18..644	4004
SKMUS20029200	1562	174..1130	4005
SKMUS20031630	1563	171..485	4006
SKMUS20046670	1564	234..617	4007
SKMUS20048970	1565	104..1132	4008
SKMUS20049030	1566	191..1096	4009
SKMUS20077400	1567	170..772	4010
SKMUS20084740	1568	83..>1516	4011
SKNMS20006220	1569	1176..1856	4012
SKNSH20008190	1570	490..2289	4013
SKNSH20020540	1571	2184..2924	4014
SKNSH20028660	1572	192..581	4015
SKNSH20031740	1573	120..563	4016
SKNSH20034660	1574	562..996	4017
SKNSH20051940	1575	1006..1488	4018
SKNSH20062340	1576	85..453	4019
SKNSH20063040	1577	91..768	4020
SKNSH20080430	1578	81..524	4021
SKNSH20087770	1579	107..>1808	4022
SKNSH20089400	1580	34..1092	4023
SKNSH20091970	1581	181..489	4024
SMINT20001760	1582	267..1706	4025
SMINT20005410	1583	138..557	4026
SMINT20008240	1584	1123..1500	4027
SMINT20009840	1585	31..750	4028
SMINT20011140	1586	1254..1664	4029
SMINT20011580	1587	131..811	4030

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SMINT20011990	1588	132..512	4031
	SMINT20013480	1589	87..686	4032
	SMINT20014580	1590	57..410	4033
	SMINT20015590	1591	1375..1818	4034
	SMINT20022020	1592	133..726	4035
10	SMINT20023280	1593	890..1345	4036
	SMINT20024570	1594	1852..2370	4037
	SMINT20026890	1595	541..2790	4038
	SMINT20028820	1596	1240..1749	4039
15	SMINT20029760	1597	236..1282	4040
	SMINT20033170	1598	539..931	4041
	SMINT20033400	1599	20..778	4042
	SMINT20035690	1600	11..1411	4043
	SMINT20040860	1601	39..1169	4044
20	SMINT20042990	1602	397..750	4045
	SMINT20047810	1603	109..588	4046
	SMINT20049090	1604	99..641	4047
	SMINT20050750	1605	101..907	4048
25	SMINT20051610	1606	56..1513	4049
	SMINT20053300	1607	1251..1598	4050
	SMINT20053870	1608	85..894	4051
	SMINT20056210	1609	356..754	4052
	SMINT20058000	1610	200..565	4053
30	SMINT20060780	1611	18..554	4054
	SMINT20065960	1612	859..1314	4055
	SMINT20068010	1613	136..1026	4056
	SMINT20071400	1614	212..1183	4057
35	SMINT20073650	1615	59..1549	4058
	SMINT20076470	1616	1678..1983	4059
	SMINT20080540	1617	1280..1606	4060
	SMINT20089170	1618	54..530	4061
	SMINT20092330	1619	169..858	4062
40	SMINT20092720	1620	1640..2293	4063
	SMINT20095050	1621	733..1107	4064
	SMINT20098320	1622	112..465	4065
	SMINT20100680	1623	237..614	4066
45	SMINT20101440	1624	187..2109	4067
	SMINT20102780	1625	26..1642	4068
	SMINT20103690	1626	208..960	4069
	SMINT20105000	1627	194..514	4070
	SMINT20105330	1628	1580..2020	4071
50	SMINT20106290	1629	501..1802	4072
	SMINT20106720	1630	80..1498	4073
	SMINT20108530	1631	185..523	4074
	SMINT20109970	1632	1444..>1974	4075
	SMINT20110330	1633	1398..2222	4076
55	SMINT20110660	1634	1108..1500	4077
	SMINT20112730	1635	80..1564	4078
	SMINT20115880	1636	679..1746	4079

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SMINT20121220	1637	263..>1798	4080
	SMINT20121950	1638	6..443	4081
	SMINT20122850	1639	454..777	4082
	SMINT20122910	1640	1516..2094	4083
	SMINT20127350	1641	622..1449	4084
10	SMINT20127930	1642	67..1554	4085
	SMINT20130320	1643	178..2601	4086
	SMINT20131810	1644	583..1257	4087
	SMINT20132280	1645	293..655	4088
15	SMINT20136130	1646	1291..1752	4089
	SMINT20138900	1647	87..1439	4090
	SMINT20144430	1648	54..647	4091
	SMINT20144800	1649	171..1394	4092
	SMINT20144890	1650	209..520	4093
20	SMINT20152940	1651	386..985	4094
	SMINT20153260	1652	135..1838	4095
	SMINT20153530	1653	1186..1524	4096
	SMINT20154540	1654	107..1339	4097
25	SMINT20155180	1655	20..763	4098
	SMINT20157450	1656	669..1118	4099
	SMINT20158100	1657	30..587	4100
	SMINT20161220	1658	397..1977	4101
	SMINT20162860	1659	36..494	4102
30	SMINT20163960	1660	665..1036	4103
	SMINT20164400	1661	125..706	4104
	SMINT20164770	1662	529..870	4105
	SMINT20168570	1663	1593..2069	4106
35	SMINT20173190	1664	251..829	4107
	SMINT20173240	1665	253..582	4108
	SMINT20174360	1666	978..1733	4109
	SMINT20177360	1667	172..771	4110
	SMINT20178550	1668	51..692	4111
40	SMINT20179740	1669	78..1865	4112
	SMINT20183530	1670	1130..2530	4113
	SMINT20190170	1671	80..1567	4114
	SMINT20191420	1672	49..1365	4115
45	SMINT20191530	1673	40..2040	4116
	SMINT20192000	1674	49..435	4117
	SPLEN10000830	1675	1586..2053	4118
	SPLEN20000640	1676	27..755	4119
	SPLEN20002220	1677	87..434	4120
50	SPLEN20003070	1678	684..1046	4121
	SPLEN20006070	1679	78..2837	4122
	SPLEN20008390	1680	375..2378	4123
	SPLEN20008740	1681	66..1547	4124
55	SPLEN20008820	1682	31..1872	4125
	SPLEN20011410	1683	199..2394	4126
	SPLEN20013540	1684	978..1310	4127
	SPLEN20016260	1685	906..1748	4128

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 SPLEN20019450	1686	180..680	4129
SPLEN20020070	1687	65..451	4130
SPLEN20021660	1688	130..771	4131
SPLEN20022230	1689	133..1026	4132
SPLEN20023140	1690	1153..1605	4133
10 SPLEN20026950	1691	855..3383	4134
SPLEN20027440	1692	29..2488	4135
SPLEN20029310	1693	70..585	4136
SPLEN20031600	1694	1658..2083	4137
SPLEN20032040	1695	357..746	4138
15 SPLEN20032190	1696	441..785	4139
SPLEN20033960	1697	16..1026	4140
SPLEN20039240	1698	1177..1929	4141
SPLEN20040600	1699	60..368	4142
20 SPLEN20054290	1700	187..2421	4143
SPLEN20076530	1701	254..586	4144
SPLEN20077500	1702	79..1941	4145
SPLEN20079260	1703	535..1506	4146
SPLEN20079510	1704	1880..>2197	4147
25 SPLEN20084600	1705	13..1878	4148
SPLEN20095410	1706	816..1541	4149
SPLEN20095550	1707	193..>2558	4150
SPLEN20095810	1708	248..670	4151
30 SPLEN20097330	1709	1448..1849	4152
SPLEN20099700	1710	91..>3025	4153
SPLEN20101190	1711	1864..2250	4154
SPLEN20103950	1712	25..507	4155
SPLEN20106250	1713	295..711	4156
35 SPLEN20117660	1714	662..1099	4157
SPLEN20118300	1715	332..1486	4158
SPLEN20119810	1716	526..1644	4159
SPLEN20121750	1717	464..1021	4160
40 SPLEN20126190	1718	274..2688	4161
SPLEN20128000	1719	96..1664	4162
SPLEN20129610	1720	207..557	4163
SPLEN20140800	1721	387..2144	4164
SPLEN20141360	1722	491..799	4165
45 SPLEN20141990	1723	443..745	4166
SPLEN20142100	1724	301..996	4167
SPLEN20143180	1725	50..448	4168
SPLEN20144520	1726	2002..2463	4169
50 SPLEN20145720	1727	1205..>1939	4170
SPLEN20146450	1728	362..862	4171
SPLEN20146690	1729	1966..2550	4172
SPLEN20147110	1730	313..2067	4173
SPLEN20147390	1731	169..1479	4174
55 SPLEN20149110	1732	2..769	4175
SPLEN20149190	1733	26..364	4176
SPLEN20149240	1734	787..2490	4177

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
SPLN20150940	1735	79..2385	4178
SPLN20151210	1736	66..1715	4179
SPLN20152610	1737	986..1453	4180
SPLN20152760	1738	284..628	4181
SPLN20157300	1739	426..728	4182
SPLN20157880	1740	35..769	4183
SPLN20158900	1741	1643..2032	4184
SPLN20158990	1742	843..1172	4185
SPLN20160450	1743	552..1115	4186
SPLN20160690	1744	734..1099	4187
SPLN20160980	1745	124..456	4188
SPLN20162680	1746	646..2007	4189
SPLN20163560	1747	86..2173	4190
SPLN20165310	1748	80..1492	4191
SPLN20166270	1749	1134..1814	4192
SPLN20167200	1750	223..570	4193
SPLN20169220	1751	160..576	4194
SPLN20169720	1752	72..2492	4195
SPLN20170310	1753	125..1039	4196
SPLN20171210	1754	7..837	4197
SPLN20171470	1755	41..2272	4198
SPLN20171890	1756	1312..1716	4199
SPLN20172120	1757	138..500	4200
SPLN20173510	1758	235..1785	4201
SPLN20174260	1759	99..428	4202
SPLN20176200	1760	36..431	4203
SPLN20179180	1761	173..1201	4204
SPLN20179810	1762	1374..3224	4205
SPLN20181810	1763	641..1183	4206
SPLN20186430	1764	80..979	4207
SPLN20193110	1765	1744..2118	4208
SPLN20194050	1766	1351..2331	4209
SPLN20198110	1767	1260..1562	4210
SPLN20204170	1768	202..594	4211
SPLN20211220	1769	601..1500	4212
SPLN20211570	1770	174..521	4213
SPLN20211940	1771	241..1155	4214
SPLN20212730	1772	979..1830	4215
SPLN20212950	1773	283..2055	4216
SPLN20213830	1774	137..460	4217
SPLN20214400	1775	28..387	4218
SPLN20214580	1776	300..602	4219
SPLN20222270	1777	241..927	4220
SPLN20225220	1778	672..1199	4221
SPLN20242320	1779	136..522	4222
SPLN20242730	1780	2343..2732	4223
SPLN20243830	1781	197..556	4224
SPLN20245300	1782	945..1529	4225
SPLN20249560	1783	889..1584	4226

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SPLN20250170	1784	457..3012	4227
	SPLN20250390	1785	1327..1788	4228
	SPLN20252190	1786	1413..2609	4229
	SPLN20261440	1787	511..894	4230
	SPLN20264110	1788	1195..1662	4231
10	SPLN20267650	1789	39..1331	4232
	SPLN20273950	1790	608..1222	4233
	SPLN20279950	1791	1874..2518	4234
	SPLN20280660	1792	1286..1612	4235
15	SPLN20283650	1793	13..621	4236
	SPLN20284240	1794	282..1175	4237
	SPLN20292950	1795	9..2456	4238
	SPLN20293800	1796	73..858	4239
	SPLN20303970	1797	778..1104	4240
20	SPLN20304950	1798	7..1011	4241
	SPLN20305620	1799	1356..1853	4242
	SPLN20329240	1800	5..361	4243
	STOMA20001830	1801	81..1574	4244
25	STOMA20005390	1802	59..1567	4245
	STOMA20005670	1803	81..1478	4246
	STOMA20006400	1804	80..1687	4247
	STOMA20006780	1805	41..1975	4248
	STOMA20006860	1806	1272..1988	4249
30	STOMA20008880	1807	112..1485	4250
	STOMA20010250	1808	66..419	4251
	STOMA20013890	1809	2151..2486	4252
	STOMA20026880	1810	548..874	4253
35	STOMA20032890	1811	1710..2600	4254
	STOMA20034770	1812	81..1583	4255
	STOMA20036460	1813	311..772	4256
	STOMA20046680	1814	768..1154	4257
	STOMA20048520	1815	160..663	4258
40	STOMA20048840	1816	936..1487	4259
	STOMA20051200	1817	140..619	4260
	STOMA20056640	1818	49..555	4261
	STOMA20056670	1819	81..1556	4262
45	STOMA20057820	1820	60..1226	4263
	STOMA20062130	1821	35..427	4264
	STOMA20062290	1822	289..693	4265
	STOMA20063250	1823	109..438	4266
	STOMA20063980	1824	97..480	4267
50	STOMA20064470	1825	78..1118	4268
	STOMA20067800	1826	35..397	4269
	STOMA20069040	1827	364..792	4270
	STOMA20072690	1828	351..701	4271
	STOMA20076800	1829	311..784	4272
55	STOMA20077450	1830	780..2300	4273
	STOMA20080500	1831	59..1735	4274
	STOMA20083610	1832	80..1564	4275

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
STOMA20086140	1833	201.. 746	4276
STOMA20088380	1834	48.. 1535	4277
STOMA20092530	1835	80.. 1501	4278
STOMA20092560	1836	68.. 439	4279
STOMA20092890	1837	105.. 1223	4280
SYNOV20001520	1838	25.. 735	4281
SYNOV20001730	1839	56..1480	4282
SYNOV20002510	1840	79..1629	4283
SYNOV20002790	1841	59..1480	4284
SYNOV20002970	1842	56..1471	4285
SYNOV20003970	1843	357..881	4286
SYNOV20004260	1844	80..1489	4287
SYNOV20007000	1845	55..1485	4288
SYNOV20008240	1846	61..1494	4289
SYNOV20009230	1847	40..1515	4290
SYNOV20010880	1848	61..1479	4291
SYNOV20011110	1849	56..1468	4292
SYNOV20013000	1850	30..1433	4293
SYNOV20013560	1851	79..1494	4294
SYNOV20013900	1852	81..1499	4295
SYNOV20017080	1853	466..1905	4296
SYNOV30001840	1854	146..2443	4297
TBAES20000590	1855	1697.. >2237	4298
TBAES20002550	1856	16.. 1896	4299
TBAES20003150	1857	42.. 1064	4300
TBAES20003770	1858	117.. 3437	4301
TCOLN20001390	1859	237.. 1106	4302
TESOP20000900	1860	110.. 448	4303
TESOP20003120	1861	42.. 929	4304
TESOP20004000	1862	295.. 1125	4305
TESOP20005270	1863	568.. 921	4306
TESOP20005690	1864	230.. 574	4307
TESTI10000940	1865	127..1752	4308
TESTI20001000	1866	129..944	4309
TESTI20001170	1867	107..1291	4310
TESTI20001720	1868	204..722	4311
TESTI20002720	1869	92..>2187	4312
TESTI20002780	1870	821..1471	4313
TESTI20004890	1871	140..1231	4314
TESTI20011200	1872	1615..1968	4315
TESTI20017950	1873	62..2023	4316
TESTI20018230	1874	506..1024	4317
TESTI20023510	1875	100..1935	4318
TESTI20029930	1876	597..1847	4319
TESTI20030310	1877	1362..1757	4320
TESTI20030890	1878	1736..2167	4321
TESTI20031270	1879	820..1332	4322
TESTI20031810	1880	235..1926	4323
TESTI20035960	1881	80..1327	4324

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20036380	1882	125..2110	4325
	TESTI20037560	1883	16..1986	4326
	TESTI20038270	1884	42..347	4327
	TESTI20039400	1885	63..1430	4328
	TESTI20041690	1886	194..2320	4329
10	TESTI20044230	1887	76..1308	4330
	TESTI20044310	1888	307..1899	4331
	TESTI20046750	1889	56..871	4332
	TESTI20057750	1890	154..495	4333
15	TESTI20060400	1891	102..1754	4334
	TESTI20061110	1892	102..1574	4335
	TESTI20063830	1893	186..1793	4336
	TESTI20066670	1894	345..1823	4337
	TESTI20066770	1895	867..1937	4338
20	TESTI20067200	1896	25..1149	4339
	TESTI20076850	1897	864..1307	4340
	TESTI20082330	1898	12..2249	4341
	TESTI20083200	1899	80..967	4342
25	TESTI20083940	1900	60..1973	4343
	TESTI20086210	1901	65..1465	4344
	TESTI20087620	1902	116..2191	4345
	TESTI20088220	1903	318..2435	4346
	TESTI20094020	1904	341..1885	4347
30	TESTI20094120	1905	402..1184	4348
	TESTI20094230	1906	1397..2158	4349
	TESTI20094470	1907	428..1540	4350
	TESTI20098350	1908	137..1849	4351
35	TESTI20098530	1909	220..564	4352
	TESTI20102800	1910	278..640	4353
	TESTI20105720	1911	1542..1901	4354
	TESTI20108720	1912	101..1123	4355
	TESTI20110280	1913	212..1396	4356
40	TESTI20112940	1914	579..899	4357
	TESTI20114070	1915	1575..1937	4358
	TESTI20116650	1916	43..387	4359
	TESTI20116830	1917	825..1208	4360
45	TESTI20121550	1918	191..1900	4361
	TESTI20122310	1919	149..826	4362
	TESTI20123080	1920	432..767	4363
	TESTI20123560	1921	249..816	4364
	TESTI20127760	1922	149..1141	4365
50	TESTI20128350	1923	178..591	4366
	TESTI20129150	1924	241..969	4367
	TESTI20129220	1925	366..773	4368
	TESTI20130010	1926	866..1420	4369
55	TESTI20130120	1927	119..748	4370
	TESTI20135660	1928	961..1374	4371
	TESTI20136100	1929	71..406	4372
	TESTI20136710	1930	14..>1826	4373

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 TESTI20136990	1931	1903..2292	4374
TESTI20137370	1932	37..339	4375
TESTI20137570	1933	181..561	4376
TESTI20143240	1934	486..908	4377
TESTI20143390	1935	52..1068	4378
10 TESTI20143520	1936	970..1332	4379
TESTI20148000	1937	250..2004	4380
TESTI20152460	1938	222..1499	4381
TESTI20155900	1939	1095..1499	4382
15 TESTI20156100	1940	31..1200	4383
TESTI20157100	1941	481..1149	4384
TESTI20157520	1942	55..>1880	4385
TESTI20159140	1943	424..>1611	4386
TESTI20161970	1944	138..1658	4387
20 TESTI20164100	1945	60..470	4388
TESTI20168480	1946	91..1341	4389
TESTI20168530	1947	1219..1608	4390
TESTI20168960	1948	37..570	4391
25 TESTI20169960	1949	801..1139	4392
TESTI20170350	1950	1106..1429	4393
TESTI20171020	1951	11..>2194	4394
TESTI20178160	1952	1084..1452	4395
TESTI20179320	1953	191..664	4396
30 TESTI20183370	1954	190..870	4397
TESTI20184520	1955	123..2417	4398
TESTI20185550	1956	75..1904	4399
TESTI20185810	1957	243..587	4400
35 TESTI20189410	1958	16..>1759	4401
TESTI20192280	1959	10..906	4402
TESTI20192800	1960	193..>2366	4403
TESTI20193360	1961	66..854	4404
TESTI20194300	1962	70..576	4405
40 TESTI20194810	1963	78..473	4406
TESTI20197940	1964	771..>1987	4407
TESTI20199170	1965	244..558	4408
TESTI20199750	1966	92..1957	4409
45 TESTI20200260	1967	307..846	4410
TESTI20200710	1968	190..1749	4411
TESTI20202550	1969	55..1299	4412
TESTI20203440	1970	1109..1600	4413
TESTI20204450	1971	417..1916	4414
50 TESTI20208400	1972	1027..1782	4415
TESTI20208710	1973	70..2046	4416
TESTI20209460	1974	1035..1400	4417
TESTI20209810	1975	872..1405	4418
TESTI20209990	1976	106..549	4419
55 TESTI20211160	1977	627..1424	4420
TESTI20211220	1978	1561..1944	4421
TESTI20211240	1979	150..>1469	4422

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20213150	1980	380..1303	4423
	TESTI20213580	1981	338..697	4424
	TESTI20214250	1982	46..933	4425
	TESTI20215990	1983	428..2635	4426
	TESTI20216370	1984	572..1195	4427
10	TESTI20220100	1985	539..1264	4428
	TESTI20220650	1986	164..481	4429
	TESTI20224620	1987	221..532	4430
	TESTI20226230	1988	335..>1500	4431
	TESTI20226490	1989	1044..1367	4432
15	TESTI20229600	1990	342..2669	4433
	TESTI20230250	1991	1310..1693	4434
	TESTI20230850	1992	246..2567	4435
	TESTI20231920	1993	949..1392	4436
20	TESTI20231940	1994	382..975	4437
	TESTI20232140	1995	26..1237	4438
	TESTI20234140	1996	182..1738	4439
	TESTI20234270	1997	334..642	4440
25	TESTI20234360	1998	23..460	4441
	TESTI20237520	1999	172..1734	4442
	TESTI20238000	2000	978..1322	4443
	TESTI20238610	2001	150..1373	4444
	TESTI20239470	2002	132..2294	4445
30	TESTI20239510	2003	701..1333	4446
	TESTI20240090	2004	10..1179	4447
	TESTI20241530	2005	594..1985	4448
	TESTI20241920	2006	1309..1632	4449
35	TESTI20242830	2007	42..2306	4450
	TESTI20242990	2008	968..1330	4451
	TESTI20244190	2009	80..1630	4452
	TESTI20244760	2010	1258..1647	4453
	TESTI20249990	2011	698..1960	4454
40	TESTI20254220	2012	81..1376	4455
	TESTI20254540	2013	997..1830	4456
	TESTI20254860	2014	205..>2004	4457
	TESTI20255820	2015	120..1565	4458
45	TESTI20258460	2016	37..1212	4459
	TESTI20262330	2017	928..1521	4460
	TESTI20262910	2018	335..1336	4461
	TESTI20265250	2019	1751..2095	4462
	TESTI20265370	2020	46..378	4463
50	TESTI20265970	2021	258..1961	4464
	TESTI20266740	2022	88..1203	4465
	TESTI20269570	2023	643..1047	4466
	TESTI20271850	2024	202..504	4467
	TESTI20272060	2025	1379..3253	4468
55	TESTI20272390	2026	123..767	4469
	TESTI20272960	2027	982..1932	4470
	TESTI20275030	2028	98..583	4471

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20275620	2029	1508.. 1840	4472
TESTI20277360	2030	298.. 1704	4473
TESTI20278200	2031	48.. 698	4474
TESTI20278400	2032	70.. >1856	4475
TESTI20280980	2033	619.. 1071	4476
TESTI20282540	2034	310.. 1356	4477
TESTI20284880	2035	683.. 1114	4478
TESTI20285830	2036	494.. 853	4479
TESTI20288110	2037	234.. 899	4480
TESTI20288910	2038	51.. 965	4481
TESTI20289850	2039	198.. 698	4482
TESTI20291310	2040	106.. 2034	4483
TESTI20291620	2041	1611.. 2021	4484
TESTI20291960	2042	809.. 1921	4485
TESTI20294700	2043	898.. 1236	4486
TESTI20297850	2044	1.. 837	4487
TESTI20301360	2045	114.. 506	4488
TESTI20303220	2046	288.. 2711	4489
TESTI20303360	2047	767.. 2050	4490
TESTI20303420	2048	34.. 768	4491
TESTI20305540	2049	97.. 2949	4492
TESTI20305560	2050	49.. 582	4493
TESTI20307540	2051	88.. 513	4494
TESTI20307700	2052	32.. 412	4495
TESTI20308600	2053	72.. 1307	4496
TESTI20309170	2054	722.. 2233	4497
TESTI20310070	2055	205.. 2097	4498
TESTI20311290	2056	940.. 1398	4499
TESTI20314180	2057	1073.. 1744	4500
TESTI20316870	2058	25.. 813	4501
TESTI20317600	2059	107.. 1420	4502
TESTI20318090	2060	1012.. 1644	4503
TESTI20319190	2061	384.. 1481	4504
TESTI20320440	2062	200.. 1861	4505
TESTI20320670	2063	259.. 1257	4506
TESTI20326810	2064	832.. 1377	4507
TESTI20327680	2065	135.. 1730	4508
TESTI20327740	2066	132.. 518	4509
TESTI20328280	2067	87.. 2135	4510
TESTI20330310	2068	315.. 1307	4511
TESTI20332420	2069	682.. 1461	4512
TESTI20333000	2070	366.. 1586	4513
TESTI20333950	2071	76.. 1500	4514
TESTI20334410	2072	167.. 1630	4515
TESTI20335050	2073	340.. 1389	4516
TESTI20335200	2074	612.. 968	4517
TESTI20336410	2075	17.. 325	4518
TESTI20337100	2076	40.. 384	4519
TESTI20342430	2077	322.. 642	4520

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20343070	2078	530..2563	4521
	TESTI20343570	2079	900..1568	4522
	TESTI20345060	2080	15..1382	4523
	TESTI20347180	2081	3..710	4524
	TESTI20347300	2082	623..931	4525
10	TESTI20347740	2083	100..1599	4526
	TESTI20347770	2084	37..351	4527
	TESTI20351830	2085	919..1773	4528
	TESTI20352620	2086	182..907	4529
15	TESTI20355020	2087	8..1651	4530
	TESTI20357750	2088	547..951	4531
	TESTI20357930	2089	1148..1498	4532
	TESTI20357960	2090	363..725	4533
	TESTI20358980	2091	85..1332	4534
20	TESTI20361140	2092	801..1514	4535
	TESTI20366910	2093	5..1396	4536
	TESTI20367360	2094	324..629	4537
	TESTI20368330	2095	201..1856	4538
25	TESTI20369130	2096	243..611	4539
	TESTI20369220	2097	118..441	4540
	TESTI20369650	2098	633..2204	4541
	TESTI20369690	2099	306..1208	4542
	TESTI20370020	2100	346..1830	4543
30	TESTI20370550	2101	160..462	4544
	TESTI20370810	2102	223..2334	4545
	TESTI20371030	2103	209..1180	4546
	TESTI20371060	2104	140..1177	4547
35	TESTI20373820	2105	237..1109	4548
	TESTI20375340	2106	387..1559	4549
	TESTI20377230	2107	574..1314	4550
	TESTI20378190	2108	380..1795	4551
	TESTI20378450	2109	489..>2419	4552
40	TESTI20380650	2110	961..1272	4553
	TESTI20381040	2111	339..1394	4554
	TESTI20382750	2112	1159..1797	4555
	TESTI20383880	2113	419..988	4556
45	TESTI20385960	2114	684..1637	4557
	TESTI20386230	2115	748..1059	4558
	TESTI20386440	2116	185..514	4559
	TESTI20388580	2117	405..788	4560
	TESTI20390260	2118	142..522	4561
50	TESTI20390410	2119	1604..1969	4562
	TESTI20391130	2120	185..2224	4563
	TESTI20391210	2121	1259..1801	4564
	TESTI20391770	2122	237..1634	4565
55	TESTI20392090	2123	405..881	4566
	TESTI20392250	2124	1057..1941	4567
	TESTI20392270	2125	316..1185	4568
	TESTI20392760	2126	306..2279	4569

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
TESTI20393530	2127	194..1198	4570
TESTI20396130	2128	338..682	4571
TESTI20397760	2129	371..1129	4572
TESTI20400940	2130	231..2705	4573
TESTI20401020	2131	583..1281	4574
TESTI20401280	2132	53..379	4575
TESTI20401430	2133	340..651	4576
TESTI20404240	2134	1110..1550	4577
TESTI20406420	2135	186..1340	4578
TESTI20408150	2136	195..752	4579
TESTI20408970	2137	247..1170	4580
TESTI20409440	2138	17..337	4581
TESTI20409890	2139	120..1082	4582
TESTI20413300	2140	66..503	4583
TESTI20415170	2141	45..419	4584
TESTI20415640	2142	1..324	4585
TESTI20416640	2143	1092..1574	4586
TESTI20417300	2144	107..1807	4587
TESTI20419560	2145	5..331	4588
TESTI20420520	2146	334..2139	4589
TESTI20421490	2147	2188..2628	4590
TESTI20422540	2148	974..2149	4591
TESTI20423020	2149	252..>1770	4592
TESTI20424000	2150	339..842	4593
TESTI20424730	2151	928..1263	4594
TESTI20425070	2152	1145..1726	4595
TESTI20427830	2153	42..380	4596
TESTI20428060	2154	230..598	4597
TESTI20429280	2155	925..1551	4598
TESTI20429580	2156	970..1458	4599
TESTI20432750	2157	56..1399	4600
TESTI20432820	2158	18..1232	4601
TESTI20433130	2159	247..549	4602
TESTI20436560	2160	103..1578	4603
TESTI20438570	2161	1252..1719	4604
TESTI20438560	2162	2227..2622	4605
TESTI20441940	2163	613..1596	4606
TESTI20442760	2164	82..>2054	4607
TESTI20443090	2165	201..1019	4608
TESTI20444130	2166	79..417	4609
TESTI20444180	2167	26..547	4610
TESTI20447540	2168	184..516	4611
TESTI20449200	2169	672..1766	4612
TESTI20451710	2170	429..731	4613
TESTI20451990	2171	210..2264	4614
TESTI20455090	2172	489..1268	4615
TESTI20455620	2173	110..1351	4616
TESTI20456110	2174	4..1191	4617
TESTI20458190	2175	235..579	4618

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20463520	2176	998..1402	4619
	TESTI20463580	2177	577..2037	4620
	TESTI20465350	2178	317..1258	4621
	TESTI20465520	2179	535.. 1026	4622
	TESTI20465690	2180	214.. 1074	4623
10	TESTI20467210	2181	435.. 1613	4624
	TESTI20467320	2182	951.. 1922	4625
	TESTI20467970	2183	332.. 1690	4626
	TESTI20468630	2184	380.. 688	4627
15	TESTI20471410	2185	97.. 1464	4628
	TESTI20471470	2186	31.. 369	4629
	TESTI20471530	2187	2264.. 2641	4630
	TESTI20472120	2188	517.. 876	4631
	TESTI20473420	2189	140..607	4632
20	TESTI20473830	2190	951..1532	4633
	TESTI20477920	2191	1387..1860	4634
	TESTI20478010	2192	169..558	4635
	TESTI20478180	2193	428..754	4636
25	TESTI20478850	2194	949..1323	4637
	TESTI20479300	2195	663..1205	4638
	THYMU10005360	2196	48..899	4639
	THYMU10005540	2197	84..1508	4640
	THYMU20000570	2198	216..728	4641
30	THYMU20011950	2199	45.. 626	4642
	THYMU20015210	2200	1003.. 1314	4643
	THYMU20018190	2201	336.. 758	4644
	THYMU20023380	2202	1426.. 1728	4645
35	THYMU20027560	2203	63.. 602	4646
	THYMU20029100	2204	215.. 928	4647
	THYMU20032870	2205	1042.. 1404	4648
	THYMU20039810	2206	54.. 2204	4649
	THYMU20045120	2207	66.. 425	4650
40	THYMU20058070	2208	984.. 1388	4651
	THYMU20061700	2209	40..435	4652
	THYMU20066100	2210	188..814	4653
	THYMU20070360	2211	1333..1635	4654
45	THYMU20075320	2212	1186..1767	4655
	THYMU20081490	2213	127..>2055	4656
	THYMU20095960	2214	304..945	4657
	THYMU20100410	2215	219.. 1415	4658
	THYMU20101610	2216	1087.. 1446	4659
50	THYMU20101920	2217	765.. 1310	4660
	THYMU20105190	2218	850.. 1713	4661
	THYMU20106710	2219	89.. 493	4662
	THYMU20108310	2220	97.. 642	4663
55	THYMU20111180	2221	33.. 1367	4664
	THYMU20111420	2222	914.. 1303	4665
	THYMU20111830	2223	38.. 796	4666
	THYMU20114470	2224	122.. 502	4667

EP 1 347 046 A1

Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20115850	2225	1500..1805	4668
	THYMU20118060	2226	355..687	4669
	THYMU20118520	2227	220..567	4670
	THYMU20119390	2228	118..525	4671
	THYMU20122730	2229	343..1140	4672
10	THYMU20126900	2230	163..1446	4673
	THYMU20128070	2231	2..349	4674
	THYMU20128260	2232	76..411	4675
	THYMU20130890	2233	221..757	4676
15	THYMU20141670	2234	196..1152	4677
	THYMU20142040	2235	24..653	4678
	THYMU20142970	2236	495..1499	4679
	THYMU20143270	2237	524..1549	4680
	THYMU20147770	2238	80..1501	4681
20	THYMU20153160	2239	1303..1920	4682
	THYMU20158250	2240	117..488	4683
	THYMU20159430	2241	79..1581	4684
	THYMU20161640	2242	110..679	4685
25	THYMU20162190	2243	299..646	4686
	THYMU20169680	2244	718..1395	4687
	THYMU20172150	2245	375..956	4688
	THYMU20173980	2246	355..813	4689
	THYMU20180280	2247	1352..1699	4690
30	THYMU20186390	2248	461..1495	4691
	THYMU20186730	2249	194..535	4692
	THYMU20187720	2250	284..661	4693
	THYMU20193640	2251	659..1165	4694
35	THYMU20194360	2252	257..955	4695
	THYMU20194420	2253	1080..1403	4696
	THYMU20195990	2254	344..673	4697
	THYMU20201980	2255	1094..2023	4698
	THYMU20202890	2256	935..2188	4699
40	THYMU20204160	2257	654..1199	4700
	THYMU20204990	2258	65..385	4701
	THYMU20208300	2259	144..542	4702
	THYMU20209590	2260	193..2061	4703
45	THYMU20215090	2261	862.. 1380	4704
	THYMU20215970	2262	1004.. 1552	4705
	THYMU20216840	2263	605.. 2074	4706
	THYMU20222890	2264	1896.. 2198	4707
	THYMU20226600	2265	246.. 1232	4708
50	THYMU20228540	2266	109.. 426	4709
	THYMU20229220	2267	259.. 894	4710
	THYMU20232090	2268	111.. 539	4711
	THYMU20235760	2269	357.. 674	4712
	THYMU20239000	2270	44.. 1672	4713
55	THYMU20239430	2271	656.. 982	4714
	THYMU20240710	2272	680.. 2077	4715
	THYMU20241210	2273	77.. 511	4716

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
THYMU20241850	2274	63.. 890	4717
THYMU20246840	2275	110.. 415	4718
THYMU20247480	2276	4.. 1176	4719
THYMU20250420	2277	222.. 707	4720
THYMU20251890	2278	1433.. 1777	4721
THYMU20253250	2279	713.. 1540	4722
THYMU20255570	2280	882.. 1550	4723
THYMU20255720	2281	88.. 645	4724
THYMU20259090	2282	1763.. 2092	4725
THYMU20265300	2283	60.. 1949	4726
THYMU20271250	2284	681.. 1628	4727
THYMU20272490	2285	174.. 560	4728
THYMU20277390	2286	930.. 1541	4729
THYMU20279750	2287	716.. 1114	4730
THYMU20283790	2288	253.. 804	4731
THYMU20284120	2289	178.. 525	4732
THYMU20286290	2290	287.. 1981	4733
THYMU20286320	2291	1214.. 1594	4734
THYMU20286320	2292	386.. 838	4735
THYMU20286320	2293	549.. 1172	4736
THYMU20286320	2294	294.. 1133	4737
THYMU20286320	2295	143.. 1558	4738
THYMU20286320	2296	25.. 531	4739
THYMU20286320	2297	1038.. 1460	4740
THYMU20286320	2298	675.. 1454	4741
THYMU20286320	2299	348.. 713	4742
THYMU20286320	2300	77.. 613	4743
THYMU20286320	2301	244.. 1773	4744
THYMU20286320	2302	75.. 1463	4745
THYMU20286320	2303	57.. 728	4746
THYMU20286320	2304	271.. 1830	4747
THYMU20286320	2305	122.. 1132	4748
THYMU20286320	2306	112.. 1410	4749
THYMU20286320	2307	61.. 384	4750
THYMU20286320	2308	161.. 1441	4751
THYMU20286320	2309	1410.. 1859	4752
THYMU20286320	2310	830.. 1354	4753
THYMU20286320	2311	560.. 2110	4754
THYMU20286320	2312	1985.. >3328	4755
THYMU20286320	2313	1.. 309	4756
THYMU20286320	2314	424.. 1035	4757
THYMU20286320	2315	77.. 1540	4758
THYMU20286320	2316	511.. 1845	4759
THYMU20286320	2317	70.. 594	4760
THYMU20286320	2318	405.. 1055	4761
THYMU20286320	2319	1448.. 1993	4762
THYMU20286320	2320	3.. 329	4763
THYMU20286320	2321	166.. 603	4764
THYMU20286320	2322	63.. 890	4765

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 TRACH20068700	2323	144..1811	4766
TRACH20069180	2324	63..1625	4767
TRACH20076740	2325	779..1669	4768
TRACH20076760	2326	1737..2183	4769
10 TRACH20077540	2327	1859..2455	4770
TRACH20079690	2328	144..2144	4771
TRACH20082780	2329	1675..2103	4772
TRACH20084720	2330	38..1819	4773
TRACH20085400	2331	223..2346	4774
15 TRACH20085830	2332	41..1567	4775
TRACH20091230	2333	1660..2067	4776
TRACH20092680	2334	56..457	4777
TRACH20096610	2335	417..935	4778
20 TRACH20099340	2336	156..494	4779
TRACH20105870	2337	1418..2176	4780
TRACH20107710	2338	13..474	4781
TRACH20109650	2339	1421..1849	4782
TRACH20111130	2340	1548..1937	4783
25 TRACH20115740	2341	507..893	4784
TRACH20118940	2342	1781..2083	4785
TRACH20121380	2343	795..1808	4786
TRACH20128110	2344	1233..1796	4787
TRACH20128230	2345	80..1657	4788
30 TRACH20134950	2346	675..1001	4789
TRACH20135520	2347	425..2335	4790
TRACH20136710	2348	42..545	4791
TRACH20139820	2349	1630..1998	4792
35 TRACH20140820	2350	196..738	4793
TRACH20141240	2351	270..875	4794
TRACH20145440	2352	243..1511	4795
TRACH20147250	2353	834..1196	4796
TRACH20149970	2354	124..1776	4797
40 TRACH20153810	2355	216..635	4798
TRACH20154860	2356	3..1439	4799
TRACH20162860	2357	98..364	4800
TRACH20163170	2358	267..1028	4801
45 TRACH20164980	2359	657..2165	4802
TRACH20167220	2360	986..2422	4803
TRACH20168350	2361	200..589	4804
TRACH20169800	2362	1922..2359	4805
TRACH20180840	2363	1288..1593	4806
50 TRACH20183170	2364	1029..2252	4807
TRACH20184490	2365	214..1596	4808
TRACH20187180	2366	1322..1639	4809
TRACH20190240	2367	1624..2313	4810
55 TSTOM10001860	2368	96..1859	4811
TSTOM20001390	2369	241..1671	4812
TSTOM20003150	2370	103..1245	4813
TSTOM20005690	2371	370..1626	4814

EP 1 347 046 A1

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 TATER20002830	2372	172..930	4815
UMVEN10001560	2373	130..669	4816
UMVEN10001860	2374	198..>2048	4817
UMVEN20000690	2375	6..1118	4818
UMVEN20003540	2376	4..519	4819
10 UTERU20000740	2377	2062..2400	4820
UTERU20004240	2378	38..385	4821
UTERU20006290	2379	101..406	4822
UTERU20006960	2380	106..555	4823
15 UTERU20020010	2381	54..431	4824
UTERU20022940	2382	735..1232	4825
UTERU20030570	2383	184..1737	4826
UTERU20040610	2384	92..409	4827
UTERU20046640	2385	15..2699	4828
20 UTERU20046980	2386	216..926	4829
UTERU20050690	2387	619..924	4830
UTERU20054460	2388	557..>2294	4831
UTERU20055330	2389	45..632	4832
25 UTERU20055480	2390	92..1765	4833
UTERU20055930	2391	90..869	4834
UTERU20056010	2392	65..484	4835
UTERU20059050	2393	809..1459	4836
UTERU20061030	2394	994..1389	4837
30 UTERU20064000	2395	153..479	4838
UTERU20064860	2396	26..1780	4839
UTERU20065930	2397	37..2097	4840
UTERU20067050	2398	641..952	4841
35 UTERU20068990	2399	945..1319	4842
UTERU20070040	2400	36..383	4843
UTERU20070810	2401	761..1219	4844
UTERU20076390	2402	71..499	4845
UTERU20081300	2403	2063..2464	4846
40 UTERU20084260	2404	494..1321	4847
UTERU20094350	2405	293.. 802	4848
UTERU20095380	2406	872.. 1213	4849
UTERU20095400	2407	737.. 1456	4850
45 UTERU20097760	2408	1232.. 1759	4851
UTERU20099720	2409	201.. 746	4852
UTERU20101240	2410	210.. 602	4853
UTERU20114100	2411	538.. 963	4854
UTERU20115740	2412	469.. 933	4855
50 UTERU20116570	2413	327.. 1694	4856
UTERU20118110	2414	87.. 485	4857
UTERU20118970	2415	229..549	4858
UTERU20119060	2416	1192..2436	4859
UTERU20119680	2417	676..1185	4860
55 UTERU20120310	2418	68..1066	4861
UTERU20124070	2419	368..733	4862
UTERU20126880	2420	524..1045	4863

Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
UTERU20134910	2421	1070..1489	4864
UTERU20135860	2422	676..1965	4865
UTERU20143980	2423	68..370	4866
UTERU20144640	2424	231..1148	4867
UTERU20145480	2425	172..2193	4868
UTERU20146310	2426	114..1580	4869
UTERU20146680	2427	524..1045	4870
UTERU20150870	2428	47..499	4871
UTERU20151980	2429	220..981	4872
UTERU20158300	2430	342..686	4873
UTERU20158800	2431	161..1318	4874
UTERU20161570	2432	295..1209	4875
UTERU20164260	2433	54..890	4876
UTERU20168220	2434	835..1530	4877
UTERU20176130	2435	27..1184	4878
UTERU20176320	2436	108..1364	4879
UTERU20178100	2437	2178..2528	4880
UTERU20179880	2438	172..2379	4881
UTERU20183640	2439	2289..2828	4882
UTERU20185230	2440	125..1927	4883
UTERU20186740	2441	851..1156	4884
UTERU20188110	2442	125..1135	4885
UTERU20188810	2443	84..389	4886

[0028] Namely, primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention shown in SEQ ID NOs in the above Table 1. When one intends to synthesize full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0029] A method to design a primer that enables a specific amplification based on the aimed nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of 5' untranslated region (5'UTR), any part of the 5'-end, which ensures the specificity to the cDNA of interest, can be selected as the primer.

[0030] When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' → 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the full-length cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones of the present invention are clones with high probability of completeness in length, which were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the very high fullness ratio by oligo-capping, and [2] assembling the 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction).

[0032] However, the uses of primers designed based on the full-length nucleotide sequences provided by the present invention enable easily obtaining full-length cDNAs without such a special technique.

[0033] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA

contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a nucleotide sequence of novel full-length cDNA. If a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods

such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0034] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. A rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the nucleotide sequence which includes the 5'-end of the full-length cDNA clone of the present invention, and thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0035] The polypeptide encoded by the full-length cDNA of the invention can be prepared as a recombinant polypeptide or as a natural polypeptide. For example, the recombinant polypeptide can be prepared by inserting the polynucleotide encoding the polypeptide of the invention into a vector, introducing the vector into an appropriate host cell and purifying the polypeptide expressed within the transformed host cell, as described below. In contrast, the natural polypeptide can be prepared, for example, by utilizing an affinity column to which an antibody against the polypeptide of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the polypeptide of the invention.

[0036] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the polypeptides of the present invention. Using the biological activity possessed by the polypeptide of the invention as an index, it is possible to verify whether or not a particular polypeptide is functionally equivalent to the polypeptide of the invention by examining whether or not the polypeptide has said activity.

[0037] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a polypeptide (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such polypeptides can be generated by spontaneous mutations. The present invention also includes a polypeptide comprising the amino acid sequence shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have the equivalent functions to those of the polypeptides identified in the present Examples described later.

[0038] There are no limitations on the number and sites of amino acid mutations, as long as the polypeptides maintain the functions thereof. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less, or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, 5 amino acids, preferably 4 or 3 amino acids, more preferably 2 amino acids, and further preferably 1 amino acid.

[0039] From the viewpoint of maintaining the polypeptide function, it is preferable that a substituted amino acid has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0040] In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4), those skilled in the art can usually isolate a polynucleotide highly homologous to the polynucleotide encoding the polypeptide identified in the present Example based on the identified nucleotide sequence (Table 1) or a portion thereof and obtain the functionally equivalent polypeptide from the isolated polynucleotide. The present invention includes polypeptides encoded by the polynucleotides hybridizing with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to the polypeptides identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0041] Washing conditions of hybridization for the isolation of polynucleotides encoding the functionally equivalent

polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6x SSC, 40% Formamide, 25°C", and the washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C". Even more preferable are those in which the hybridization is done at "6x SSC, 50% Formamide, 37°C", and the washing at "0.1x SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C".

[0042] One skilled in the art can suitably select various conditions, such as dilution ratios of SSC, formamide concentrations, and temperatures to accomplish a similar stringency.

[0043] However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0044] The amino acid sequences of polypeptides isolated by using the hybridization techniques usually have high identity to those of the polypeptides of the present invention, which are shown in Table 1. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses a peptide, or polypeptide comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0045] As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the algorithm BLAST of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, for example, score = 50, wordlength = 3. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used. See <http://www.ncbi.nlm.nih.gov>.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4) using primers designed based on the nucleotide sequence (Table 1) or a portion thereof identified in the present Example, it is possible to isolate a polynucleotide fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent polypeptide to a particular polypeptide identified in the present Example based on the isolated polynucleotide fragment.

[0047] The present invention also provides a polynucleotide containing at least 15 nucleotides complementary to a polynucleotide comprising a nucleotide sequence of SEQ ID NOs shown in Table 1 or the complementary strand thereof. Herein, the term "complementary strand" is defined as one strand of a double strand DNA composed of A:T and G:C base pair to the other strand. Also, "complementary" is defined as not only those completely matching within a continuous region of at least 15 nucleotides, but also having a identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. The identity may be determined using the algorithm described herein.

[0048] Such a polynucleotide includes probes and primers used for the detection and amplification of a polynucleotide encoding the inventive polypeptide. When used as a primer, the polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, the polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the invention, and comprises at least 15 bp. When used as primers, such polynucleotides are complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

[0049] Furthermore, polynucleotides of the present invention include an antisense polynucleotide for suppressing the expression of a polypeptide of the invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in the gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotide encoding a polypeptide of the invention (for example, the nucleotide sequences of SEQ ID NO: 1 to 2443).

[0050] The polynucleotides or antisense polynucleotides of the present invention can be used in, for example, gene

therapy. As target diseases, for example, cancers or various inflammatory diseases may be preferable. These molecules can be used for gene therapy, for example, by administering them to patients by the *in vivo* or *ex vivo* method using virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-related virus vectors, or non-virus vectors such as liposomes.

[0051] The present invention also includes a partial peptide of the polypeptides of the invention. The partial peptide comprises a polypeptide generated as a result that a signal peptide has been removed from a secretory protein. If the polypeptide of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the polypeptide and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific for the polypeptide of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the polypeptide of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the polypeptide of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the polypeptide of the invention with an appropriate peptidase.

[0052] The present invention also relates to a vector into which a polynucleotide of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the polynucleotide of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0053] Recently, the technique of GATEWAY™ system (Invitrogen), which is an expression vector construction system for polypeptide expression, has been developed (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASE™ and LR CLONASE™) derived from lambda phage and uses BP CLONASE™-specific recombination sites for an Entry Vector and LR CLONASE™-specific recombination sites for a Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

[0054] First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, the secondary recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and highly efficiently. With the above-mentioned typical method using restriction enzyme and ligase reactions, the step of expression vector construction and expression of polypeptide of interest takes about 7 to 10 days. However, with the GATEWAY™ system, the polypeptide of interest can be expressed and prepared in only 3 to 4 days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (<http://biotech.nikkeibp.co.jp/netlink/ito/gateway/>).

[0055] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the polypeptide in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0056] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0057] Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1 or the complementary strand thereof can be used not only as a primer for synthesizing full-length cDNAs but also for testing and diagnosing the abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the polynucleotide of the invention as a primer, polynucleotide encoding the polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or sequencing. Especially, in the case where expression of the mRNA of the present invention varies according to a specific disease, analysis of the amount of expression of the mRNA using the polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of the disease.

[0058] The present invention also relates to antibodies that bind to the polypeptide of the invention. There are no

limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

[0059] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the polypeptide expressed in *E. coli*, immunizing mice with the polypeptide, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0060] The antibody binding to the polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and the polypeptide of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0061] Furthermore, the antibody binding to the polypeptide of the present invention can be utilized for treating the diseases that associates with the polypeptide of the invention. If the antibodies are used for treating patients, human antibodies, humanized antibodies, or chimeric antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0062] A cDNA of the present invention encodes, for example, an amino acid sequence of a protein that is predicted to have the following function. The use of the amino acid sequences of the polypeptides encoded by the cDNAs of the present invention enables predicting that the polypeptides have the following functions. It can be predict, from the results of homology search of SwissProt, GenBank, UniGene, or nr, that these polypeptides have such functions. Specifically, for instance, as shown in Examples, searching for a known gene or polypeptide that is homologous to the partial sequence of the full-length cDNA of the invention (2443 clone) and referring the function of the gene and of the polypeptide encoded by the gene make it possible to predict the function of the polypeptide encoded by the cDNA of the invention. In this way, each of 1216 clones out of the 2443 full-length cDNA clones of the invention was predicted to encode a polypeptide that was classified into the following categories.

- Secretory and/or membrane protein (632 clones)
- Glycoprotein-related protein (128 clones)
- Signal transduction-related protein (84 clones)
- Transcription-related protein (144 clones)
- Disease-related protein (387 clones)
- Enzyme and/or metabolism-related protein (206 clones)
- Cell division- and/or cell proliferation-related protein (33 clones)
- Cytoskeleton-related protein (75 clones)
- Nuclear protein and/or RNA synthesis-related protein (65 clones)
- Protein synthesis- and/or transport-related protein (62 clones)
- Cellular defense-related protein (15 clones)
- Development and/or differentiation-related protein (13 clones)
- DNA- and/or RNA-binding protein (174 clones)
- ATP- and/or GTP-binding protein (68 clones)

[0063] The functions of the polypeptides encoded by the cDNAs of the present invention can be predicted by assessing the presence of signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, and zinc finger motif, SH3 domain, etc. in the amino acid sequences. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Knowledge Industry), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the polypeptide is fused with another polypeptide such as GFP, the fusion polypeptide is transfected into cultured cells, and the localization is analyzed to predict the function of the original polypeptide.

[0064] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the polypeptides encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot, UniGene, and nr for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software pro-

grams such as Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) and PROSITE (<http://www.expasy.ch/prosite/>). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0065] GenBank, Swiss-Prot, UniGene and nr databases were searched for homologies of the full-length nucleotide sequences of the 2443 clones (see Example 6). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of polypeptides encoded by the clones and the categorization thereof were performed based on these results obtained. The categorization was carried out by the following method.

[1] Firstly, the cDNA clones were classified into the above-mentioned 14 functional categories based on the results of annotation-based categorization (using the keywords in the case of Swiss-Prot hit data; using Definition or Reference information in the case of GenBank, UniGene, or nr hit data), and the signal sequence search of the deduced ORFs by PSORT and the transmembrane region search by SOSUI.

[2] Secondly, clones which had been unassignable to the categories by the method of [1] were searched for functional domains and/or motifs by Pfam. Based on the results, the clones were additionally classified into the above-mentioned 14 types of categories when they had a functional domain and/or motif assignable to any one of the categories.

[0066] The following 632 clones presumably belong to secretory and/or membrane proteins.

ADIPS10000640, ADRGL10001470, ADRGL20013520, ADRGL20018540, ADRGL20035850, ASTRO20001410, ASTRO20005330, ASTRO20033160, ASTRO20055750, ASTRO20058630, ASTRO20190390, BEAST20004540, BGGI110000240, BNGH420088500, BRACE20006400, BRACE20038000, BRACE20038470, BRACE20039040, BRACE20039540, BRACE20051380, BRACE20053630, BRACE20059370, BRACE20060550, BRACE20061050, BRACE20063530, BRACE20067430, BRACE20069090, BRACE20081720, BRACE20101700, BRACE20101710, BRACE20116110, BRACE20147800, BRACE20153680, BRACE20163350, BRACE20179340, BRACE20188470, BRACE20195100, BRACE20201570, BRACE20210140, BRACE20224480, BRACE20224500, BRACE20228480, BRACE20232340, BRACE20238000, BRACE20273890, BRACE20274080, BRALZ20013500, BRALZ20054710, BRALZ20054740, BRALZ20069760, BRALZ20073760, BRALZ20077930, BRAMY20000860, BRAMY20002770, BRAMY20025840, BRAMY20039260, BRAMY20060920, BRAMY20063970, BRAMY20111960, BRAMY20112800, BRAMY20124260, BRAMY20134140, BRAMY20135900, BRAMY20136210, BRAMY20144620, BRAMY20152110, BRAMY20174550, BRAMY20181220, BRAMY20195090, BRAMY20211390, BRAMY20211420, BRAMY20215230, BRAMY20218250, BRAMY20218670, BRAMY20229800, BRAMY20231720, BRAMY20247280, BRAMY20252180, BRAMY20273960, BRAMY20277170, BRAMY20284910, BRAMY20285160, BRAWH20015350, BRAWH20015890, BRAWH20016860, BRAWH20018730, BRAWH20030250, BRAWH20064050, BRAWH20110790, BRAWH20112940, BRAWH20117950, BRAWH20118230, BRAWH20121640, BRAWH20122580, BRAWH20132190, BRCAN20064010, BRCAN20071190, BRCAN20091560, BRCAN20103740, BRCAN20224720, BRCAN20273550, BRCAN20280360, BRCAN20285450, BRCOC10000870, BRCOC20004040, BRCOC20006370, BRCOC20041750, BRCOC20077690, BRCOC20078640, BRCOC20090520, BRCOC20101230, BRCOC20107300, BRCOC20114180, BRCOC20121720, BRCOC20134480, BRCOC20136750, BRHIP10001290, BRHIP20000870, BRHIP20003120, BRHIP20103090, BRHIP20111200, BRHIP20118380, BRHIP20118910, BRHIP20121410, BRHIP20135100, BRHIP20174040, BRHIP20179200, BRHIP20183690, BRHIP20191490, BRHIP20191770, BRHIP20198190, BRHIP20207430, BRHIP20208270, BRHIP20208590, BRHIP20217620, BRHIP20233090, BRHIP20234380, BRHIP20238880, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20043040, BRSSN20066110, BRSSN20120810, BRSSN20137020, BRSSN20142940, BRSSN20146100, BRSSN20151990, BRSSN20169050, BRSTN20002200, BRTHA20004740, BRTHA20046290, BRTHA20046420, COLON10001350, COLON20093370, CTONG10000100, CTONG10000940, CTONG10001650, CTONG20004690, CTONG20009770, CTONG20092570, CTONG20092580, CTONG20095340, CTONG20099380, CTONG20103480, CTONG20105080, CTONG20114740, CTONG20119200, CTONG20120770, CTONG20124730, CTONG20131490, CTONG20132220, CTONG20133480, CTONG20139340, CTONG20149950, CTONG20155400, CTONG20158660, CTONG20159530, CTONG20161850, CTONG20267700, D3OST10001090, D3OST20036070, D3OST20038560, D3OST30002580, D6OST20005070, D9OST20002780, D9OST20015470, D9OST20023970, D9OST20026730, D9OST20035940, D9OST20040180, DFNES20025880, FCBBF10000240, FCBBF10000380, FCBBF10001150, FCBBF10001210, FCBBF10001550, FCBBF10002430, FCBBF10002700, FCBBF10003220, FCBBF10003760, FCBBF10005460, FCBBF10005740, FCBBF20032970, FCBBF20042560, FCBBF20049300, FCBBF20051220, FCBBF30008470, FCBBF30024750, FCBBF30078290, FCBBF30083620, FCBBF30086440, FCBBF30090690, FCBBF30095260, FCBBF30123470, FCBBF30172550.

EP 1 347 046 A1

FCBBF30175310, FCBBF30190850, FCBBF30215060, FCBBF30238870, FCBBF30251420, FCBBF30279030,
FEBRA20002100, FEBRA20004620, FEBRA20009090, FEBRA20029860, FEBRA20037260, FEBRA20080810,
FEBRA20086620, FEBRA20092890, FEBRA20093520, FEBRA20095880, FEBRA20111460, FEBRA20125070,
FEBRA20130190, FEBRA20140100, FEBRA20145780, FEBRA20211710, FEBRA20223220, FEBRA20229630,
5 FEBRA20235500, HCHON20000380, HCHON20008180, HCHON20015980, HCHON20016040, HCHON20016650,
HCHON20040020, HCHON20064590, HCHON20067700, HCHON20068710, HCHON20086720, HCHON20100740,
HEART20003060, HEART20005410, HEART20034320, HEART20049410, HEART20049800, HEART20072310,
HHDPC20001040, HHDPC20014320, HHDPC20034720, HHDPC20068620, HHDPC20084140, HHDPC20091780,
HHDPC20092080, HLUNG10000550, KIDNE20003940, KIDNE20007770, KIDNE20011400, KIDNE20021910,
10 KIDNE20022620, KIDNE20100070, KIDNE20101510, KIDNE20109730, KIDNE20121880, KIDNE20125630,
KIDNE20126010, KIDNE20126130, KIDNE20127450, KIDNE20130450, KIDNE20131580, KIDNE20137340,
KIDNE20181660, LIVER20035110, LIVER20045650, LIVER20055200, LIVER20062510, LIVER20064690,
LIVER20075680, LIVER20087060, LIVER20091180, MESAN10001260, MESAN20014500, MESAN20027090,
MESAN20038510, MESAN20089360, MESAN20103120, MESAN20115970, MESAN20125860, MESAN20139360,
15 MESAN20152770, MESAN20153910, MESAN20174170, NOVAR20000380, NT2NE20010050, NT2NE20021620,
NT2NE20068130, NT2NE20118960, NT2NE20124480, NT2NE20131890, NT2NE20132170, NT2NE20155110,
NT2NE20156260, NT2NE20157470, NT2NE20159740, NT2NE20177520, NT2NE20183760, NT2RI20003480,
NT2RI20023910, NT2RI20025400, NT2RI20028470, NT2RI20040930, NT2RI20054050, NT2RI20056700,
NT2RI20076290, NT2RI20086220, NT2RI20091940, NT2RI20244600, NT2RP70072690, NT2RP70081610,
20 NT2RP70122910, NT2RP70125160, NT2RP70133740, NT2RP70134990, NT2RP70137290, NT2RP70179710,
NT2RP70188020, NT2RP70192730, NT2RP70198350, NTONG20028070, NTONG20029700, NTONG20048060,
NTONG20049910, NTONG20051530, NTONG20061870, NTONG20063010, NTONG20067830, NTONG20076930,
KTONG20092330, OCBBF10001750, OCBBF20013890, OCBBF20019830, OCBBF20023570, OCBBF20026630,
OCBBF20046690, OCBBF20050770, OCBBF20059560, OCBBF20063320, OCBBF20071210, OCBBF20072320,
25 OCBBF20080350, OCBBF20086400, OCBBF20086910, OCBBF20087010, OCBBF20088140, OCBBF20091150,
OCBBF20107090, OCBBF20108630, OCBBF20116850, OCBBF20120390, OCBBF20122620, OCBBF20130910,
OCBBF20132350, OCBBF20145760, OCBBF20155060, OCBBF20178880, OCBBF20180120, OCBBF20180840,
OCBBF20188730, PANCR10000910, PEBLM10000710, PEBLM20024320, PEBLM20040150, PEBLM20074370,
PERM20075980, PERIC20004220, PLACE60086400, PLACE60121080, PLACE60161600, PLACE60177140,
30 PROST20005050, PROST20050670, PROST20107820, PROST20116600, PROST20120160, PROST20127800,
PROST20146310, PROST20164440, PROST20169800, PROST20170980, PROST20175290, PUAEN20003740,
PUAEN20030180, SALGL10001710, SKMUS20003610, SKMUS20007800, SKMUS20011640, SKMUS20020840,
SKNSH20028210, SKMUS20028400, SKMUS20077400, SKNSH20028660, SKNSH20031740, SKNSH20051940,
SKNSH20063340, SMINT20009840, SMINT20011990, SMINT20022020, SMINT20029760, SMINT20040860,
35 SMINT20050750, SMINT20053870, SMINT20073650, SMINT20095050, SMINT20100680, SMINT20105330,
SMINT20106720, SMINT20121950, SMINT20127930, SMINT20144430, SMINT20144890, SMINT20153260,
SMINT20154540, SMINT20157450, SMINT20173240, SMINT20178550, SMINT20191420, SMINT20192000,
SPLEN200033070, SPLEN20021660, SPLEN20029310, SPLEN20079510, SPLEN20095810, SPLEN20097330,
SPLEN20118300, SPLEN20141360, SPLEN20141990, SPLEN20142100, SPLEN20144520, SPLEN20152760,
40 SPLEN20157880, SPLEN20165310, SPLEN20167200, SPLEN20169220, SPLEN20169720, SPLEN20171890,
SPLEN20172120, SPLEN20179810, SPLEN20186430, SPLEN20211570, SPLEN20211940, SPLEN20213830,
SPLEN20273950, SPLEN20292950, SPLEN20293800, SPLEN20304950, SPLEN20329240, STOMA20005390,
STOMA20005670, STOMA20006400, STOMA20006780, STOMA20008880, STOMA20051200, STOMA20056640,
STOMA20056670, STOMA20062130, STOMA20077450, STOMA20080500, STOMA20088380, STOMA20092530,
45 SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790, SYNOV20002970, SYNOV20004260,
SYNOV20007300, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000,
SYNOV20013560, SYNOV20013900, SYNOV20001840, TBAES20003150, TESOP20004000, TESOP20005690,
TESTI20001720, TESTI20036380, TESTI20037560, TESTI20094120, TESTI20110280, TESTI20123080,
TESTI20123560, TESTI20128350, TESTI20136100, TESTI20136710, TESTI20143390, TESTI20148000,
50 TESTI20164100, TESTI20193360, TESTI20209810, TESTI20209990, TESTI20211220, TESTI20214250,
TESTI20216370, TESTI20230250, TESTI20231940, TESTI20242990, TESTI20244190, TESTI20254220,
TESTI20254860, TESTI20265970, TESTI20271850, TESTI20272960, TESTI20284880, TESTI20291310,
TESTI20291960, TESTI20303220, TESTI20303360, TESTI20303420, TESTI20307700, TESTI20309170,
TESTI20314180, TESTI20316870, TESTI20333000, TESTI20335200, TESTI20347180, TESTI20347300,
55 TESTI20352620, TESTI20357960, TESTI20370810, TESTI20373820, TESTI20383880, TESTI20390260,
TESTI20390410, TESTI20391770, TESTI20393530, TESTI20396130, TESTI20397760, TESTI20401020,
TESTI20401280, TESTI20415170, TESTI20421490, TESTI20422640, TESTI20441940, TESTI20442760,
TESTI20444130, TESTI20444180, TESTI20449200, TESTI20463520, TESTI20463580, TESTI20465350,

THYMU10005360, THYMU10005540, THYMU20027560, THYMU20032870, THYMU20039810, THYMU20066100,
 THYMU20081490, THYMU20100410, THYMU20106710, THYMU20111830, THYMU20141670, THYMU20147770,
 THYMU20159430, THYMU20161640, THYMU20162190, THYMU20173980, THYMU20194420, THYMU20208300,
 THYMU20216840, THYMU20222890, THYMU20229220, THYMU20241850, THYMU20277390, TKIDN20005210,
 5 TRACH20002870, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20029540, TRACH20033230,
 TRACH20034840, TRACH20042920, TRACH20050040, TRACH20067620, TRACH20068660, TRACH20069180,
 TRACH20076740, TRACH20085400, TRACH20085830, TRACH20109650, TRACH20111130, TRACH20121380,
 TRACH20128110, TRACH20128230, TRACH20134950, TRACH20136710, TRACH20139820, TRACH20140820,
 TRACH20145440, TRACH20168350, TRACH20180840, TRACH20190240, UMVEN20000690, UTERU20030570,
 10 UTERU20040610, UTERU20046980, UTERU20055480, UTERU20064860, UTERU20076390, UTERU20094350,
 UTERU20135860, UTERU20144640, UTERU20158300, UTERU20158800, UTERU20161570, UTERU20178100,
 UTERU20183640, UTERU20186740

[0067] The following 128 clones presumably belong to glycoprotein-related proteins.

ADIPS10000640, BRACE20059370, BRACE20163350, BRAMY20277170, BRAMY20285160, BRAWH20064050,
 15 BRAWH20112940, BRAWH20117950, BRAWH20118230, BRCAN20103740, BRCOC20004040, BRCOC20006370,
 BRHIP10001290, BRHIP20103090, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20146100,
 BRTHA20046290, COLON10001350, CTONG20159530, D9OST20023970, D9OST20040180, FCBBF10001150,
 FCBBF20049300, FCBBF30024750, FCBBF30083620, FCBBF30190850, FCBBF30238870, FEBRA20086620,
 FEBRA20092890, HCHON20015980, HCHON20016040, HCHON20064590, HCHON20086720, HCHON20100740,
 20 HEART20003060, HHDP20014320, HHDP20068620, HHDP20092080, KIDNE20003940, KIDNE20007770,
 KIDNE20101510, LIVER20064690, MESAN20125860, NT2NE20118960, NT2NE20157470, NT2NE20177520,
 NT2RI20003480, NT2RI20056700, NT2RP70192730, NTONG20051530, NTONG20076930, OCBBF20107090,
 OCBBF20108630, OCBBF20120390, OCBBF20145760, OCBBF20155060, PLACE60177140, SMINT20050750,
 SMINT20073650, SMINT20105330, SMINT20106720, SMINT20112730, SMINT20127930, SMINT20153260,
 25 SMINT20179740, SMINT20190170, SPLEN20021660, SPLEN20142100, SPLEN20157880, SPLEN20165310,
 SPLEN20179810, SPLEN20186430, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400,
 STOMA20008880, STOMA20034770, STOMA20056640, STOMA20056670, STOMA20083610, STOMA20088380,
 STOMA20092530, SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790, SYNOV20002970,
 SYNOV20004260, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110,
 30 SYNOV20013000, SYNOV20013560, SYNOV20013900, TESOP20004000, TESTI20136100, TESTI20216370,
 TESTI20244190, TESTI20254860, TESTI20303220, TESTI20335200, TESTI20352620, TESTI20358980,
 TESTI20442760, TESTI20449200, TESTI20455090, THYMU10005360, THYMU10005540, THYMU20147770,
 THYMU20159430, THYMU20241850, TRACH20016210, TRACH20050040, TRACH20067620, TRACH20069180,
 TRACH20076740, TRACH20128230, UTERU20046980, UTERU20064860, UTERU20144640, UTERU20158800,
 35 UTERU20161570, UTERU20183640

[0068] The following 84 clones presumably belong to signal transduction-related proteins.

ASTRO20108190, BRACE20115920, BRACE20154120, BRACE20177200, BRACE20237270, BRAMY20104640,
 BRAMY20242470, BRAMY20271400, BRAWH20016620, BRAWH20103290, BRAWH20149340, BRCOC20021550,
 40 BRCOC20091960, BRHIP20189980, BRHIP20218580, BRHIP20238600, BRSSN20038200, CD34C30004240,
 CTONG20118150, CTONG20127450, CTONG20200310, FCBBF30012350, FCBBF40001730, FEBRA10001880,
 FEBRA20004620, FEBRA20132740, FEBRA20144170, FEHRT20003250, HCHON20007510, HLUNG20033780,
 IMR3220002430, KIDNE20008010, KIDNE20102710, KIDNE20107620, NT2NE20080170, NT2NE20181650,
 NT2RP70027380, NT2RP70036880, NT2RP70063950, NT2RP70078420, NT2RP70159960, NTONG20046140,
 NTONG20056570, OCBBF20028050, OCBBF20053430, OCBBF20054760, OCBBF20124360, OCBBF20127140,
 45 OCBBF20149280, OCBBF20173980, PEBLM20013120, PEBLM20085760, PROST20161950, PUAEN20015260,
 PUAEN20015860, PUAEN20083140, SMINT20028820, SMINT20049090, SMINT20110660, SMINT20011410,
 SPLEN20121750, SPLEN20170310, SPLEN20181810, SPLEN20222270, SPLEN20250170, SPLEN20283650,
 TESTI20035960, TESTI20288910, TESTI20305540, TESTI20326810, TESTI20369650, TESTI20392250,
 TESTI20416640, TESTI20432750, TESTI20467320, THYMU20169680, THYMU20172150, THYMU20201980,
 50 THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20057690, UMVEN10001860, UTERU20146310

[0069] The following 144 clones presumably belong to transcription-related proteins.

3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890,
 BRACE20060890, BRACE20068590, BRACE20257100, BRAMY20210400, BRAMY20260910, BRAMY20270730,
 BRAWH20028110, BRAWH20075700, BRAWH20096780, BRCAN20280210, BRCOC20144000, BRCOC20178270,
 55 BRHIP20005340, BRHIP20096170, BRHIP20119330, BRHIP20191860, BRHIP20195890, BRHIP20222280,
 BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950,
 CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20133390, CTONG20133520,
 D9OST20033970, FCBBF10001710, FCBBF20059090, FCBBF20068820, FCBBF30007680,

EP 1 347 046 A1

FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630, FCBBF30240960, FCBBF30246230, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20171380, FEBRA20195820, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130, HHDP20000830, HHDP20030490, HHDP20031130, KIDNE20027250, KIDNE20027950, KIDNE20182690, LIVER20055440, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900, NT2RP60000770, NT2RP70043480, NT2RP70063950, NT2RP70102350, NT2RP70157890, NTONG20070200, OCBBF10001850, OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20054200, OCBBF20066390, OCBBF20071840, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280, PEBLM20060360, PEBLM20078320, PERIC20003870, PROST10003220, PROST20047390, PROST20066880, PROST20185830, PROST20189770, PROST20191640, SKNSH20008190, SMINT20001760, SMINT20028820, SMINT20130320, SMINT20144800, SPLEN20026950, SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20117660, SPLEN20140800, SPLEN20147390, SPLEN20160450, SPLEN20162680, SPLEN20243830, SPLEN20250170, SPLEN20252190, SPLEN20267650, STOMA20032890, STOMA20063250, TESTI20039400, TESTI20041690, TESTI20067200, TESTI20088220, TESTI20130010, TESTI20156100, TESTI20230850, TESTI20318090, TESTI20320670, TESTI20378190, TESTI20385960, TESTI20409890, TESTI20420620, TESTI20432820, TESTI20456110, THYMU20247480, TRACH20079690, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130

[0070] The following 387 clones presumably belong to disease-related proteins.

ADIPS20004250, ADRGL10001470, ADRGL20011190, ADRGL20018300, ADRGL20035850, ADRGL20078100, ASTRO10001650, ASTRO20008010, ASTRO20027430, ASTRO20106150, ASTRO20108190, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20038480, BRACE20039540, BRACE20059370, BRACE20108130, BRACE20108880, BRACE20115920, BRACE20116460, BRACE20232840, BRACE20248260, BRACE20253330, BRACE20284100, BRALZ20013500, BRALZ20017430, BRALZ20018340, BRAMY20000520, BRAMY20025840, BRAMY20120910, BRAMY20134140, BRAMY20135900, BRAMY20162510, BRAMY20174550, BRAMY20210400, BRAMY20211390, BRAMY20242470, BRAMY20245300, BRAMY20266850, BRAMY20285160, BRAWH20016620, BRAWH20028110, BRAWH20064050, BRAWH20096780, BRAWH20110960, BRAWH20113430, BRAWH20114000, BRAWH20118230, BRAWH20121640, BRAWH20128270, BRAWH20137480, BRCAN20103740, BRCAN20224720, BRCAN20279700, BRCAN20280210, BRCAN20283190, BRCOC20001860, BRCOC20006370, BRCOC20027510, BRCOC20055420, BRCOC20099370, BRCOC20178270, BRCOC20178560, BRHIP20003120, BRHIP20005340, BRHIP20174040, BRHIP20176420, BRHIP20191490, BRHIP20191860, BRHIP20194940, BRHIP20195890, BRHIP20222280, BRHIP20249110, BRHIP20285930, BRHIP30004880, BRSSN20013420, BRSSN20038200, BRSSN20039370, BRSSN20046790, BRSSN20066110, BRSSN20101100, BRSSN20120810, BRSSN20187310, BRTHA20046290, CD34C20004240, COLON10001350, CTONG20004690, CTONG20052650, CTONG20099550, CTONG20124220, CTONG20125640, CTONG20128430, CTONG20131560, CTONG20133390, CTONG20153300, CTONG20153580, CTONG20158040, CTONG20159530, D6OST20003580, D9OST20023970, DFNES20001530, DFNES20037420, FCBBF10001210, FCBBF10001710, FCBBF10003770, FCBBF20059090, FCBBF20064520, FCBBF20068820, FCBBF30010810, FCBBF30024750, FCBBF30025560, FCBBF30039020, FCBBF30049550, FCBBF30057290, FCBBF30083620, FCBBF30129630, FCBBF30190850, FCBBF30238870, FCBBF30240960, FCBBF30243640, FCBBF30279030, FCBBF30281880, FCBBF40001730, FEBRA10001880, FEBRA20004620, FEBRA20010120, FEBRA20018690, FEBRA20082010, FEBRA20097310, FEBRA20130190, FEBRA20132740, FEBRA20144170, FEBRA20195820, FEBRA20223220, FEBRA20233770, FEBRA20235500, FEHRT20003250, HCHON10001760, HCHON20007380, HCHON20008320, HCHON20009560, HCHON20015230, HCHON20015980, HCHON20016040, HCHON20035130, HCHON20036420, HCHON20064590, HCHON20067700, HCHON20086720, HCHON20100740, HEART20003060, HEART20017730, HEART20025980, HEART20049410, HHDP20014320, HHDP20030490, HHDP20084140, HHDP20091140, HHDP20091780, HHDP20092080, HLUNG20033780, IMR3220002430, KIDNE20007770, KIDNE20020150, KIDNE20021680, KIDNE20022620, KIDNE20024830, KIDNE20027950, KIDNE20101370, KIDNE20101510, KIDNE20182690, LIVER20002160, LIVER20055200, LIVER20055440, LIVER20059810, LIVER20064690, MESAN20101140, MESAN20125860, MESAN20130220, MESAN20154010, MESAN20174170, NOVAR10000910, NT2NE20010490, NT2NE20118960, NT2NE20157470, NT2RI20040990, NT2RI20041880, NT2RI20048840, NT2RI20050960, NT2RI20240080, NT2RP60000770, NT2RP70027380, NT2RP70032610, NT2RP70037240, NT2RP70192730, NT2RP70198350, NTONG20013620, NTONG20015870, NTONG20028070, NTONG20067830, NTONG20070200, NTONG20090600, NTONG20092330, OCBBF20006770, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20053490, OCBBF20053730, OCBBF20054760, OCBBF20071840, OCBBF20072240, OCBBF20078920, OCBBF20108430, OCBBF20108580, OCBBF20127140, OCBBF20129360, OCBBF20145760, OCBBF20153350, OCBBF20173980, OCBBF20178880, PEBLM10000710, PEBLM20013120, PERIC10000250, PLACE60060420, PLACE60177140, PROST20100460, PROST20159240, PROST20169800, PROST20176170, PUAEN20018820, PUAEN20030180, PUAEN20055020, PUAEN20083140, SKMUS20018230, SKMUS20018500, SKMUS20021530, SKMUS20024750, SKMUS20029200,

EP 1 347 046 A1

SKMUS20048970, SKMUS20049030, SKNSH20008190, SKNSH20089400, SMINT20001760, SMINT20026890, SMINT20028820, SMINT20050750, SMINT20073650, SMINT20105330, SMINT20112730, SMINT20121220, SMINT20127350, SMINT20127930, SMINT20136130, SMINT20138900, SMINT20153260, SMINT20155180, SMINT20179740, SMINT20190170, SMINT20191420, SPLEN20006070, SPLEN20011410, SPLEN20026950, 5 SPLEN20027440, SPLEN20039240, SPLEN20079260, SPLEN20095410, SPLEN20146450, SPLEN20147390, SPLEN20151210, SPLEN20160450, SPLEN20170310, SPLEN20179180, SPLEN20186430, SPLEN20212730, SPLEN20243830, SPLEN20245300, SPLEN20250390, SPLEN20252190, SPLEN20267650, SPLEN20305620, STOMA20001830, STOMA20005390, STOMA20008880, STOMA20010250, STOMA20034770, STOMA20046680, STOMA20056670, STOMA20064470, STOMA20077450, STOMA20080500, STOMA20083610, STOMA20088380, 10 SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, TBAES20003770, TESOP20004000, TESOP20005270, TESTI20031270, TESTI20036380, TESTI20044310, TESTI20067200, TESTI20116830, TESTI20121550, TESTI20156100, TESTI20168480, TESTI20208400, TESTI20215990, TESTI20231940, TESTI20234360, TESTI20237520, TESTI20238610, TESTI20239510, TESTI20249990, TESTI20266740, TESTI20316870, 15 TESTI20318090, TESTI20335050, TESTI20335200, TESTI20343570, TESTI20352620, TESTI20368330, TESTI20369650, TESTI20385960, TESTI20392250, TESTI20400940, TESTI20404240, TESTI20420620, TESTI20436560, TESTI20438570, TESTI20441940, TESTI20442760, TESTI20443090, TESTI20449200, TESTI20455090, TESTI20455620, TESTI20456110, TESTI20463580, TESTI20465350, TESTI20465690, TESTI20467210, THYMU20122730, THYMU20126900, THYMU20130890, THYMU20159430, THYMU20169680, 20 THYMU20172150, THYMU20180280, THYMU20193640, THYMU20209590, THYMU20232090, THYMU20247480, TKIDN10000010, TKIDN20004640, TKIDN20047480, TRACH20016210, TRACH20019960, TRACH20050040, TRACH20057690, TRACH20067620, TRACH20077540, TRACH20079690, TRACH20096610, TRACH20105870, TRACH20121380, TRACH20154860, TRACH20162860, TRACH20163170, TRACH20164980, TRACH20190240, TSTOM20005590, TUTER20002830, UTERU20030570, UTERU20116570, UTERU20144640, UTERU20151980, 25 UTERU20158800, UTERU20183640, UTERU20185230

[0071] The following 206 clones presumably belong to the category of enzymes and/or metabolism-related proteins.

3N:B6910001910, ADRGL10001470, ADRGL20035850, ADRGL20078100, ASTRO20105820, ASTRO20106150, ASTRO20130500, ASTRO20145760, BRACE20027620, BRACE20038000, BRACE20062640, BRACE20096200, BRACE20107530, BRACE20108130, BRACE20108880, BRACE20116460, BRACE20148240, BRACE20185680, 30 BRACE20253160, BRALZ20017430, BRALZ20018340, BRAMY20104640, BRAMY20134140, BRAMY20153110, BRAMY20213100, BRAWH20016620, BRAWH20105840, BRAWH20112940, BRAWH20114000, BRAWH20117950, BRAWH20125380, BRAWH20132190, BRAWH20171030, BRCAN20054490, BRCAN20224720, BRCAN20280360, BRCAN20283190, BRCAN20283380, BRCOC20001860, BRCOC20031250, BRCOC20055420, BRCOC20091960, BRCOC20144000, BRHIP10001290, BRHIP20005530, BRHIP20096850, BRHIP20103090, 35 BRHIP20174040, BRHIP20249110, BRSSN20013420, BRSSN20015790, BRSSN20120810, BRSSN20146100, CTONG20095340, CTONG20106520, CTONG20118250, CTONG20127450, CTONG20140580, CTONG20153300, CTONG20158040, D3OST20006180, D6OST20003580, DFNES20031920, DFNES20071130, FCBBF10001820, FCBBF10033670, FCBBF30012350, FCBBF30012810, FCBBF30175310, FCBBF30243640, FEBRA10001880, FEBRA20007620, FEBRA20130190, FEBRA20144170, FEBRA20167390, FEBRA20196630, FEHRT20003250, 40 HCHON10001760, HCHON20003220, HCHON20015350, HEART20034320, HEART20090000, HHDPC20014320, KIDNE20002520, KIDNE20008010, KIDNE20021680, KIDNE20022620, KIDNE20028390, KIDNE20028720, KIDNE20107620, LIVER20059810, MESAN20154010, NT2NE20118960, NT2NE20157470, NT2RI20005750, NT2RI20244630, NT2RI20273230, NT2RP70032610, NT2RP70045590, NT2RP70192730, NT2RP70195430, NTONG20009770, NTONG20013620, NTONG20046140, OCBBF20028650, OCBBF20030910, OCBBF20046690, 45 OCBBF20050770, OCBBF20053430, OCBBF20053490, OCBBF20053730, OCBBF20054760, OCBBF20078920, OCBBF20124360, OCBBF20129360, OCBBF20178880, PEBLM20044520, PEBLM20052820, PEBLM20060490, PERIC10000250, PLACE50000660, PROST20083600, PROST20169800, PUAEN20015260, PUAEN20030180, SKMJS200018230, SMINT20028820, SMINT20049090, SMINT20102780, SMINT20105330, SMINT20106290, SMINT20110660, SMINT20152940, SMINT20191420, SMINT20191530, SPLEN20021660, SPLEN20026950, 50 SPLEN20121750, SPLEN20145720, SPLEN20149240, SPLEN20150940, SPLEN20151210, SPLEN20173510, SPLEN20212730, SPLEN20250390, SPLEN20305620, STOMA20006860, STOMA20077450, TBAES20002550, TBAES20003150, TESOP20004000, TESOP20005270, TESTI20001000, TESTI20002720, TESTI20002780, TESTI20060400, TESTI20066670, TESTI20082330, TESTI20083200, TESTI20108720, TESTI20116830, TESTI20143390, TESTI20148000, TESTI20216370, TESTI20232140, TESTI20234360, TESTI20237520, 55 TESTI20239510, TESTI20266740, TESTI20314180, TESTI20334410, TESTI20343570, TESTI20352620, TESTI20355020, TESTI20366910, TESTI20368330, TESTI20369650, TESTI20375340, TESTI20397760, TESTI20416640, TESTI20432750, TESTI20463580, TESTI20465350, TESTI20471410, TESTI20473830, THYMU20023380, THYMU20111830, THYMU20126900, THYMU20169680, THYMU20202890, TKIDN20004640,

EP 1 347 046 A1

TKIDN20047480, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20041830, TRACH20057690, TRACH20067620, TRACH20084720, TRACH20085830, TRACH20162860, UTERU20064860, UTERU20144640, UTERU20146310, UTERU20151980

[0072] The following 33 clones presumably belong to the category of cell division- and/or cell proliferation-related proteins.

BRALZ20077900, BRAMY20135900, BRAWH20002320, BRAWH20128270, BRCAN20071190, BRCAN20273640, BRHIP20096170, CTONG10000940, CTONG20124220, FCBBF30247930, FEBRA20113560, HCASM10000500, HCHON20097490, MESAN20025190, NT2RI20050960, OCBBF20039250, OCBBF20054760, OCBBF20072240, SMINT20051610, SPLEN20147110, SPLEN20284240, TESOP20005690, TESTI20234360, TESTI20305540, TESTI20332420, TESTI20335050, TESTI20368330, TESTI20392760, TESTI20400940, THYMU20161640, TKIDN20047480, UTERU20097760, UTERU20185230

[0073] The following 75 clones presumably belong to the category of cytoskeleton-related proteins.

ADRGL20011190, ADRGL20018300, ASTRO10001650, ASTRO20055750, BRACE20003070, BRACE20059370, BRACE20163350, BRAMY20121620, BRAMY20157820, BRAMY20242470, BRAWH20028110, BRAWH20137480, BRCAN20003460, BRCOC20008160, BRCOC20059510, BRHIP20115080, BRHIP20137230, BRHIP20167880, BRHIP20283030, BRHIP20285830, BRSSN20187310, CTONG10002770, CTONG20052900, CTONG20121580, FCBBF10001150, FCBBF30013770, FCBBF30015940, FCBBF30049550, FEBRA20024100, FEBRA20237640, HCHON20015980, HCHON20068410, HEART20017730, HEART20025980, HEART20061950, HEART20077670, HLUNG20016330, KIDNE20118580, MESAN20004570, NT2RI20040990, NT2RI20041880, NT2RP70037240, NT2RP70062230, NTONG20015870, NTONG20056570, NTONG20067830, NTONG20090600, OCBBF20107090, OCBBF20155060, PLACE60079250, PUEN20040670, SKMUS20001980, SKMUS20016220, SKMUS20048970, SKMUS20049030, SMINT20024570, SMINT20026890, SMINT20121220, SMINT20138900, SPLEN20006070, SPLEN20027440, SPLEN20142100, TESTI20063830, TESTI20094230, TESTI20278400, TESTI20371030, TESTI20417300, TESTI20436560, TESTI20455090, THYMU20105190, THYMU20172150, THYMU20209590, TRACH20096610, UMVEN10001560, UTERU20116570

[0074] The following 65 clones presumably belong to the category of nuclear proteins and/or RNA synthesis-related proteins.

BRACE20057190, BRACE20064880, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20120910, BRAWH20113430, BRAWH20171030, BRCAN10001490, BRCAN20283190, BRCOC20037320, BRCOC20178560, BRHIP20106100, BRHIP20176420, BRHIP20243470, BRSSN20101100, CTONG20114290, CTONG20125540, CTONG20131560, CTONG20140580, DFNES20001530, FCBBF20064520, FEBRA20007620, FEBRA20010120, FEBRA20097310, FEBRA20144170, FEBRA20174410, FEBRA20215500, IMR3220002430, MESAN20101140, NT2RI20273230, OCBBF20028650, OCBBF20030910, OCBBF20078920, PROST20104000, PUEN20018820, SKMUS20007010, SMINT20127350, SMINT20177360, SMINT20191530, SPLEN20008740, SPLEN20146450, STOMA20046680, TESTI20082330, TESTI20094470, TESTI20121550, TESTI20208400, TESTI20234360, TESTI20237520, TESTI20249990, TESTI20334410, TESTI20355020, TESTI20368330, TESTI20392760, TESTI20408970, TESTI20436560, TESTI20438570, TESTI20443090, THYMU20193640, THYMU20202890, THYMU20241210, TRACH20096610, TATER20002830, UTERU20151980, UTERU20176320

[0075] The following 62 clones presumably belong to the category of protein synthesis- and/or protein transport-related proteins.

3NB6910001910, ASTRO20106150, ASTRO20130500, ASTRO20141350, BRACE20038480, BRACE20052160, BRACE20057620, BRACE20106840, BRACE20172980, BRACE20192440, BRAWH20110960, BRCOC20037320, BRHIP20005530, BRSSN20120810, BRSTN20005360, CTONG20009770, CTONG20114290, CTONG20125640, CTONG20153300, D6OST20003580, DFNES20037420, FCBBF30012810, FEBRA20080810, HCHON20064590, HHDPC20014320, HHDPC20084140, HLUNG20017120, LIVER20064690, NT2NE20132170, NT2NE20157470, NT2RP70133740, NTONG20009770, NTONG20075220, NTONG20076930, OCBBF20030910, OCBBF20035930, OCBBF20153340, PLACE60060420, SMINT20152940, SPLEN20008740, SPLEN20103950, SPLEN20118300, SPLEN20212730, SPLEN20250390, STOMA20077450, TBAES20002550, TESOP20004000, TESTI20239510, TESTI20278400, TESTI20314180, TESTI20463580, THYMU20111830, THYMU20122730, THYMU20130890, THYMU20232090, TKIDN10000010, TRACH20084720, TRACH20105870, TRACH20139820, TRACH20149970, UTERU20120310, UTERU20188110

[0076] The following 15 clones presumably belong to the category of cellular defense-related proteins.

BRCOC20144000, CTONG20092680, KIDNE20020150, LIVER20002160, NT2RI20050960, NT2RP70045590, OCBBF20128120, PLACE60003480, SKNSH20089400, SMINT20106290, SPLEN20039240, TESTI20001000, TESTI20455620, TRACH20028030, UTERU20176320

[0077] The following 13 clones presumably belong to the category of development and/or differentiation-related proteins.

3NB6920014590, BRAMY20211390, CTONG20091080, CTONG20121010, FCBBF30024750, KIDNE20027250,

EP 1 347 046 A1

NT2NE20142210, OCBBF20054200, PROST10003220, SKMUS20007010, SPLEN20179810, STOMA20063250, TESTI20291960

[0078] The following 174 clones presumably belong to the category of DNA- and/or RNA-binding proteins.

3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890,
 5 BRACE20057620, BRACE20060890, BRACE20064880, BRACE20068590, BRACE20248260, BRACE20253160,
 BRAMY20000520, BRAMY20213100, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700,
 BRAWH20096780, BRAWH20113430, BRCAN10001490, BRCAN20280210, BRCAN20283190, BRCOC20144000,
 BRCOC20178270, BRCOC20178560, BRHIP20005340, BRHIP20106100, BRHIP20119330, BRHIP20153600,
 10 BRHIP20176420, BRHIP20191860, BRHIP20195890, BRHIP20222280, BRSSN20039370, BRSSN20046790,
 BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950, CTONG20091080, CTONG20092700,
 CTONG20121010, CTONG20124220, CTONG20125540, CTONG20133390, CTONG20133520, CTONG20140580,
 CTONG20156780, D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20064520,
 FCBBF20068820, FCBBF30007680, FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290,
 FCBBF30083820, FCBBF30129630, FCBBF30240960, FCBBF30246230, FEBRA20010120, FEBRA20018690,
 15 FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20097310, FEBRA20171380,
 FEBRA20195820, FEBRA20196630, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130,
 HHDP20000830, HHDP20031130, KIDNE20017130, KIDNE20027250, KIDNE20027950, KIDNE20107390,
 KIDNE20182690, LIVER20055440, MESAN20101140, NT2NE20010490, NT2NE20089970, NT2NE20142210,
 NT2NE20184900, NT2RP60000770, NT2RP70044280, NT2RP70102350, NT2RP70157890, NTONG20070200,
 20 OCBBF10001850, OCBBF20020830, OCBBF20037440, OCBBF20046120, OCBBF20049300, OCBBF20066390,
 OCBBF20071840, OCBBF20078920, OCBBF20080410, OCBBF20108190, OCBBF20125530, OCBBF20148280,
 PEBLM20060360, PEBLM20060490, PEBLM20078320, PERIC10000250, PROST10003220, PROST20047390,
 PROST20066880, PROST20185830, PROST20189770, PROST20191640, PUAEN20018820, SKNSH20008190,
 SKNSH20089400, SMINT20001760, SMINT20127350, SMINT20144800, SMINT20177360, SMINT20191530,
 25 SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20140800, SPLEN20147390, SPLEN20160450,
 SPLEN20252190, SPLEN20267650, STOMA20010250, STOMA20032890, STOMA20046680, STOMA20063250,
 TESTI20039400, TESTI20067200, TESTI20088220, TESTI20094470, TESTI20121550, TESTI20130010,
 TESTI20156100, TESTI20204450, TESTI20230850, TESTI20237520, TESTI20266740, TESTI20318090,
 TESTI20320670, TESTI20334410, TESTI20355020, TESTI20378190, TESTI20385960, TESTI20432820,
 30 TESTI20443090, TESTI20456110, THYMU20193640, THYMU20241210, THYMU20247480, TRACH20079690,
 TRACH20105870, TRACH20139820, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490,
 TATER20002830, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130, UTERU20185230

[0079] The following 68 clones presumably belong to the category of ATP- and/or GTP-binding proteins.

3NB6910001910, BRACE20108130, BRACE20148240, BRAMY20134140, BRAMY20157820, BRAMY20174550,
 35 BRAWH20164460, BRCAN20003460, BRCAN20054490, BRCAN20283190, BRCOC20059510, BRCOC20144000,
 BRHIP20103090, BRHIP20115080, BRHIP20167880, BRSTN20005360, CD34C30004240, CTONG20095340,
 CTONG20121580, CTONG20200310, DFNES20037420, FCBBF20067810, FCBBF30012350, FCBBF30015940,
 FEBRA20007620, FEBRA20024100, FEBRA20144170, KIDNE20020150, KIDNE20028720, LIVER20002160,
 LIVER20087060, NT2RI20005750, NT2RI20041880, NT2RI20048840, NT2RI20273230, OCBBF20028650,
 40 OCBBF20046690, OCBBF20054760, OCBBF20108430, OCBBF20108630, SMINT20121220, SMINT20183530,
 SMINT20191530, SPLEN20026950, SPLEN20039240, SPLEN20099700, SPLEN20145720, SPLEN20179180,
 STOMA20006860, TESTI20035960, TESTI20355020, TESTI20397760, TESTI20400940, TESTI20417300,
 TESTI20443090, TESTI20455620, THYMU20105190, THYMU20202890, THYMU20209590, TKIDN20004640,
 TKIDN20047480, TRACH20005400, TRACH20019960, TRACH20057690, TRACH20084720, UTERU20168220,
 45 UTERU20176320, UTERU20185230

[0080] Among the clones other than the ones shown above, BRAMY20248490, FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, THYMU20279750, TRACH20167220, are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

50 FCBBF10002800, NTONG20092290, OCBBF20127040, SMINT20163960, TESTI20478850, THYMU20279750

[0081] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20060720, BRACE20223330, BRALZ20058880, BRAMY20148130, BRAWH20101360, BRCAN20124080,
 BRHIP20253660, CTONG10000620, CTONG20014280, CTONG20124010, KIDNE20109890, MESAN20171520,
 55 OCBBF20109310, OCBBF20140640, PROST20079500, PUAEN20078980, SPLEN20077500, SPLEN20143180,
 TESTI20017950, TESTI20184620, TESTI20208710, TESTI20211160, TESTI20226230, TESTI20234140,
 TESTI20258460, TESTI20275030

[0082] The 26 clones shown above are clones which were predicted to highly possibly belong to the category of

EP 1 347 046 A1

signal transduction-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRALZ20058880, BRHIP20207990, CTONG20093950, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, KIDNE20109890, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, NT2NE20130190, PEBLM20060310, PERIC20004780, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, TESTI20023510, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, UTERU20050690

[0083] The 36 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BGGI120006160, BRACE20053480, BRACE20190040, BRACE20223330, BRAWH20101360, BRAWH20185060, BRCOC20023230, BRHIP20252450, BRSSN20105870, BRSSN20117990, BRTHA20000570, CTONG20098440, CTONG20129960, CTONG20146300, CTONG20155180, FEBRA20025270, HEART20083640, KIDNE20009470, LIVER20035680, MESAN20029400, MESAN20031900, MESAN20186700, NOVARI10000150, NTONG20029480, OCBBF20079310, OCBBF20082830, PEBLM20042900, PLACE60136500, PLACE60136720, PROST20114390, SKNSH20020540, SMINT20013480, SMINT20174360, SPLEN20077500, SPLEN20119810, SPLEN20126190, SPLEN20174260, SPLEN20211220, TESTI20046750, TESTI20057750, TESTI20061110, TESTI20197940, TESTI20211160, TESTI20226230, TESTI20255820, TESTI20317600, TESTI20377230, THYMU20111180, THYMU20115850, THYMU20143270, THYMU20240710, UTERU20055330, UTERU20055930, UTERU20064000, UTERU20119060

[0084] The 55 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

TESTI20127760, TESTI20392270

[0085] The 2 clone shown above is a clone which was predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

FCBBF30262510, MESAN20031900, NT2NE20125050, SMINT20068010, SPLEN20163560, STOMA20092890, TESTI20382750

[0086] The 7 clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

THYMU20118520

[0087] The clone shown above is clone which was predicted to highly possibly belong to the category of Nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

BRACE20053480, BRACE20240740, KIDNE20009470, OCBBF20140890, SMINT20035690, UTERU20064000

[0088] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of Protein synthesis- and/or transport-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRACE20190040, BRACE20223330, BRALZ20058880, BRAMY20103570, BRCOC20023230, BRHIP20207990, BRTHA20000570, CTONG20093950, CTONG20129960, CTONG20146300, CTONG20155180, CTONG20160560, FCBBF10004120, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, HCHON20008150, HEART20083640, KIDNE20109890, LIVER20035680, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, MESAN20186700, NT2NE20130190, NT2RI20025640, NTONG20029480, PEBLM20060310, PERIC20004780, PROST20114390, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, SPLEN20119810, TESTI20023510, TESTI20057750, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, THYMU20115850, UTERU20050690, UTERU20055330

[0089] The 57 clones shown above are clones which were predicted to highly possibly belong to the category of DNA- and/or RNA-binding protein based on the result of domain search by Pfam.

PLACE60136720

[0090] The clone shown above is a clone which was predicted to highly possibly belong to the category of ATP- and/or GTP-binding proteins based on the result of domain search by Pfam.

[0091] The 213 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search using their full-length nucleotide sequences and motif search in their estimated ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (/), are shown below.

ADRGL20028570//Rattus norvegicus MG87 mRNA, complete cds.
ADRGL20061930//transposon-derived Buster1 transposase-like protein
ASTRO20012490//Eukaryotic initiation factor 1A
ASTRO20072210//PERIAXIN.

EP 1 347 046 A1

ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds.
 ASTRO20125520//dnaj protein [Schizosaccharomyces pombe]
 ASTRO20143630//KH domain// Bacterial regulatory proteins, crp family
 ASTRO20155290//TPR Domain// TPR Domain// TPR Domain
 5 ASTRO20181690//oocyte-specific protein P100
 BGGI110001930//UBX domain
 BRACE20011070//Mus musculus F-box protein FBX15 mRNA, partial cds.
 BRACE20039440//Drosophila melanogaster CHARYBDE (charybde) mRNA, complete cds.
 BRACE20050900//TPR Domain// TPR Domain// TPR Domain// TPR Domain
 10 BRACE20053280//Mus musculus Pdz-containing protein (Pdzx) mRNA, complete cds.
 BRACE20057730//toxin sensitivity protein KT112 homolog
 BRACE20058580//Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds.
 BRACE20063780//NOL1/NOP2/sun family
 BRACE20269200//Heat-labile enterotoxin alpha chain
 15 BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
 BRACE20286360//Alpha adaptin carboxyl-terminal domain
 BRAMY10001300//Homo sapiens MAG-E1b mRNA, complete cds.
 BRAMY20045240//Flagellar L-ring protein
 BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.
 20 BRAMY20167060//Collagen triple helix repeat (20 copies)
 BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds.
 BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete
 cds, alternatively spliced.
 BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds.
 25 BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, com-
 plete cds.
 BRAWH20004600//Mus musculus mRNA for NAKAP95, complete cds.
 BRAWH20011710//cytoplasmic linker 2
 BRAWH20012390//Trichomonas vaginalis mRNA for centrin (ce1 gene).
 30 BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds.
 BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds.
 BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds.
 BRCOC20008500//Human ras inhibitor mRNA, 3' end.
 BRCOC20026640//Gag P30 core shell protein
 35 BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION FACTOR L SUBU-
 NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E).
 BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT).
 BRCOC20110100//Integrase core domain
 BRCOC20176520//Rattus norvegicus mRNA for type II brain 4.1, complete cds.
 40 BRHIP20001630//Protein of unknown function DUF16
 BRHIP20132860//Homo sapiens raphilin-like protein mRNA, complete cds.
 BRHIP20143730//MYND finger
 BRHIP20175420//Mus musculus partial mRNA for stretch responsive protein 278 (sr278 gene).
 BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin)
 45 BRSSN20014260//RIBONUCLEASE INHIBITOR.
 BRSSN20018690//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
 BRSSN20021600//RING CANAL PROTEIN (KELCH PROTEIN).
 BRSSN20177570//Phosducin
 BRSTN10000830//Kelch motif// Kelch motif// Kelch motif
 50 CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
 CTONG10000930//Armadillo/beta-catenin-like repeats
 CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat
 CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A).
 CTONG20096750//Disintegrin
 55 CTONG20100240//Mus musculus radial spokehead-L protein (Rshl1) mRNA, complete cds.
 CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.
 CTONG20143690//MYND finger
 CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN).

EP 1 347 046 A1

CTONG20165050//Keratin, high sulfur B2 protein
CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN).
D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC).
D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds.
5 D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene).
DFNES20014040//TRICHOHYALIN.
FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds.
FCBBF10000770//Homo sapiens REC8 mRNA, partial cds.
FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
10 FCBBF10005500//Keratin, high sulfur B2 protein
FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-
DOZEPINE) (EP).
FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds.
FCBBF30016320//SecA protein, amino terminal region
15 FCBBF30033050//Sm protein
FCBBF30054440//PLAT/LH2 domain
FCBBF30225660//Ank repeat// Ank repeat// Ank repeat// K+ channel tetramerisation domain// BTB/POZ domain
FCBBF30233680//G10 protein
FCBBF30246630//H.sapiens mRNA for ZYG homologue.
20 FCBBF30250730//TRICHOHYALIN.
FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds.
FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING
AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN
CAP43).
25 FCBBF30252850//Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA, complete
cds.
FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family
FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE
CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-
PHA C SUBUNIT).
30 FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds.
FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
35 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
FEBRA20225040//high-glucose-regulated protein 8
HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4.
HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.
HCHON20010990//TPR Domain
40 HCHON20059870//Hypothetical protein.
HHDPC20034390//Cereal trypsin/alpha-amylase inhibito
HHDPC20057420//Mus musculus proline-rich protein (Bprp) mRNA, complete cds.
HHDPC20064600//SUPPRESSOR PROTEIN SRP40.
HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds.
45 KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene).
KIDNE20028830//K-box region
KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds.
KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds.
KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds.
50 KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (TTS-2.1 gene).
KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds.
LIVER10004790//EF hand
LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds.
LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds.
55 LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds.
MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds.
MESAN20036460//Corticotropin-releasing factor family
MESAN20127350//mvelin expression factor-3

EP 1 347 046 A1

MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Docl) mRNA, complete cds.

NT2NE20010400//Homo sapiens GL013 mRNA, complete cds.

NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN.

5 NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803).

NT2RI20001330//Homo sapiens KE03 protein mRNA, partial cds.

NT2RI20009870//lunatic fringe precursor [Mus musculus]

NT2RI20046080//recA bacterial DNA recombination proteins

NT2RI20091730//Molluscan rhodopsin C-terminal tail

10 NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds.

NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an

NT2RP70105210//Myc amino-terminal region

NT2RP70188710//Yeast PIR proteins

NT2RP70194450//Bacterial regulatory proteins, crp family

15 NTONG20052650//Gallus gallus Xin mRNA, complete cds.

NTONG20064400//REPETIN.

NTONG20064840//Mus musculus s1p1 mRNA for synaptotagmin-like protein 1, complete cds.

NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds.

NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds.

20 NTONG20070340//collagen alpha 1(IX) chain

NTONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR Domain

NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds.

OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds.

25 OCBBF20019380//seizure related gene 6

OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds.

OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds.

OCBBF20046470//ARFAPTIN 1.

OCBBF20049840//Homo sapiens mRNA for neurabin II protein.

30 OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds.

OCBBF20071960//Coturnix coturnix japonica qMEF2D gene.

OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds.

OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN).

OCBBF20127550//Outer Capsid protein VP4 (Hemagglutinin)

35 OCBBF20148730//RING CANAL PROTEIN (KELCH PROTEIN).

OCBBF20178150//Plasmodium falciparum ADA2-like protein gene, partial cds.

PEBLM10000240//Domain found in Dishevelled, Eg1-10 and Ple

PROST20047270//CRAL/TRIO domain.

PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif)

40 PUAEN10000850//Uncharacterized protein family UPF0025// SecI family

PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds.

PUAEN20051100//Mus musculus otogelin mRNA, complete cds.

PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds.

SKMUS20084740//Syndecan domain

45 SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.

SMINT20071400//NOL1/NOP2/sun family

SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds.

SMINT20110330//pKID domain

SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds.

50 SMINT20131810//ENV polyprotein (coat polyprotein)

SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene).

SPLEN20008390//Human placenta (Diff48) mRNA, complete cds.

SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN).

SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds.

55 SPLEN20149110//Dishevelled specific domain

SPLEN20171470//Keratin, high sulfur B2 protein

SPLEN20194050//Homo sapiens HOTTL protein mRNA, complete cds

SPLEN20214580//Mus musculus mdg1-1 mRNA, complete cds.

EP 1 347 046 A1

STOMA20057820//Uncharacterized protein family UPF0024
 STOMA20063980//Collagen triple helix repeat (20 copies)
 STOMA20069040//Keratin, high sulfur B2 protein
 SYNOV20017080//UBX domain
 5 TBAES20000590//Cytochrome P450// Cytochrome P450
 TESTI2000170//HORMA domain
 TESTI20031810//Bacterial luciferase// Domain of unknown function DUF28
 TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspyl) mRNA, complete cds.
 TESTI20098350//VAT-Nn domain
 10 TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain
 TESTI20170350//Cystine-knot domain
 TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.
 TESTI20199750//TRICHOHYALIN.
 TESTI20202650//Repeat in HS1/Cortactin
 15 TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds.
 TESTI20231920//Gag P30 core shell protein
 TESTI20242830//E2 (early) protein, C terminal// Syndecan domain
 TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.
 TESTI20320440//THIOREDOXIN.
 20 TESTI20327680//EF hand// EF hand
 TESTI20328280//KE2 family protein// Troponin
 TESTI20351830//K-box region
 TESTI20370020//Bleomycin resistance protein
 TESTI20391210//IQ calmodulin-binding motif
 25 TESTI20408150//Keratin, high sulfur B2 protein
 TESTI20451990//SAP domain
 TESTI20467970//Neurohypophysial hormones N-terminal Domain// Neurohypophysial hormones, N-terminal Do-
 main// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neu-
 rohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophy-
 30 sial hormones N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hor-
 mones N-terminal Domain
 THYMU20108300//Mouse NCBP-29 mRNA for PW29, complete cds.
 THYMU20142040//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).
 THYMU20194360//Kelch motif
 35 THYMU20239000//collagen alpha 1(XI) chain
 TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 TRACH20005020//Ank repeat// MutT-like domain
 TRACH20007020//TRICHOHYALIN.
 TRACH20048450//PROTEIN K4 (PROTEIN K3).
 40 TRACH20068700//Homo sapiens adaptor protein CIKS mRNA, complete cds.
 TRACH20076760//Keratin, high sulfur B2 protein
 TRACH20141240//Mus musculus G21 protein mRNA, complete cds.
 TRACH20183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA, complete cds.
 45 UTERU20000740//Human fusion protein mRNA, complete cds.
 UTERU20004240//CGI-96 protein
 UTERU20005960//endoplasmic reticulum resident protein 58
 UTERU20022940//Human (p23) mRNA, complete cds.
 UTERU20046640//Mus musculus 1dIBp (LDLB) mRNA, complete cds.
 50 UTERU20065930//GTP-RHO BINDING PROTEIN 1 (RHOPHILIN).
 UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.
 UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain

[0092] Further the reason is that a polypeptide does not always belong solely to a single category of the above-
 55 described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories.
 Besides additional functions can be found for the clones classified into these functional categories by further analyses.

[0093] Since the polypeptide encoded by clones of the invention contains full-length amino acid sequence, it is pos-
 sible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation

EP 1 347 046 A1

by expressing the polypeptide as a recombinant polypeptide using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the polypeptide.

[0094] The biological activities of respective polypeptides can be analyzed by the methods as shown below.

5 Secretory protein, transmembrane protein:

[0095]

10 "Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),
"Growth Factors" (Eds., I. McKay, I. Leigh, 1993),
"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995) ;

Glycoprotein-related protein:

15 [0096]

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The Practical Approach Series" (IRL PRESS),
"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F.Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

20

Signal transduction-related protein:

[0097]

25 "Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),
"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or
"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J.Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

30 Transcription-related protein:

[0098]

35 "Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),
"Transcription Factors" (Ed., D.S.Latchman, 1993);

Enzyme and/or metabolism-related protein:

[0099]

40 "Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS) ; Cell division and/or cell proliferation-related protein:
"Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS) ;

45

Cytoskeleton-related protein:

[0100]

50 "Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),
"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana Press) series; Nuclear protein and/or RNA synthesis-related protein:
"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),
55 "RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

Protein synthesis and/or transport-related protein:

[0101]

5 "Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS),
 "Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana
 Press) series;

Cellular defense-related protein:

10

[0102]

"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,
 "Chaperonin Protocols" (Eds., Schneider, Christine, 2000); Development and/or differentiation-related protein:
 15 "Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in
 Molecular Biology" (Humana Press) series;

DNA- and/or RNA-binding protein:

20

[0103]

"DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biol-
 ogy" (Humana Press) series,
 "RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

25

ATP- and/or GTP-binding protein:

[0104]

30 "Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology"
 (Humana Press) series.

[0105] In the categorization, the clone predicted to belong to the category of secretory and/or membrane protein
 means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane,
 35 membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium
 channel, cell adhesion, collagen, connective tissue, etc., suggesting that it was a secretory or membrane protein, or
 a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane region was
 suggested by the results of PSORT and SOSUI analyses for deduced ORF.

40

[0106] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data
 with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0107] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit
 data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain,
 etc., suggesting that the clone encodes a signal transduction-related protein.

45

[0108] The clone predicted to belong to the category of transcription-related protein means a clone having hit data
 with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes
 a transcription-related protein.

[0109] The clone predicted to belong to the category of disease-related protein means a clone having hit data with
 some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related
 protein, or a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, UniGene, or nr, where
 50 the hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in
 Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database described later.

[0110] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone
 having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number),
 etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

55

[0111] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means
 a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth,
 apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0112] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data

with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0113] The clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0114] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0115] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0116] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0117] The clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0118] The clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0119] As to a protein involved in a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database OMIM, which is a database of human genes and diseases, to analyze the protein. Further, new information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database. The proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0120] Also, as for a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are involved in many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins related to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan Vol 17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). When cancer is used as an example, as described in "Biology of Cancer" (S. Matsubara, 1992) of Life Science series (Shokabo), many proteins are involved in cancers which include enzyme and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins. As clearly seen by the above example, it is evident that not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, etc. are often involved in diseases, and thus they can be useful targets in the field of medical industry.

[0121] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

- (1) secretion protein.
- (2) membrane protein.
- (3) channel and
- (4) extracellular matrix were used.

[0122] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein

[0123] 354 entries found, searching for "secretion protein"

*604667, *104760, *176860, *151675, *139320, *107400, *604029, *118910, #200100, *176880, *603850, *147572, *604028, *179513, *125950, *139250, *246700, *600946, *600560, *602926, 185860, *605083, *603215, *602421, *157147, *179512, *600174, *109270, *604710, *138120, *179510, *600998, *179509, *170280, *179511, *600626, *603831, *601489, *154545, *179490, *603826, *122559, *603216, *102720, *147290, *164160, *603062, *112262, *602672, *605435, *605322, *131230,

EP 1 347 046 A1

*601652, *603166, *601746, *601591, *179508, #160900, *104311, *600759, *147545, *167805, #104300, *167770, #219700, *168470, *601684, *602049, *601146, *605227, *602434, *602534, *114840, *603489, *604323, *107470, *600753, *600768, *118825, *600564, *604252, *173120, *134370, *192340, *308230, *600322, *605359, *600046, *300090, 106160, *600041, #262500, *605563, *150390, *158106, *182590, #103580, *104610, #173900, *134797, *143890, #145980, *306900, *308700, *176300, *227500, *137350, #154700, *138079, *600760, *107730, *142410, *147670, *124092, *590050, *152760, *600509, *605646, *201910, *227600, *152790, *300200, *300300, 300800, *138160, *107741, *120150, *601199, *120180, *120160, *176730, *133170, *122560, *107300, *137241, *120140, *101000, *193400, *217000, *272800, *600937, #201710, *600377, #174800, *106100, #274600, *173350, #177170, *147620, *214500, *131244, *202110, *120120, *601007, *191160, *147470, *603372, *600733, *252800, *190160, *138040, *158070, *162151, #125700, *130070, *113811, *603355, *171060, *136435, #184700, *603732, *190180, *164008, *186590, *120220, *604312, *152200, *138130, *605085, *605353, *600840, #166210, *188545, *207750, *173360, *601933, #194050, *153450, *138850, *253200, *307030, *157145, *600514, *600262, *264080, *147380, *600281, #204000, #227810, *232200, *188826, *232800, *161561, #166200, *188400, *153620, *182099, *218040, #265800, *172400, #177200, *176805, #211600, #214700, #176410, *152780, *600633, *601771, *301500, *605402, *601922, *307800, *147892, *147720, *312060, #520000, *147660, *106150, *602358, *107270, *601769, *147440, *604558, *131530, *600270, *601610, *603692, *603401, *600423, *601604, *603345, #125853, *602843, *142640, *603044, *605740, *134830, *602779, *130660, *139191, *137035, *600761, *601340, *600823, *107740, *130160, *600877, *605110, *600945, *130080, *600957, #130050, *605580, *118444, *601124, *124020, 122470, *120700, *603201, *137216, *601185, *138945, *218030, *600839, #240600, #262400, #162300, *162330, *188450, #265850, *263200, *162641, *300159, *601038, #191390, *201810, *601398, *602384, *131240, *602423, *139392, *142703, *602663, *232700, *602682, #602722, *602730, *600734, *188540, *182452, *601538, *603061, *146880, *603140, *603160, *142704, #252650, *182280, *125255, *603252, #131750, *182139, *182100, #259420, #261100, *603493, *601745, *182098, *603795, *123812, *600264, *147940, *180246, *180245, *118888, #604284, *168450, *118455, *604398, *604433, *601919, *118445, *600031, *604961, *605032, *605033, *171050, #171300, *131243, *109160, *605254, 274900, #171400, *600042, *151670, *184600, *605470, *605546, *176760, *602008, *102200, *605720, *600732, *605901

2) Membrane protein

[0124] 1489 entries found, searching for "membrane protein"

*130500, *605704, *305360, *153330, *173610, *109270, *170995, *170993, *104776, *602333, *309060, *605703, *120920, *605943, *602690, *159430, *600897, *133090, *601178, *602413, *602003, *604405, *605940, *603237, *109280, *600378, *602173, *107776, *602334, *602335, *125305, *601134, *309845, *605731, *154045, *603241, *603718, *600594, *603214, *185881, *603657, *600182, *603177, *605331, *601476, *605456, *601114, *605190, *600723, *603904, *136950, *300222, *602879, *185880, *605348, *300096, *602257, *177070, *310200, *603062, *603344, *600039, *602977, *300100, *128240, *600959, *600322, *227400, *186945, *600946, *602534, *602048, *182900, *601097, *600267, *602625, *136430, *602421, *601047, *107450, *143450, *603141, *184756, *164730, *159440, *154050, *600579, *312080, *604202, *603700, *600447, *256540, *604691, *158343, *600403, *602414, *137290, *176640, *176981, *600179, *600754, *604456, *604693, *605875, *604605, *188860, *300172, *602910, *604323, *219800, *601848, *603179, *600279, *602251, #222700, *603831, *605072, *605377, *601028, *604155, *108733, *104225, *601896, *601510, *173335, *107770, *601767, *600046, *603850, *600040, *603784, *603234, 188560, *605863, *121015, *605862, *605861, *186946, *604252, *603215, *142461, *604597, *603143, *605264, *603735, *176860, *605536, *176801, *180721, *603355, *104760, *131560, *310300, *602631, *304700, #309400, *603142, *143890, *605431, *600753, *115501, *176790, *600266, *601691, *168468, *601239, *602216, #104300, *605613, *601595, *605550, *125950, *605475, *602217, *602261, *603534, *602262, *604631, *190315, *601313, *604306, *104311, *604672, *605000, *602461, *605548, *602296, *604376, *121014, *121011, *600691, *604262, *139310, *304040, *605445, *179514, *179512, *151460, #160900, *120130, *128239, *601158, *601403, *176943, *601014, 300800, *300294, *601757, *185470, *273800, *605034, *602887, #185000, *604871, *603593, *603583, *605454, *104775, *605872, *141180, *602713, *603531, *139150, *601531, *601832, *605452, *134651, *604156, *120620, *605883, *604142, *166945, *605324, *600816, *604699, *300112, *605182, *600164, *182180, *605071,

EP 1 347 046 A1

*300023, *605057, *308240, *300249, *176947, *176894, *605081, *605035, *602044, *182860, *107271, *305100,
 *153390, *113730, *602689, *180069, *603518, *300017, *191275, *177061, *601693, *601789, *604241, *600934,
 *138160, *604424, *603868, *600174, *600718, *600523, *604141, *601009, *605251, *600481, *600874, *155550,
 *605227, *601017, *162230, 601138,
 5 *604157, *601212, *600763, *604110, *604158, *601107, *601326, 600621, *600587, 601137, *600917, *600855,
 *605058, *194355, *605194, *603291, *102720, *136425, *170715, *603216, *605547, *135630, *602926, *600168,
 *605002, *602474, *600157, *603025, *603893, *231200, *120090, *601966, *131230, *604722, *604721, *604515,
 *246700, *602101, *605628, *303630,
 *605787, *602857, *602285, *605708, *602488, *605025, *603817, *300051, *603293, *176878, *603646, 605707,
 10 185860, *112205, *300187, *602654, *120070, *603648, *604850, *602655, *602514, *300118, *182309, *179590,
 *602701, *600759, *204200, *604170, *175100, #103580, *147670, *306400, *143100, *182870, *257220, *180380,
 #116920, *301000, *193300, *157147,
 *131550, *139200, *139130, *190195, *605406, *155760, *155960, *605734, *155970, *605385, *111700, *155975,
 *150370, 605709, *151430, *605438, *151510, *116952, *157655, *158105, *605777, *176877, *153619, *120131,
 15 *185430, *109190, *120190, *109170, *605093, *605250, *153432, *107777, *186590, *160993, *605699, *605698,
 *605813, *605697, *605616, *605300,
 *162060, *605219, *163970, *135620, *165040, *605478, *604964, *103195, *604932, *604923, *605906, *605496,
 *605914, *166490, *138277, *604915, *114070, *605213, *605933, *180297, *101000, *191163, *191164, *605101,
 *603167, *600772, *603164, *600708, *604001, *191328, *313440, *602672, *604009, *604299, *192974, *604256,
 20 *603048, *600515, *604221, *602632,
 *604196, *601179, 603290, *604661, *601023, *601110, *304800, *203200, *300212, *602933, *603352, *208900,
 *604418, *604838, *600551, #212140, *604837, *602049, *600552, *600553, *300213, *602574, *600583, *600932,
 *603452, *604775, *516020, *604617, *604464, *603498, *300145, *601523, *602694, *600632, *604762, *604492,
 *400015, *604504, *601717, *601728,
 25 *300242, *602426, *604194, *603821, *604730, *600695, *603823, *603869, *300241, *600707, *603822, *602370,
 *602202, *601193, *601181, *604089, *602507, *604195, *602306, *300284, *601805, *601275, *604660,
 *600752, *603820, *604192, *602207, *308230, *600894, *312600, *603199, *604029, *602500, *102680, *235200,
 #256300, *601633, #219700, 262890,
 *156225, *73470, *193400, *173910, *600354, *113705, *600065, *107741, *107400, *600024, *131195, *113811,
 30 #118220, *601638, *300011, *276903, *604144, *311770, *601758, #173900, *604592, *120120, *179605, *603130,
 *603372, *10750, *222900, *602509, *256100, *602469, *602281, *229300, *224100, *110900, *190180, *261600,
 *602997, *603616, *603189, 601791,
 *601567, *312700, *171060, *308700, *604027, *162643, *516000, *176261, *604028, *314850, #145980, *601383,
 *600930, *305900, *601253, *136350, *605537, *138140, *604033, *605070, *139250, *300500, *603967, *300041,
 35 *603866, #130600, *120150, *601050, *604942, *605204, *605248, *272750, *600163, *604235, *600682, *107266,
 *306900, *91092, #262500, *600106,
 *152790, *86720, *227650, *153700, *308380, *103390, *605646, *164920, *604478, #252650, *173850, *173350,
 *602505, *246530, *194380, *602575, *603030, #209920, *212138, #214100, *605767, *600582, *189980, #176200,
 *604652, *604678, *256550, *300037, *253700, #253300, #226700, *604766, #244400, *190000, *188040, *604824,
 40 *214500, #237500, *232300, *605014,
 *604477, *90930, *605124, *604475, *604594, #227810, *306700, #301050, *600135, *600143, *605145, #269920,
 *300104, *277900, *300135, *300231, *192500, *182138, *191190, *176805, *600185, *186591, *604889, *603051,
 *165360, *47545, *601040, #156575, *107269, *603009, *602934, *123825, *601081, *602924, *163890, *600381,
 *602909, *50330, *109690, *123900,
 45 *603434, *603491, *110700, *602581, *125647, #154700, *114760, *141900, *603690, *120220, *601199, #145500,
 *601309, *602382, *120325, *600877, *604205, *604090, *601497, *602377, *605464, *138720, *603728, *120950,
 *604026, *600580, *601610, *137167, *603960, *603931, *601880, *603126, *138190, *130130, *601997, *601975,
 *600395, *516040, *600418, *600650,
 *605245, *605172, *600509, *164761, *310400, *600308, *605109, *600544, *600359, *600103, *605267, *312610,
 50 *176100, *308100, *158070, *605123, *173325, #312750, *600839, *158120, #604369, *604465, *173510, #161200,
 *151525, *605369, *604237, *516050, #600886, *604517, *165180, *605381, *605399, *307800, *604365, *155740,
 *147795, 601709, *604673, *147730,
 *602122, *147557, *193245, *600978, *604990, *603261, *603274, *601007, *131100, *602941, *107941, *146710,
 *276901, *131244, *602872, *603411, *186357, *176290, *601066, *185050, *232200, *143030, *601843, #236700,
 55 *604122, *142800, *134638, *604985, *182380, *603930, *142410, *137060, *604586, *601193, *120650, *252500,
 *253800, *120930, *604858, *605874,
 601274, *602158, *605873, *193210, *203100, *601295, *604095, #201710, *126150, *108740, #205400, *601373,
 *300167, *109545, *602894, *603361, #300257, *266200, *603401, *131390, *180470, *605908, *604798, #221770,

EP 1 347 046 A1

*223360, *180901, *605641, *605745, *604018, *300200, *604603, *230800, *602676, #604004, *605692, *602640, *601599, *134637, *245900, *118425, 601614, *605725, *120110, *300189, *300035, *603102, *250800, *602282, *602458, *123610, *603754, *300278, *601463, *300224, *601581, *182160, *601653, *139191, *601733, *600748, *142460, *601194, *152390, *153620, 5 *601615, *601814, *601617, *601613, *300191, #308300, *600798, 601858, *601872, *601597, #601588, *600821, *147840, *152427, *138850, *600823, *601492, *300256, *600840, *300267, *601411, *139080, *139090, 600851, *300334, *179080, *602095, *601284, *601282, #177200, *601681, *601252, *176000, *602184, *602188, #266510, #154020, *186711, *257200, *601711, *600667, *602241, *186745, *255125, *300126, *600644, *123890, #255120, #175200, *600004, *302060, *123580, 10 *186760, *122561, *602316, *600017, *120940, 140300, *151690, *120700, *602354, *600019, *600857, *182175, *600536, *158380, *600516, *120290, *600493, *182310, #252010, *182530, *186830, *601839, *142790, *159465, *118990, *250790, *248600, #248250, *186845, *601153, *142600, *116930, *114860, *171834, #303600, *186880, *600444, *142871, *601852, *602602, *602607, *114207, *186910, #232220, 15 600880, *134635, *112203, #112100, *111680, *231680, *311030, *111250, *111200, *134390, #226670, #145600, *226200, *602714, *171760, *133550, *602727, *161555, *602744, *602746, #131705, *602835, *600423, *176267, *602859, #600918, 277175, *602874, *601020, *109770, *600170, *217070, *173515, *602893, *147280, *154360, *171050, *108780, *176257, *600979, *600377, *108360, *204500, *170260, *146880, *154582, *601011, *600997, *602992, *201475, *603005, *190198, 20 *147360, #270400, *600238, #164970, *306250, #126600, *193065, #181350, *106180, *602136, *600937, *603086, *603087, *307030, *182099, *103320, *601683, #192430, *103180, *102681, *192321, *600244, *191740, *191315, *603152, *102642, *191305, #266140, *100500, *600867, *604585, *604404, *604345, *603201, *605430, *603207, *603208, *605433, *604101, *603969, *605896, *604616, *605851, *605768, *604576, *605754, *605730, *605477, *603263, *605538, *603283, *604402, 25 *605453, *605427, *603302, *605458, 603313, *604415, *603345, *605541, *603353, *605295, *603879, *605268, *605266, *605246, *603377, *603380, *605181, *604203, *603425, *603867, *605106, *605017, *603842, *604936, *603510, *604857, *605932, *605816, *603765, *603551, *605357, *605237, *604204, *603594, *605110, *604190, *603861, *604962, *603639, *603644, *605007, *605349, *604943, *604918, *604907, *603667, *603681, *605396, *605561, *603712, *603713, *605688, 30 *605942, *604878, *604843, *604659, *604671, *603798, *604682, *604056, *604705, *603749, 602586, *603647, *602515, #602475, *603717, *602359, *602372, *602380, *602518, *603652, *602573, *603626, 602587, *603598, *602871, *603613, *603750, *603875, *602608, *602666, *602345, *602935, *603564, *603548, *603927, 601876, *602343, *603943, *603787, *601730, *601611, *602679, *603788, *602243, 35 603790, *601535, *603796, *601488, *601485, *602314, *601478, *604047, *604048, *602297, *604057, *602715, *602192, *601459, *601416, *603833, *602190, *604102, *602106, *604111, *602724, *603499, *602736, *601123, *601002, *600923, *601987, *604149, *601929, *600910, *600900, *600864, *604165, *600782, *602836, *600769, *600742, *602783, *601905, *600535, *604198, *601901, *600534, *602876, *603356, *600530, *604216, *604217, *602890, *602905, *600465, *600464, 40 *600446, *602891, *603366, *601894, *604272, *603926, *603312, *600368, *602914, *600327, *603151, *603202, 602911, *602974, *603006, *601883, *603008, *600074, *603007, *603046, #603903, *604433, *600016, *603925, *516005, *516004, *516003, *601756, *604487, *516001, *313475, *313470, #307810, *604527, *604528, *601745, *604551, *604555, *603243, *603242, *603061, *603063, *603217, *300335, *300283, *300281, *604600, *300197, *603097, *603220, *601625, *604623, 45 *603118, *601590, *604646, *300008, *601568, *300007, *275630, *601533, #275200, *270200, #261550, *604031, *604683, #254800, *251100, #242300, *604058, *604720, *240500, *233690, #232240, #226730, *223100, *222100, #220100, *216950, *604832, 212750, 212067, *604066, *193067, 601315, *193001, *604862, *604870, *191306, *600385, *604879, *191191, *601296, *604914, *190181, *604119, #188550, *604925, *188410, #601287, *604939, *188380, *604126, *604945, *604148, 50 *188060, *604982, *186854, *604988, *186360, *186355, *185250, *600916, *605008, *605009, 185020, *600734, *605024, *182331, *605032, *605033, *182305, *180903, #179800, *179610, *605060, *179410, *178990, *176802, *605080, *176266, *176263, *176260, *600732, *173490, *604199, *173445, *173391, 172290, *605147, *605149, *171890, *600528, *171833, *605185, #170500, *605193, #168000, *605196, 55 *167055, *605205, *605208, 166900, *605216, *162651, *162010, *600504, #161400, *604253, #160800, *159460, *154540, *605254, *605261, *153634, *600429, *153337, *600424, *605292, #604286, #152700, 152423, *152310, *151625, *600153, *604313, *151523, *150325, *150320, *150292, *603150, *150290, *150210, *605410, *605415, *605416, *605417, *605421, *603149,

EP 1 347 046 A1

*604349, *147940, *600282, *147880, *146928, *146661, *600150, *146630, *142622, *600018, *605461, *138981, *138590, *600023, *138330, *605495, *138297, *605512, *138230, #136900, #301310, *516006, *605545, *605546, *136131, *134660, *134350, *516002, *605589, *131235, #130050, *605625, *126455, *126064, #125310, *605670, *604534, *125240, *123836, *123830, *123620, *605702, #122200, *120980, *120360, *118510, *114835, *605710, *605716, *605722, *114217, *604561, *113810, *111740, #110800, *605748, *605752, *604564, *110600, *603160, *109610, *605784, #107480, *107273, *603192, *300169, *106195, *105210, *104615, *104614, *104210, *103850, 103581, *605876, *605877, *605879, *103220, *605887, *300150, *102910, *102670, *102576, *605916, *604629, *102575, *102573, *300132, *101800, *605947

3) Channel (member of membrane protein)

[0125] 361 entries found, searching for "channel"

*176266, *600724, *182390, *123825, *114208, *114206, *176267, *114205, *601784, *600937, *114204, *603415, *600053, *114207, *114209, *605427, *604527, *604528, *600760, *601011, *192500, *118425, *600228, *176261, *602235, *600761, *600359, *300008, *182389, *600877, *602232, *176263, *182391, *601328, *600054, *603939, *602208, *601534, *600504, *602323, *603208, *601958, *603537, *601012, *601327, *600734, *602780, *602781, *604433, *603220, *182392, *605874, *605873, *601745, *603888, *603219, *602604, *603796, *302910, *602866, *601013, *602905, *602906, *603967, *600163, #170500, *152427, *180901, *176260, #601462, *603951, *601141, *604492, *600702, *602023, *600308, *602754, *107776, *176257, *602024, *601949, *605222, *601142, *602983, *193245, *600681, *176265, *600235, *176262, *176258, *605206, *604427, *605411, *603305, *601219, *600150, *604065, *602343, *605223, *605720, *603906, *138249, *138253, *600843, *604385, *600003, *600935, *603940, *602727, *602158, 602911, *600397, *602726, *600845, *605080, *600580, *602872, *602106, *176264, *603953, *605722, *300110, *138252, *604111, *602717, *602420, *600570, 600844, *603493, *600932, *605716, *138254, *603652, *300138, *605410, *176268, *605214, *605696, *300334, *604660, *176256, *605879, *603749, *603583, *602345, *604661, *603787, 603313, *602982, *604337, *600846, *604662, *300328, *300281, *602566, *602836, *604003, *603788, *603651, *602421, *107777, #177200, *100725, *219700, *100690, *100710, #160800, #603830, #183086, *600509, #220400, #601144, *173910, *180902, *605692, #264350, #160900, #145600, #255700, *602076, *603061, *601313, *154275, #604233, *604532, #108500, #121201, #170400, *300225, *121014, *139311, #125800, #160120, *118503, 601439, #141500, #168300, *304040, #601887, #256450, *186945, *154276, #300009, #216900, *600040, *601014, *601042, *602512, *601383, *605445, *602368, *603831, #117000, *601218, *108745, *605248, #177735, #173900, *601212, *182139, *601059, *600039, *601485, *180903, *186360, *603319, #600101, *118509, *600109, #121200, *600170, *604187, *176975, *137163, #310468, #263800, #262300, *603750, *600229, *124030, *602251, #603829, *137143, #145500, *600669, *147450, *154050, *603353, *600516, *601157, *600855, *601154, *602522, *249210, *600968, #252650, *171060, *600919, *156490, #259700, #601678, *601764, #310500, *131244, *300041, *121011, *125950, *114180, *602974, *600637, *113730, *118504, *605145, *604669, *118800, *121013, *121015, *138491, *600421, *104610, *604045, *604594, *131230, *605487, *138247, *600467, #602485, *602481, *138251, *137192, *602403, 600851, *277900, *603785, *603152, *603199, *603475, #168600, #272120, *170280, *603852, #241200, *603053, *600465, #603034, *142461, *164920, *137164, *600884, *600442, *123885, *604001, *600232, *232200, *171050, *602103, *602014, *300211, *600983, *602887, *604415, *604418, *300242, #300071, *604471, *600837, 168350, *118511, 193007, *600300, *604654, #601820, *180297, *600046, *603853, *604678, *604693, #604772, *118508, *603855, *605204, #254210, *182099, *182307, #130600, *601109, *114080, *300103, *182860, *605438, *601129, *603964, *600019, *516060, #185000, *138079, *104210, *605818, *603418, *305990, *305450

4) Extracellular matrix

[0126] 218 entries found, searching for "extracellular matrix"

*605912, *603479, *602201, *604633, *601418, *601548, *115437, *154870, *600754, *602261, *602285, *602262, *134797, *120361, *604629, *604871, *603321, *603320, *601807, #154700, *116935, *185261, *120360, *185250, *605470, *603767, *253700, *190180, *128239, *308700, *276901, *193300, *120324, *188826, *602109, *155760, *600514, *600261, #177170, *600536, *147557, #116920, *150240, *601313, *120140, 601614, *605158, *120150, *120180, #200610, *605127, *193400,

*192240, #173900, *152200, #136900, *135821, #130070, *120320, *120220, *112260, *310200, *600900, *600262, *605670, *600985, *179590, #245150, *602574, *601463, 183850, *601211, *604241, *600758, *186745, *604710, *602369, *602090, *190182, *192975.
 *602178, *230740, *600065, *601652, *158106, *190181, *156790, *158810, *193210, *155120, *192977, *193065, #226700, *187380, *231050, *182120, *188060, *186355, 163200, *164010, #156550, *151510, *150370, *253800, *156225, *150325, #194050, *150290, *216550, *147620, *600215, *222600, *147559, *165380, *182888, *600491, *146650, *146640, *600564, *600596,
 *600616, *600700, *600742, *138297, *182889, *154705, *600930, *301870, *153619, *601050, *601090, *601105, *165070, *305370, *135820, *130660, *310300, *601492, *128240, *601587, #126600, *601636, *600119, *601692, *601728, *125485, 601858, *601915, *602048, *175100, *602108, *121010, *600245, *120470, *120328, *120325, *602264, *120280, *602366, *600309,
 *602402, *602415, *602428, *602453, *602505, #166210, *602600, *602941, *603005, *603196, 603209, *603221, *603234, *603319, *120250, *120210, *120120, *603489, *603551, *118938, *603799, *603842, *603924, *603963, *604042, *604063, *604149, *604160, *601028, *604467, *604510, *604592, *116930, *116806, *601284, *604724, *604806, *604807, *604808, *107269,
 *605007, *605008, *605009, *600214, *600076, *605174, *605175, *605292, *605343, *605351, #600204, *605497, *605546, *605587, *605623, *600211, *605702, *103320

[0127] In addition to these, the various keywords shown in the above-mentioned categorization or others can be used for the OMIM search and the result may suggest the involvement thereof in diseases.

[0128] Further, the use of nucleotide sequences of cDNAs of the present invention enables analyzing the expression frequency of genes corresponding to the cDNAs. In addition, functions of the genes can be predicted based on the information obtained by the expression frequency analysis.

[0129] There are several methods for analyzing the expression levels of genes involved in diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods using, for example, Northern hybridization, RT-PCR, DNA microarray, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujunsha (2000)). By computer analysis, in addition to these analysis methods, the nucleotide sequences of expressed genes can be compared to analyze the expression frequency. For example, there is a database called "BODYMAP"; gene clones are extracted at random from cDNA libraries of various tissues and/or cells, and the clones homologous to one another are assigned to a single cluster based on the information of nucleotide sequence homology at the 3'-end; genes are classified into any clusters, and the numbers of clones in the respective clusters are compared to gain the information on expression frequency (<http://bodymap.ims.u-tokyo.ac.jp/>).

[0130] When explicit difference in the expression levels between diseased tissues and normal tissues is observed for a gene by these analytical methods, it can be concluded that the gene is closely involved in a disease or disorder. Instead of diseased tissues, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely involved in a disease or disorder.

[0131] From the 2443 clones whose full-length nucleotide sequences had been revealed, genes involved in particular pathology or functions were selected by the use of databases shown below (see Example 7; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains nucleotide sequences of 1,402,070 clones, and the population of the database is large enough for the analysis. The sequence information in the database was obtained by selecting cDNA clones at random from cDNA libraries derived from the various tissues and cells shown in Example 1 and determining the 5'-end sequences thereof.

[0132] Then, the nucleotide sequences of respective clones in this database were categorized (clustered) based on the nucleotide sequence homology determined with a search program: the number of clones belonging to every cluster of each library was determined and normalized; thus, the ratio of a certain gene in a cDNA library was determined. This analysis provided the information of the expression frequency of a gene in a tissue or cell that is the source of the cDNA library.

[0133] Then, in order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells, which had been used in the large-scale cDNA analyses, were taken as subjects to compare the expression levels between different tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which 600 or more cDNA clones whose nucleotide sequences had been analyzed were derived. The result of this analysis showed that the cDNA clones corresponded to the genes involved in the pathology and functions, which are indicated below. Each value in Tables 3 to 51 indicated below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0134] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset correlates to the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38. 642-648. (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0135] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38. 642-648. (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D3OST, D6OST or D9OST) showed that the genes whose expression levels were different between the two were 56 clones indicated in Table 3. These clones are involved in osteoporosis.

Genes involved in neural cell differentiation

[0136] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0137] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were 288 clones indicated in Table 4. These genes are neurological disease-related genes.

Cancer-related genes

[0138] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression thereof can contribute to the carcinogenesis in tissues and cells. Thus, genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0139] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were 35 clones indicated in Table 5.

[0140] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were 11 clones indicated in Table 6.

[0141] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were 25 clones indicated in Table 7.

[0142] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were 41 clones indicated in Table 8.

[0143] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were 175 clones indicated in Table 9.

[0144] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were 30 clones indicated in Table 10.

[0145] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were 62 clones indicated in Table 11.

[0146] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were 23 clones indicated in Table 12.

[0147] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were 70 clones indicated

in Table 13.

[0148] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were 236 clones indicated in Table 14.

[0149] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were 232 clones indicated in Table 15.

[0150] These genes are involved in cancers.

[0151] Further, there is a method to search for genes involved in development and differentiation, which is the expression frequency analysis in which the expression levels of genes are compared between developing and/or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0152] By using the information of gene expression frequency gained from the database of 5'-end nucleotide sequences described above, genes involved in development or differentiation of particular tissues were selected from the 2443 clones whose full-length nucleotide sequence had been revealed (see Example 7).

[0153] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were 1195 clones indicated in Tables 16 to 48.

[0154] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were 45 clones indicated in Table 49.

[0155] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were 118 clones indicated in Table 50.

[0156] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were 63 clones indicated in Table 51. These genes are involved in regeneration of tissues and/or cells.

[0157] The expression frequency or the like can be analyzed by PCR based on the nucleotide sequences of cDNAs of the present invention. There are some known methods for comparing the quantities of amplification products obtained by PCR. For example, the band intensities can be determined by ethidium bromide staining. With RI-labeled or fluorescently labeled primers, the RI signal or fluorescence intensity can be assayed for the quantity of labeled amplification products. Alternatively, the quantity of amplification products can also be determined by measuring the RI signal or the fluorescence intensity from the RI-labeled or fluorescently labeled probe hybridizing to the products. The assay results thus obtained are compared and then the clones exhibiting differences in the expression levels can be selected.

[0158] There are some quantitative PCR methods: a PCR method using internal standards; a competitive PCR, in which the quantification is achieved by adding, to a sample, a dilution series of a known quantity of a template RNA and by comparing the quantity of an amplification product derived from the RNA of interest with the quantity of an amplification product derived from the template RNA. These methods overcome the problems of errors in the amount of amplification products among tubes and of the plateau effect. ATAC-PCR (Adaptor-tagged competitive PCR) is a method of competitive PCR which is practiced by using multiple adapters of different sizes attached to a gene whose 3'-end nucleotide sequence has previously been determined. The ratio of expression frequency of a single mRNA species from a number of tissues (cells) can be assayed in a single step (Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Microarray and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112).

[0159] If it is observed, by using these analytical methods, that the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-related genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes involved in diseases and/or disorders affecting the tissues.

[0160] For example, inflammation is an important biological response that is known to be involved in various diseases. The representative inflammation-inducing factors include TNF- α (Tumor Necrosis Factor-alpha). There exists a signaling cascade activated by TNF- α stimulations, wherein NF- κ B is a transducing molecule (Cell 1995, 80:529-532). It has also been revealed that many inflammation-related genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes whose expression levels are varied in response to the stimulation of TNF- α also participate in inflammation.

[0161] Further, the infection of *Helicobacter pylori* to the gastric epithelia is known to cause gastritis and gastroduodenal ulcer (Mebio 2000, July, 17(7): 16-33). Thus, the genes whose expression levels are altered depending on co-

culturing cells with *Helicobacter pylori* may be involved in gastritis and gastroduodenal ulcer. A recent study has suggested that *Helicobacter pylori* strongly activates the NF- κ B pathway (Gastroenterology 2000, 119: 97-108).

[0162] THP-1 cell, which is a human monocyte cell line, was cultured in the presence of TNF- α (Tumor Necrosis Factor- α). The genes whose expression levels were altered owing to the presence of TNF- α were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of TNF- α were

ASTRO20152140, BRACE20057620, BRACE20060720, BRACE20090440, BRACE20152870, BRACE20229280, BRAMY20002770, BRAMY20266850, BRAMY20280720, BRAWH20106180, BRAWH20122770, BRHIP20096170, BRHIP20111200, BRHIP20186120, BRHIP20194940, BRHIP20207430, BRSSN20152380, CTONG20095270, CTONG20100240, CTONG20158150,

CTONG20265130, D3OST20006540, D9OST20031370, FCBBF20071860, FCBBF30251420, FCBBF30252520, FCBBF40001420, FEBRA20017050, FEBRA20082100, HCHON20011160, KIDNE20141190, KIDNE20163880, KIDNE20182690, LIVER10004790, LIVER20038540, LIVER20085800, MESAN20130220, MESAN20174170, NT2NE20158600, NT2RI20005750, NT2RP70110860, NT2RP70169110, NT2RP70175670, NT2RP70188710, PERIC20002140, PLACE60155130, PROST20120160, PROST20149250, PROST20161950, PUAEN20015260,

SKNSH20080430, SMINT20051610, SMINT20060780, SMINT20161220, SMINT20163960, SPLEN20101190, SPLEN20157300, SPLEN20163560, SPLEN20214580, SPLEN20279950, STOMA20048520, TESTI20076850, TESTI20087620, TESTI20108720, TESTI20220100, TESTI20239510, TESTI20266740, TESTI20342430, TESTI20370020, TESTI20391210, TESTI20401020, TESTI20415640, THYMU20130890, THYMU20286290, TRACH20060150, TRACH20099340, UTERU20004240, UTERU20068990, UTERU20119060.

[0163] On the other hand, the clones whose expression levels were decreased owing to the presence of TNF- α were

ASTRO20032120, ASTRO20084250, ASTRO20181690, BRACE20062640, BRACE20067430, BRACE20235400, BRALZ20018340, BRALZ20069760, BRALZ20075450, BRAMY20163270, BRAMY20204450, BRAMY20218670, BRAMY20229800, BRAWH10000930, BRAWH20107540, BRAWH20132190, BRAWH20158530, BRCAN20273340, BRHIP20105710, BRHIP20186120,

BRSSN20176820, CTONG20095290, DFNES20031920, FCBBF30033050, FCBBF30071520, FCBBF30083820, HCHON20008980, HCHON20022470, HHDP20034390, KIDNE20028720, KIDNE20079440, KIDNE20127750, KIDNE20148900, LIVER20011130, MAMGL10000830, MESAN20127350, NT2NE20181650, NT2RI20023160, NT2RP70102350, NT2RP70157890, NTONG20029480, OCBBF20020830, OCBBF20041680, OCBBF20061720, OCBBF20127040, OCBBF20139260, OCBBF20178990, PEBLM20013120, PLACE60003480, PLACE60181070,

PROST20151240, PUAEN20003740, PUAEN20011880, PUAEN20078980, PUAEN20085150, SKNSH20080430, SMINT20001760, SMINT20047810, SMINT20108530, SPLEN20158990, SPLEN20283650, STOMA20010250, STOMA20057820, TESTI20060400, TESTI20161970, TESTI20275620, TESTI20369690, TESTI20386230, TESTI20392250, TESTI20409440, TESTI20424730, THYMU20095960, THYMU20111180, THYMU20226600, THYMU20253250, THYMU20272490, TRACH20153810, UTERU20176130, UTERU20186740.

[0164] These clones are inflammation-related genes.

[0165] MKN45, which is a gastric cancer cell line, was co-cultured with *Helicobacter pylori*. The genes whose expression levels were altered owing to the presence of *Helicobacter pylori* were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of *Helicobacter pylori* were

ADRL20067670, BLADE20004630, BRACE20039040, BRACE20151320, BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20060920, BRAMY20184670, BRAMY20218670, BRAMY20229800, BRCAN20147880, BRHIP20196410, BRHIP30004880, BRSSN20187310, CD34C30004940, CTONG20265130, DFNES20031920, FCBBF30278630, FCBBF40001420,

HHDP20095280, KIDNE20130450, LIVER20011130, LIVER20038540, NT2NE20172590, NT2RP70169110, OCBBF20085200, OCBBF20180840, PEBLM10000240, PLACE60003480, PROST20120160, PROST20151240, PUAEN20011880, SKMUS20031680, SKNSH20080430, SMINT20056210, SMINT20105000, SPLEN20019450, SPLEN20211570, STOMA20048520, TESTI20004890, TESTI20083940, TESTI20168480, TESTI20239510, TESTI20308600, TESTI20478010, UTERU20126880.

[0166] On the other hand, the clones whose expression levels were decreased owing to the presence of *Helicobacter pylori* were

ASTRO20032120, BRACE20090440, BRACE20114780, BRALZ20064740, BRAMY20002770, BRAMY20210400, BRAMY20215230, BRAMY20247280, BRAMY20267130, BRAWH20029630, BRAWH20100690, BRAWH20118230, BRCOC20105100, BRHIP20218580, BRSSN20046570, CTONG20138030, CTONG20146970, CTONG20158150, D3OST20037970, FCBBF30001840, FCBBF30033050, FEBRA20082100, HCHON20035130, HCHON20043590, HCHON20067220, NT2NE20174920, NT2RI20009870, NT2RI20023160, NT2RP70062230, NT2RP70130020,

NTONG20070340, OCBBF20020150, OCBBF20094240, OCBBF20107920, PROST20144220, PROST20149160, PROST20153320, PUAEN20003740, PUAEN20025680, PUAEN20040670, SMINT20014580, SPLEN20101190, STOMA20076800, TESTI20087620, TESTI20098530, TESTI20123080, TESTI20161970, TESTI20234140, TESTI20288110, TESTI20357960, TESTI20391210, TESTI20424730, THYMU20158250, THYMU20226600,

TRACH20005020, TRACH20134950, TRACH20184490, TSTOM20001390, UTERU20119060, UTERU20134910, UTERU20176130.

[0167] These clones are involved in gastritis or gastroduodenal ulcer.

[0168] For example, if the polypeptide encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible to screen low molecular weight compounds, etc. by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows.

[0169] First the polypeptide is expressed and purified as recombinant. The purified polypeptide is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be involved in a particular change of cellular conditions may be detected by the amount of mRNA or polypeptide. Alternatively, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (polypeptide) which is known to be involved in a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.

[0170] Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be involved in a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit the function of the polypeptide of the invention, it can be applied for developing medicines.

[0171] If the polypeptide encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein involved in signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0172] In case of a membrane protein, it is most likely to be a polypeptide that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0173] For example, a ligand against the polypeptide of the invention can be screened in the following manner. Namely a ligand that binds to a specific polypeptide can be screened by a method comprising the steps of: (a) contacting a test sample with the polypeptide of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

[0174] On the other hand, for example, screening using cells expressing the polypeptide of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific polypeptide by using procedures (a) attaching the sample cells to the polypeptide of the invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

[0175] In a following screening as an example, first the polypeptide of the invention is expressed, and the recombinant polypeptide is purified. Next, the purified polypeptide is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the invention can be labeled with RI such as ^{125}I , and enzyme (alkaline phosphatase etc.)

[0176] Alternatively, a polypeptide of the invention may be used without labeling and then detected by using a labeled antibody against the polypeptide. The cells that are selected by the above screening methods, which express a receptor of the polypeptide of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0177] Once the ligand binding to the polypeptide of the invention, the receptor of the polypeptide of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor for example) by utilizing the binding activities.

[0178] When the polypeptide of the invention is a receptor, the screening method comprises the steps of (a) contacting the polypeptide of the invention or cells expressing the polypeptide of the invention with the ligand, in the presence of a test sample (b) detecting the binding activity between said polypeptide or cells expressing said polypeptide and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the polypeptide of the invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the polypeptide and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0179] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the polypeptide of the invention can also be used as a sample.

[0180] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the polypeptide. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the polypeptide and its associated proteins (including a receptor) *in vivo*. Such compounds can be used for developing drugs for precaution or cures of a disease in which the polypeptide is involved.

[0181] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0182] The screening can be performed, for example, as follows. First, the polypeptide of the invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and polypeptide. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (polypeptide) that is known to function in a certain cellular change is used for the detection.

[0183] Once the screening reveals that the polypeptide of the invention can regulate cellular conditions or the functions, it is possible to apply the polypeptide as a pharmaceutical and diagnostic medicine for related diseases by itself or by altering a part of it into an appropriate composition.

[0184] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the polypeptide of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the polypeptide may play a certain role.

[0185] Proteins involved in signal transduction or transcription may be a factor that affects a certain polypeptide or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a polypeptide or gene by expressing the polypeptide provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular polypeptide or gene.

[0186] The screening may be performed as follows. First, a transformed cell line expressing the polypeptide is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or polypeptide. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) that is changed by the function of a certain gene product (polypeptide) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, β -galactosidase, etc.) into a cell, expressing the polypeptide provided by the invention into the cell, and estimating the activity of a marker gene product (polypeptide).

[0187] If the polypeptide or gene of the invention is involved in diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the polypeptide of the present invention.

[0188] For example, the polypeptide of the invention is expressed and purified as a recombinant polypeptide. Then, the polypeptide or gene that interacts with the polypeptide of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the polypeptide of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0189] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases in which the polypeptide of the present invention is involved. Similarly, if the regulatory factor obtained in the screening is turn out to be a polypeptide, compounds that can newly affect the expression or activity of the polypeptide may be used as a medicine for the diseases in which the polypeptide of the invention is involved.

[0190] If the polypeptide of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins involved in signal transduction, glycoprotein, transcription, or diseases, a screening

may be performed by adding a compound to the polypeptide of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the polypeptide.

[0191] In a screening given as an example, the polypeptide of the invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified polypeptide, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified polypeptide is added, and the amount of the substrate and the reaction products is examined.

[0192] The compounds obtained in the screening may be used as a medicine for diseases in which the polypeptide of the invention is involved. Also they can be applied for tests that examine whether the polypeptide of the invention functions normally *in vivo*.

[0193] Whether the secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in diseases or not is determined in another method than described above, by obtaining a specific antibody against the polypeptide of the invention, and examining the relationship between the expression or activity of the polypeptide and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit. (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0194] Proteins involved in diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the related disease or a target of gene therapy.

[0195] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by polynucleotide, the polynucleotide can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the polynucleotide and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0196] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 1. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0197] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0198] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known polypeptides. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0199] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the polypeptide encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-

length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0200] The present invention has provided 2443 polynucleotides. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. It is known that secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are involved in many diseases. The genes and proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0201] In particular, cDNA assumed to encode secretory proteins, which were provided by this invention, are very important for the industry since the encoded proteins themselves are expected to be useful as pharmaceutical agents and many disease-related genes may be included in them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases, etc. These cDNA are also very important for the industry, which are expected to regulate the activity or expression of the encoded protein to treat diseases, etc.

[0202] Any patents, patent applications, and publications cited herein are incorporated by reference.

[0203] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA

[0204] Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989). Further, by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) which had been cultivated by the methods described in the catalogs.

[0205] The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Extraction of mRNA from human tissues>

[0206]

NTONG Normal tongue;
CTONG Tongue cancer;
FCBBF Fetal brain;
OCBBF Fetal brain;
PLACE Placenta;
SYNOV Synovial membrane tissue (from rheumatoid arthritis);
CORDB Cord blood.

<Extraction of mRNA from culture cells>

[0207]

BNGH4 H4 cells (ATCC #HTB-148);
IMR32 IMR32 cells (ATCC #CCL-127);
SKNMC SK-N-MC cells (ATCC #HTB-10);
3NB69 NB69 cells (RCB #RCB0480);
BGG11 G11 cells (RCB #RCB0763);
NB9N4 NB9 cells (RCB #RCB0477);
SKNSH SK-N-SH cells (RCB #RCB0426);
AHMSC Human mesenchymal (HMSC) cells;
CHONS Chondrocytes;
ERLTF TF-1 cells (erythroleukemia);
HELAC HeLa cells;

EP 1 347 046 A1

JCMCLC: Leukemia, myelogenous;
 MESTC: Mesenchyme stem cells;
 N1ESE: Mesenchymal stem cells;
 NCRRM: Embryonal carcinoma;
 5 NCRRP: Embryonal carcinoma treated with retinoic acid (RA) to induce the differentiation;
 T1ESE: Mesenchymal stem cells treated with trichostatin and 5-azacytidine to induce the differentiation;
 NT2RM: NT2 cells (STARATAGENE #204101);
 NT2RP: NT2 cells treated with retinoic acid (RA) for 5 weeks to induce the differentiation;
 NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth
 10 inhibitor for 2 weeks;
 NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant
 neurons were concentrated and harvested (NT2 Neuron) ;
 NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for 5 weeks to induce the differentiation, and
 then treated with the growth inhibitor for 2 weeks; mRNA was prepared from the cells and a cDNA library was
 15 constructed from the mRNA; the cDNAs of the library whose nucleotide sequences were shared by those of mRNAs
 from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01); the subtracted
 library (NT2RI-NT2RM) was provided by this procedure.

[0208] RCB indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and
 20 Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.

<Extraction of mRNA from primary culture cells>

[0209]

ASTRO Normal human astrocyte NHA5732, Takara Shuzo #CC2565;
 DFNES Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;
 MFSAN Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;
 NHNPC Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;
 30 PEBLM Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;
 HSYRA Human synoviocyte HS-RA (from rheumatoid arthritis), Toyobo #T404K-05;
 PUAEN Normal human pulmonary artery endothelial cells, Toyobo #T302K-05;
 UMYEN Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;
 HCASM Normal human coronary artery smooth muscle cell HCASMC, Toyobo #T305K-05;
 35 HCHON Normal human chondrocyte HC, Toyobo #T402K-05;
 HHDPG Normal human dermal papilla cell HDPC, Toyobo #THPCK-001;
 CD34C CD34+ cells (AllCells, LLC #CB14435M) ;
 D3OST CD34+ cells treated with the osteoclast differentiation factor (ODF) for 3 days to induce the differentiation;
 D6OST CD34+ cells treated with ODF for 6 days to induce the differentiation;
 40 D9OST CD34+ cells treated with ODF for 9 days to induce the differentiation;
 ACTVT Activated T-cells;
 LYMPB Lymphoblasts, EB virus transferred B cells;
 NETRP Neutrophils.

[0210] Then total RNAs extracted from the following human tissues were purchased and used as mRNA sources.
 The library names and the origins are indicated below in the order of "Library name: Origin". When a library was
 prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

[0211]

ADRGL: Adrenal gland, CLONTECH #64016-1;
 BRACE: Brain (cerebellum), CLONTECH #64035-1;
 55 BRAWH: Whole brain, CLONTECH #64020-1;
 FEBRA: Fetal brain, CLONTECH #64019-1;
 FELIV: Fetal liver, CLONTECH #64018-1;
 HEART: Heart, CLONTECH #64025-1;

EP 1 347 046 A1

HLUNG: Lung, CLONTECH #64023-1;
 KIDNE: Kidney, CLONTECH #64030-1;
 LIVER: Liver, CLONTECH #64022-1;
 MAMGL: Mammary Gland, CLONTECH #64037-1;
 5 PANCR: Pancreas, CLONTECH #64031-1;
 PROST: Prostate, CLONTECH #64038-1;
 SALGL: Salivary Gland, CLONTECH #64026-1;
 SKMUS: Skeletal Muscle, CLONTECH #64033-1;
 SMINT: Small Intestine, CLONTECH #64039-1;
 10 SPLEN: Spleen, CLONTECH #64034-1;
 STOMA: Stomach, CLONTECH #64090-1;
 TBAS: Breast (Tumor), CLONTECH #64015-1;
 TCERX: Cervix (Tumor), CLONTECH #64010-1;
 TCOLN: Colon (Tumor), CLONTECH #64014-1;
 15 TESTI: Testis, CLONTECH #64027-1;
 THYMU: Thymus, CLONTECH #64028-1;
 TLUNG: Lung (Tumor), CLONTECH #64013-1;
 TOVAR: Ovary (Tumor), CLONTECH #64011-1;
 T-RACH: Trachea, CLONTECH #64091-1;
 20 TUTER: Uterus (Tumor), CLONTECH #64008-1;
 UTERU: Uterus, CLONTECH #64029-1;
 ADIPS: Adipose, Invitrogen #D6005-01;
 BLADE: Bladder, Invitrogen #D6020-01;
 BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01;
 25 CERVX: Cervix, Invitrogen #D6047-01;
 COLON: Colon, Invitrogen #D6050-01;
 NESOP: Esophagus, Invitrogen #D6060-01;
 PERIC: Pericardium, Invitrogen #D6105-01;
 RECTM: Rectum, Invitrogen #D6110-01;
 30 TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
 TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
 TLIVE: Liver (Tumor), Invitrogen #D6880-01;
 TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
 BEAST: Adult breast, STARATAGENE #735044;
 35 FEHRT: Fetal heart, STARATAGENE #738012;
 FEKID: Fetal kidney, STARATAGENE #738014;
 FELNG: Fetal lung, STARATAGENE #738020;
 NOVAR: Adult ovary, STARATAGENE #735260;
 BRASW: subtracted library (BRALZ-BRAWH). A cDNA library was constructed from mRNA prepared from tissues
 40 of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain,
 cortex, Alzheimer). Invitrogen #D6830-01]; the cDNAs of this library whose nucleotide sequences were shared
 by those of mRNAs from whole brain tissue [BRAWH: Whole brain, CLONTECH #64020-1] were subtracted by
 using a Subtract Kit (Invitrogen #K4320-01).

45 [0212] Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were pur-
 chased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue had been
 combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole
 brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and the origins are indicated below
 in the order of "Library name: Origin".

50 <Purchase of mRNAs of human tissues as poly A(+) RNAs>

[0213]

55 BRAMY: Brain (amygdala), CLONTECH #6574-1;
 BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
 BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
 BRHIP: Brain (hippocampus), CLONTECH #6578-1;

EP 1 347 046 A1

BRSSN: Brain (substantia nigra), CLONTECH #6580-1;
 BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;
 BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA library

[0214] cDNA library was prepared from each RNA by the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase) treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (SEQ ID NO: 5455) and oligo dT primer (SEQ ID NO: 5456), as described in WO 01/04286. Then, the single-stranded cDNA was converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (SEQ ID NO: 5457) and 3' (SEQ ID NO: 5458) PCR primers, and then digested with *Sfi*. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *DraIII*-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); the cDNA library was thus prepared.

[0215] The names of cDNA libraries, which were used in the analysis of full-length cDNA sequences, and their origins are shown in Table 2.

Table 2

Library	Type	Origin, etc.
3NB69	Culture cell	NB69 cells (RCB #RCB0480)
ADIPS	Tissue	Adipose (Invitrogen #D6005-01)
ADRL	Tissue	Adrenal gland (CLONTECH #64016-1)
ASTRO	Primary culture cell	Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565)
BEAST	Tissue	Adult Breast (STARATAGENE #735044)
BGGI1	Culture cell	GI1 cells (RCB #RCB0763)
BLADE	Tissue	Bladder (Invitrogen #D6020-01)
BNGH4	Culture cell	H4 cells (ATCC #HTB-148)
BRACE	Tissue	Brain, cerebellum (CLONTECH #64035-1)
BRALZ	Tissue	Brain, cortex, Alzheimer (Invitrogen #D6830-01)
BRAMY	Tissue	Brain, amygdala (CLONTECH #6574-1)
BRAWH	Tissue	Brain, whole (CLONTECH #64020-1)
BRCAN	Tissue	Brain, caudate nucleus (CLONTECH #6575-1)
BRCOC	Tissue	Brain, corpus callosum (CLONTECH #6577-1)
BRHIP	Tissue	Brain, hippocampus (CLONTECH #6578-1)
BRSSN	Tissue	Brain, substantia nigra (CLONTECH #6580-1)
BRSTN	Tissue	Brain, subthalamic nucleus (CLONTECH #6581-1)
BRTHA	Tissue	Brain, thalamus (CLONTECH #6582-1)
CD34C	Primary culture cell	CD34+ cells (AllCells, LLC #CB14435M)
COLON	Tissue	Colon (Invitrogen #D6050-0)
CTONG	Tissue	Tongue, Cancer
D3OST	Primary culture cell	CD34+ cells (ODF induction for 3 days)
D6OST	Primary culture cell	CD34+ cells (ODF induction for 6 days)
D9OS	Primary culture cell	CD34+ cells (ODF induction for 9 days)
DFNES	Primary culture cell	Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509)

EP 1 347 046 A1

Table 2 (continued)

Library	Type	Origin, etc.
FCBBF	Tissue	Brain, Fetal
5 FEBRA	Tissue	Brain, Fetal (CLONTECH #64019-1)
FEHRT	Tissue	Heart, Fetal (STARATAGENE #738012)
FELNG	Tissue	Lung, Fetal (STARATAGENE #738020)
10 HCASM	Primary culture cell	Human coronary artery smooth muscle cells HCASMC (Toyobo #T305K-05)
HCHON	Primary culture cell	Human Chondrocytes HC (Toyobo #T402K-05)
HEART	Tissue	Heart (CLONTECH #64025-1)
15 HHDP	Primary culture cell	Human dermal papilla cells HDPC (Toyobo #THPCK-001)
HLUNG	Tissue	Lung (CLONTECH #64023-1)
IMR32	Culture cell	IMR32 cells (ATCC #CCL-127)
KIDNE	Tissue	Kidney (CLONTECH #64030-1)
20 LIVER	Tissue	Liver (CLONTECH #64022-1)
MAVGL	Tissue	Mammary Gland (CLONTECH #64037-1)
MESAN	Primary culture cell	Normal human mesangial cells NHMC56046-2 (Takara Shuzo #CC2559)
NESOP	Tissue	Esophagus (Invitrogen #D6060-01)
25 NOVAR	Tissue	Adult Ovary (STARATAGENE #735260)
NT2NE	Culture cell	NT2 cells concentrated after differentiation (NT2 Neuron)
NT2HI	Culture cell	NT2 cells treated by growth inhibitor for 2 weeks after RA induction for 5 weeks
30 NT2RP	Culture cell	NT2 cells treated by RA for 5 weeks
NTONG	Tissue	Tongue
OC3BF	Tissue	Brain, Fetal
PANCR	Tissue	Pancreas (CLONTECH #64031-1)
35 PEBLM	Primary culture cell	Human peripheral blood mononuclear cells HPBMC5939 (Takara Shuzo #CC2702)
PERIC	Tissue	Pericardium (Invitrogen #D6105-01)
40 PLACE	Tissue	Placenta
PROST	Tissue	Prostate (CLONTECH #64038-1)
PUAEN	Primary culture cell	Human pulmonary artery endothelial cells (Toyobo #T302K-05)
RECTM	Tissue	Rectum (Invitrogen #D6110-01)
45 SALGL	Tissue	Salivary Gland (CLONTECH #64026-1)
SKMUS	Tissue	Skeletal Muscle (CLONTECH #64033-1)
SKNMC	Culture cell	SK-N-MC cells (ATCC #HTB-10)
50 SKNSH	Culture cell	SK-N-SH cells (RCB #RCB0426)
SMINT	Tissue	Small Intestine (CLONTECH #64039-1)
SPLEN	Tissue	Spleen (CLONTECH #64034-1)
STOMA	Tissue	Stomach (CLONTECH #64090-1)
55 SYNOV	Tissue	Synovial membrane tissue from rheumatoid arthritis
TBAES	Tissue	Breast, Tumor (CLONTECH #64015-1)

Table 2 (continued)

Library	Type	Origin, etc.
TCOLN	Tissue	Colon, Tumor (CLONTECH #64014-1)
TESOP	Tissue	Esophageal, Tumor (Invitrogen #D6860-01)
TESTI	Tissue	Testis (CLONTECH #64027-1)
THYMU	Tissue	Thymus (CLONTECH #64028-1)
TKIDN	Tissue	Kidney, Tumor (Invitrogen #D6870-01)
TOVAR	Tissue	Ovary, Tumor (CLONTECH #64011-1)
TRACH	Tissue	Trachea (CLONTECH #64091-1)
TSTOM	Tissue	Stomach, Tumor (Invitrogen #D6920-01)
TUTER	Tissue	Uterus, Tumor (CLONTECH #64008-1)
UMVEN	Primary culture cell	Human umbilical vein endothelial cells HUVEC (Toyobo #T2OOK-05)
UTERU	Tissue	Uterus (CLONTECH #64029-1)

[0216] The cDNA library with the high fullness ratio (the fullness ratio of 5'-end, which was calculated for each cDNA library by using the protein coding region found in known mRNA species as an index, was 90% in average) prepared by the improved oligo-capping method was constructed by using a eukaryotic expression vector pME18SFL3. The vector contains SR α promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

(3) Assessment of the 5'-end completeness of clones derived from the cDNA library prepared by oligo-capping

[0217] With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

[0218] The 5'-end completeness of about 1110,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined by the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA; or even though the 5'-end sequence was shorter, if it contained the translation initiation codon it was judged to have the "full-length" sequence. Clones which did not contain the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparing with known human mRNA. As a result, the fullness ratio of the 5'-ends was 90%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high in the human cDNA clones obtained by the oligo-capping method.

EXAMPLE 2

Sequencing analysis of cDNA ends and selection of full-length clones

[0219] With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

[0220] For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequenc-

es, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

EXAMPLE 3

Analysis of the full-length nucleotide sequences

[0221] The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

[0222] Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

[0223] Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

EXAMPLE 4

Functional prediction by homology search

[0224] For the determined nucleotide sequences, GenBank, SwissProt, UniGene, and nr were searched by BLAST. The clones exhibiting higher homology, which were convenient to predict their functions based on the nucleotide sequences and deduced amino acid sequences, were selected based on the BLAST search hit data whose P value or E value was 10^{-4} or lower and for which the length of consensus sequence \times homology = 30 or higher in the amino acid database search. Further, from them, representative clones were selected, which are shown as Homology Search Result Data in the last part herein. Accordingly, the data shown herein are merely the representative data, and the molecule exhibiting homology to each clone is not limited thereto. Further, with respect to a part of clones, the BLAST search hit data that did not meet the criteria as described above are not shown herein.

EXAMPLE 5

Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

[0225] With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., Bioinformatics, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). In addition, the functional domain search can also be carried out on the PROSITE.

[0226] The search results obtained with the respective programs are shown below.

EP 1 347 046 A1

[0227] The clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADRGL20013520, ASTRO20005330, ASTRO20055750, BNGH420088500, BRACE20038000, BRACE20081720, BRACE20101710, BRACE20224480, BRACE20257100, BRACE20273890, BRALZ20013500, BRALZ20054710, BRALZ20077930, BRAMY20063970, BRAMY20284910, BRAWH20016860, BRAWH20064050, BRCOC10000870, BRCOC20078640, BRCOC20090520, BRCOC20101230, BRCOC20114180, BRCOC20121720, BRCOC20134480, BRCOC20136750, BRHIP20179200, BRHIP20198190, BRHIP20217620, BRSSN20003120, BRSSN20137020, COLON10001350, COLON20093370, CTONG20158660, CTONG20267700, D3OST20036070, D3OST20038560, D6OST20005070, FCBBF10001210, FCBBF10002430, FCBBF10003760, FCBBF10005740, FCBBF20042560, FCBBF30086440, FCBBF30095260, FCBBF30172550, FCBBF30238870, FEBRA20009090, FEBRA20029860, FEBRA20086620, FEBRA20092890, FEBRA20111460, FEBRA20130190, FEBRA20145780, FEBRA20235500, HCHON20064590, HCHON20067700, HCHON20086720, HEART20049410, HHDP20001040, HHDP20014320, KIDNE20011400, KIDNE20022620, KIDNE20126130, KIDNE20127450, LIVER20064690, MESAN10001260, MESAN20038510, MESAN20115970, MESAN20152770, MESAN20153910, NT2NE20118960, NT2NE20124480, NT2NE20183760, NT2RI20003480, NT2RI20023910, NT2RI20028470, NT2RI20040930, NT2RP70134990, NTONG20029700, NTONG20063010, OCBBF20019830, OCBBF20078920, OCBBF20086400, OCBBF20087010, OCBBF20116850, OCBBF20122620, OCBBF20130910, OCBBF20188730, PEBLM20075980, PLACE60086400, PROST20175290, SKNSH20028660, SMINT20009840, SMINT20022020, SMINT20073650, SMINT20095050, SMINT20105330, SMINT20127930, SMINT20153260, SMINT20157450, SMINT20173240, SMINT20178550, SMINT20191420, SMINT20192000, SPLEN20079510, SPLEN20095810, SPLEN20118300, SPLEN20141360, SPLEN20157880, SPLEN20171890, SPLEN20213830, STOMA20005390, STOMA20056640, STOMA20080500, STOMA20088380, SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970, SYNOV20004260, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000, TESOP20005690, TESTI20123560, TESTI20208400, TESTI20211220, TESTI20272960, TESTI20309170, TESTI20316870, TESTI20385960, TESTI20390260, TESTI20391770, TESTI20396130, TESTI20415170, TESTI20421490, TESTI20441940, TESTI20444180, TESTI20463580, THYMU10005360, THYMU20027560, THYMU20032870, THYMU20039810, THYMU20066100, THYMU20106710, THYMU20111830, THYMU20161640, THYMU20162190, THYMU20194420, THYMU20222890, THYMU20241850, TKIDN20005210, TRACH20029540, TRACH20034840, TRACH20050040, TRACH20069180, TRACH20085400, TRACH20136710, TRACH20145440, TRACH20180840, UTERU20158300, UTERU20158800, UTERU20161570

[0228] The clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid sequences. Of the search result, the clone name and the number of transmembrane domains are demarcated by a double slash mark (/).

ADIPS10000640//3, ADRGL20018540//1, ADRGL20035850//2, ASTRO20001410//1, ASTRO20005330//3, ASTRO20058630//4, ASTRO20190390//1, BEAST20004540//1, BGGI110000240//2, BRACE20006400//1, BRACE20038470//1, BRACE20039040//1, BRACE20039540//1, BRACE20051380//1, BRACE20059370//1, BRACE20061050//1, BRACE20063630//2, BRACE20067430//1, BRACE20069090//2, BRACE20101700//2, BRACE20116110//2, BRACE20147800//1, BRACE20153680//5, BRACE20163350//1, BRACE20179340//6, BRACE20188470//4, BRACE20195100//1, BRACE20201570//1, BRACE20210140//1, BRACE20224480//1, BRACE20224500//1, BRACE20228480//1, BRACE20232840//1, BRACE20238000//2, BRACE20274080//1, BRALZ20013500//2, BRALZ20064740//1, BRALZ20069760//3, BRALZ20073760//3, BRAMY20000860//2, BRAMY20002770//2, BRAMY20025840//1, BRAMY20039260//3, BRAMY20060920//1, BRAMY20063970//3, BRAMY20111960//1, BRAMY20112800//2, BRAMY20134140//2, BRAMY20135900//1, BRAMY20136210//1, BRAMY20144620//3, BRAMY20152110//1, BRAMY20174550//4, BRAMY20181220//2, BRAMY20195090//1, BRAMY20211390//1, BRAMY20211420//10, BRAMY20215230//1, BRAMY20218250//10, BRAMY20218670//3, BRAMY20229800//1, BRAMY20231720//1, BRAMY20247280//1, BRAMY20252180//2, BRAMY20273960//1, BRAMY20277170//5, BRAWH20015350//1, BRAWH20015890//2, BRAWH20016860//3, BRAWH20018730//10, BRAWH20030250//4, BRAWH20110790//3, BRAWH20121640//11, BRAWH20122580//2, BRAWH20132190//2, BRCAN20064010//2, BRCAN20071190//1, BRCAN20091560//1, BRCAN20103740//1, BRCAN20224720//1, BRCAN20273550//5, BRCAN20280360//6, BRCAN20285450//2, BRCOC20004040//4, BRCOC20006370//2, BRCOC20041750//1, BRCOC20077690//2, BRCOC20090520//1, BRCOC20091960//2, BRCOC20101230//6, BRCOC20107300//1, BRCOC20114180//3, BRCOC20121720//7, BRCOC20134480//3, BRCOC20136750//2, BRHIP20000870//2, BRHIP20003120//3, BRHIP20112000//1, BRHIP20118380//1, BRHIP20118910//2, BRHIP20121410//3, BRHIP20135100//1, BRHIP20183690//9, BRHIP20191490//2, BRHIP20191770//1, BRHIP20207430//1, BRHIP20208270//1, BRHIP20208590//2, BRHIP20217620//1, BRHIP20233090//1, BRHIP20234380//1, BRHIP20238880//1, BRHIP20283030//1, BRSSN20003120//7, BRSSN20043040//2, BRSSN20066110//2, BRSSN20137020//2, BRSSN20142940//1, BRSSN20146100//3, BRSSN20151990//2,

EP 1 347 046 A1

BRSSN20169050//2, BRSTN20002200//1, BRTHA20046290//2, BRTHA20046420//5, CTONG10000100//6,
CTONG10000940//1, CTONG10001650//1, CTONG20004690//5, CTONG20092570//7, CTONG20092580//2,
CTONG20095340//5, CTONG20099380//2, CTONG20103480//1, CTONG20105080//9, CTONG20114290//2,
CTONG20114740//3, CTONG20119200//2, CTONG20120770//1, CTONG20124220//3, CTONG20124730//1,
5 CTONG20131490//1, CTONG20132220//1, CTONG20133480//2, CTONG20139340//2, CTONG20149950//1,
CTONG20155400//1, CTONG20158660//9, CTONG20161850//2, CTONG20267700//1, D3OST10001090//5,
D3OST20036070//1, D3OST20038560//1, D3OST30002580//2, D9OST20002780//2, D9OST20015470//2,
D9OST20026730//1, D9OST20040180//7, DFNES20025880//1, FCBBF10000240//8, FCBBF10000380//1,
FCBBF10001150//1, FCBBF10001210//2, FCBBF10001550//1, FCBBF10002700//2, FCBBF10003220//1,
10 FCBBF10005460//1, FCBBF20032970//1, FCBBF20042560//3, FCBBF20051220//2, FCBBF30008470//2,
FCBBF30012350//1, FCBBF30024750//1, FCBBF30078290//1, FCBBF30086440//3, FCBBF30090690//1,
FCBBF30095260//2, FCBBF30123470//3, FCBBF30172550//1, FCBBF30175310//9, FCBBF30190850//1,
FCBBF30215060//4, FCBBF30238870//1, FCBBF30251420//1, ECBBF30279030//5, FEBRA20002100//5,
FEBRA20037260//1, FEBRA20080810//5, FEBRA20093520//1, FEBRA20095880//1, FEBRA20111460//1,
15 FEBRA20125070//1, FEBRA20130190//1, FEBRA20140100//3, FEBRA20145780//2, FEBRA20211710//1,
FEBRA20229630//3, FEBRA20235500//10, HCHON20000380//2, HCHON20007510//1, HCHON20008180//1,
HCHON20016650//7, HCHON20035130//1, HCHON20040020//1, HCHON20067700//1, HCHON20068710//4,
HEART20003060//1, HEART20005410//1, HEART20034320//2, HEART20049800//1, HEART20072310//2,
HHDPC10000830//3, HHDPC20001040//1, HHDPC20014320//1, HHDPC20034720//1, HHDPC20068620//1,
20 HHDPC20084140//1, HHDPC20091780//2, HLUNG10000550//2, KIDNE20003940//10, KIDNE20007770//2,
KIDNE20021910//4, KIDNE20022620//1, KIDNE20100070//2, KIDNE20101510//2, KIDNE20109730//2,
KIDNE20121880//5, KIDNE20125630//2, KIDNE20126010//1, KIDNE20130450//2, KIDNE20131580//7,
KIDNE20137340//4, KIDNE20181660//1, LIVER20035110//1, LIVER20045650//1, LIVER20062510//1,
LIVER20075680//1, LIVER20087060//1, LIVER20091180//1, MESAN20014500//6, MESAN20027090//2,
25 MESAN20038510//1, MESAN20089360//1, MESAN20103120//5, MESAN20115970//4, MESAN20139360//1,
MESAN20153910//1, NOVAR20000380//1, NT2NE20010050//1, NT2NE20021620//1, NT2NE20118960//4,
NT2NE20131890//1, NT2NE20132170//9, NT2NE20155110//1, NT2NE20156260//1, NT2NE20159740//3,
NT2NE20177520//2, NT2RI20023910//2, NT2RI20025400//2, NT2RI20054050//8, NT2RI20076290//8,
NT2RI20086220//4, NT2RI20091940//3, NT2RI20244600//6, NT2RP70072690//1, NT2RP70081610//6,
30 NT2RP70122910//2, NT2RP70125160//3, NT2RP70133740//4, NT2RP70137290//1, NT2RP70179710//1,
NT2RP70188020//1, NTONG20028070//1, NTONG20048060//1, NTONG20049910//1, NTONG20051530//1,
NTONG20061870//1, NTONG20067830//1, NTONG20092330//2, OCBBF10001750//2, OCBBF20013890//3,
OCBBF20023570//1, OCBBF20026630//1, OCBBF20037440//1, OCBBF20050770//1, OCBBF20059560//2,
OCBBF20063320//1, OCBBF20072320//1, OCBBF20080050//2, OCBBF20086400//1, OCBBF20086910//1,
35 OCBBF20088140//1, OCBBF20091150//1, OCBBF20107090//2, OCBBF20116850//2, OCBBF20120390//12,
OCBBF20130910//2, OCBBF20132850//3, OCBBF20155060//2, OCBBF20178880//1, OCBBF20180120//10,
OCBBF20180840//1, PANCR10000910//3, PEBLM20024320//2, PEBLM20040150//2, PEBLM20074370//1,
PERIC20004220//4, PLACE60121080//1, PLACE60161600//2, PLACE60177140//6, PROST20005050//1,
PROST20050670//1, PROST20107820//4, PROST20116600//2, PROST20120160//1, PROST20127800//3,
40 PROST20146010//3, PROST20164440//3, PROST20169800//1, PROST20170980//1, PROST20191640//1,
PUAEN20003740//2, PUAEN20030180//2, SALGL10001710//5, SKMUS20007800//7, SKMUS20011640//3,
SKMUS20020840//3, SKMUS20028210//1, SKMUS20028400//1, SKMUS20077400//1, SKNSH20031740//1,
SKNSH20051940//1, SKNSH20063040//3, SMINT20011990//1, SMINT20022020//4, SMINT20029760//1,
SMINT20040860//7, SMINT20049090//1, SMINT20053870//1, SMINT20095050//2, SMINT20100680//1,
45 SMINT20105330//1, SMINT20144890//1, SMINT20157450//5, SMINT20173240//3, SMINT20178550//3,
SMINT20192000//1, SPLEN20003070//2, SPLEN20008740//4, SPLEN20026950//1, SPLEN20029310//3,
SPLEN20095810//1, SPLEN20097330//1, SPLEN20118300//9, SPLEN20141360//1, SPLEN20141990//1,
SPLEN20144520//3, SPLEN20152760//2, SPLEN20157880//1, SPLEN20165310//1, SPLEN20167200//1,
SPLEN20169220//2, SPLEN20169720//1, SPLEN20171890//4, SPLEN20172120//2, SPLEN20186430//6,
50 SPLEN20211570//2, SPLEN20211940//3, SPLEN20213830//2, SPLEN20273950//1, SPLEN20292950//7,
SPLEN20293800//4, SPLEN20304950//2, SPLEN20329240//1, STOMA20006780//2, STOMA20008880//1,
STOMA20051200//1, STOMA20056670//1, STOMA20062130//1, STOMA20077450//2, STOMA20080500//4,
SYNOV20013560//1, SYNOV30001840//4, TBAES20003150//2, TESOP20005690//3, TESTI20001720//3,
TESTI20036380//6, TESTI20037560//1, TESTI20082330//1, TESTI20094120//8, TESTI20110280//1,
55 TESTI20123080//1, TESTI20123560//3, TESTI20128350//1, TESTI20136100//2, TESTI20136710//2,
TESTI20143390//8, TESTI20148000//1, TESTI20164100//3, TESTI20193360//1, TESTI20209810//1,
TESTI20209990//1, TESTI20214250//2, TESTI20230250//1, TESTI20231940//1, TESTI20237520//2,
TESTI20242990//2, TESTI20254220//7, TESTI20254860//1, TESTI20265970//2, TESTI20271850//2,

EP 1 347 046 A1

TESTI20272960//8, TESTI20284880//2, TESTI20291310//4, TESTI20291960//5, TESTI20303360//1,
TESTI20303420//1, TESTI20307700//2, TESTI20316870//1, TESTI20333000//2, TESTI20347180//6,
TESTI20347300//1, TESTI20355020//1, TESTI20357960//1, TESTI20370810//9, TESTI20373820//1,
TESTI20383880//1, TESTI20390410//1, TESTI20391770//3, TESTI20393530//1, TESTI20397760//2,
TESTI20401280//1, TESTI20422640//2, TESTI20441940//5, TESTI20444130//1, TESTI20449200//6,
TESTI20463520//1, TESTI20463580//1, THYMU20027560//4, THYMU20032870//1, THYMU20039810//3,
THYMU20040100//2, THYMU20106710//1, THYMU20111830//1, THYMU20141670//1, THYMU20147770//1,
THYMU20054300//1, THYMU20161640//4, THYMU20162190//2, THYMU20173980//2, THYMU20208300//1,
THYMU20216840//2, THYMU20229220//1, THYMU20241850//2, THYMU20277390//7, TRACH20002870//3,
TRACH20003590//1, TRACH20016210//1, TRACH20029540//1, TRACH20033230//6, TRACH20042920//6,
TRACH20050340//2, TRACH20068660//6, TRACH20076740//4, TRACH20085400//2, TRACH20085830//1,
TRACH20109550//2, TRACH20111130//1, TRACH20128110//5, TRACH20134950//1, TRACH20140820//1,
TRACH20145440//1, TRACH20168350//1, UMVEN20000690//1, UTERU20030570//5, UTERU20040610//1,
UTERU20055800//2, UTERU20076390//4, UTERU20094350//1, UTERU20135860//2, UTERU20158300//3,
UTERU20158400//2, UTERU20161570//6, UTERU20178100//1, UTERU20186740//1

[0229] The Names of clones whose deduced amino acid sequences were detected to have functional domains with P2am and the name of hit functional domains are as follows. The search result is indicated as "clone name//functional domain name" When the clone has multiple hit functional domains, they are listed and demarcated by a double slash mark (/); When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

3NB6910001910//tRNA synthetases class II (A)// tRNA synthetases class II (A)// DHHA1 domain

3NB6920014590//Homeobox domain

ADIPS2000+250//Zinc finger, C2H2 type// DNA binding domain with preference for// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// UvrD/REP helicase// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

ADRL1C001470//Cytochrome P450// Cytochrome P450

ADRG_L2C011190//Calponin homology (CH) domain// Calponin homology (CH) domain// Pou domain - N-terminal to homeobox domain

ADRG12C013300//TPR Domain// TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain

AD RGL2C035850//Cytochrome P450

ADRL2C043330//PHD-finger// Rabphilin-3A effector domain// C2 domain// C2 domain

ASTRO2C003010//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type ASTRO20012490//Eukaryotic initiation factor 1A

ASTRO2C027430//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//

Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

ASTRO2C033160//Mitochond carrier proteins// Mitochondrial carrier proteins// Mitochondrial carrier proteins

ASTRO2C055750//Collagen triple helix repeat (20 copies)// Heavy-metal-associated domain

ASTRO2C058630//Vacuolar sorting protein 9 (VPS9) domain

ASTRO2C064750//Zinc finger, C2H2 type// Nuclear transition protein 2 ASTRO20072210//PDZ domain (Also known as DFR or GLGE).

ASTRO2C084250//KH domain// Zinc finger, C3HC4 type (RING finger) ASTRO20105820//FAD binding domain

ASTRO2C106150//Calpain family cysteine protease// Calpain large subunit, domain III

ASTRO2C108190//Rap/ran-GAP

AS1K02C125520//DnaJ domain

ASTRO2C13500//ThiF family// Repeat in ubiquitin-activating (UBA) pro ASTRO20143630//KH domain// Bacterial regulatory proteins - cro family ASTRO20155290//TPR Domain// TPR Domain// TPR Domain

ASTRO2C163470//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type.

type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BGG110001930//UBX domain

BGGI120006160//Fumarylacetoacetate (FAA) hydrolase fam

BLADE2003400//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc
finger, C2H2 type// Zinc finger, C2H2 type

BLADE2003890//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc
finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2

type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2

type// Zinc finger C2H2 type

EP 1 347 046 A1

BNGH420088500//SAM domain (Sterile alpha motif)
 BRACE20003070//SAM domain (Sterile alpha motif)
 BRACE20011070//F-box domain.
 BRACE20027620//Dienelactone hydrolase family// Dienelactone hydrolase family
 5 BRACE20038000//ATP synthase, Delta/Epsilon chain// Dual specificity phosphatase, catalytic d
 BRACE20039540//Immunoglobulin domain// Adenovirus E3 region protein CR2
 BRACE20050900//TPR Domain// TPR Domain// TPR Domain// TPR Domain
 BRACE20052160//SAM domain (Sterile alpha motif)
 BRACE20053280//PDZ domain (Also known as DHR or GLGF).
 10 BRACE20053480//Ribosomal protein L22p/L17e// Glycosyl hydrolases family 38
 BRACE20053630//Plant thionins// Mitochondrial carrier proteins// Mitochondrial carrier proteins
 BRACE20057620//Eukaryotic initiation factor 4E
 BRACE20058580//L1 (late) protein
 BRACE20059370//FERM domain (Band 4.1 family)
 15 BRACE20060550//Ank repeat// Ank repeat// Ank repeat// PEP-utilizing enzymes
 BRACE20060720//WD domain, G-beta repeat// WD domain, G-beta repeat
 BRACE20060890//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRACE20062640//Alanine racemase// RNB-like proteins
 20 BRACE20063780//NOL1/NOP2/sun family
 BRACE20064880//KH domain// KH domain// KH domain
 BRACE20068590//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 25 BRACE20096200//Sir2 family// Sir2 family
 BRACE20107530//short chain dehydrogenase
 BRACE20115920//Spectrin repeat// Fes/CIP4 homology domain// Interleukin 10
 BRACE20148240//Ras family
 BRACE20151320//Zinc finger, C3HC4 type (RING finger)
 30 BRACE20153680//Sir2 family// Ion transport protein
 BRACE20163350//Immunoglobulin domain// Immunoglobulin domain
 BRACE20177200//RanBP1 domain.
 BRACE20188470//ABC transporter// Thymidylate kinase
 BRACE20190040//Integrase DNA binding domain
 35 BRACE20192440//Translation initiation factor IF-3
 BRACE20223330//3'-5' exonuclease// Adenylylsulfate kinase// Protein of unknown function DUF82
 BRACE20232840//4Fe-4S binding domain// ABC transporter// ABC transporter// ATPases associated with various
 cellular act
 BRACE20240740//Ribosomal protein L36
 40 BRACE20253330//PDZ domain (Also known as DHR or GLGF).
 BRACE20269200//Heat-labile enterotoxin alpha chain
 BRACE20273890//UBA domain
 BRACE20284100//Polysaccharide lyase family 8
 BRACE20286360//Alpha adaptin carboxyl-terminal domain
 45 BRALZ20013500//Keratin, high sulfur B2 protein// u-PAR/Ly-6 domain
 BRALZ20054710//Zinc finger, C3HC4 type (RING finger)// TRAF-type zinc finger
 BRALZ20058880//STAT protein
 BRALZ20077930//Ribosomal protein S27a
 BRAMY20000520//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 50 BRAMY20002770//DB module
 BRAMY20025840//Sec7 domain
 BRAMY20045240//Flagellar L-ring protein
 BRAMY20054880//Pou domain - N-terminal to homeobox domain
 BRAMY20103570//DNA binding domain with preference for A/T r
 55 BRAMY20104640//Eukaryotic protein kinase domain// Protein kinase C terminal domain
 BRAMY20111960//Ribosomal protein L36
 BRAMY20121620//TPR Domain// TPR Domain// TPR Domain// TPR Domain// PPR repeat
 BRAMY20124260//ZU5 domain// Death domain

EP 1 347 046 A1

BRAMY20148130//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// TBC domain
 BRAMY20153110//ACT domain// Biopterin-dependent aromatic amino acid hydroxylase
 BRAMY20157820//Kinesin motor domain
 5 BRAMY20162510//MAGE family
 BRAMY20167060//Collagen triple helix repeat (20 copies)
 BRAMY20174550//ABC transporter transmembrane region// Phosphoribulokinase// Adenylylsulfate kinase// FtsK/SpoIIIE family// ABC transporter
 BRAMY20211390//Zinc finger, C3HC4 type (RING finger)
 10 BRAMY20211420//Transient receptor// GGL domain
 BRAMY20213100//LIM domain containing proteins// GATA zinc finger// 'Paired box' domain
 BRAMY20215230//ribonuclease.
 BRAMY20217460//EF hand// EF hand// EF hand
 BRAMY20218250//Ion transport protein// Sir2 family// Ion transport protein
 15 BRAMY20240040//Nuclear transition protein 2
 BRAMY20245300//Fanconi anaemia group C protein// Metallo-beta-lactamase superfamily
 BRAMY20248490//Sodium:sulfate symporter transmembrane
 BRAMY20260910//Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 20 BRAMY20270730//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C3HC4 type (RING finger)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRAMY20271400//Phorb esters/diacylglycerol binding dom// PHD-finger
 25 BRAMY20277170//K_i channel tetramerisation domain// NADH-ubiquinone/plastoquinone oxidoreduc// Ion transport protein// Transmembrane region cyclic Nucleotide G
 BRAMY20285160//NTR/C345C module
 BRAWH20002320//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 BRAWH20011710//Ank repeat// Ank repeat// Ank repeat// CAP-Gly domain// CAP-Gly domain
 30 BRAWH20012390//EF hand// EF hand// EF hand
 BRAWH20016620//Eukaryotic protein kinase domain// EIAV coat protein. gp90 BRAWH20018730//Sugar (and other) transporter
 BRAWH20028110//4Fe-4S binding domain// LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins// Villin headpiece domain
 35 BRAWH20030250//jmyN domain
 BRAWH20064050//Sushi domain (SCR repeat)// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like domain// Granulins// Granulins// EGF-like domain
 BRAWH20075700//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 40 Zinc finger, C2H2 type
 BRAWH20096780//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 45 BRAWH20101360//Hexokinase
 BRAWH20103290//CRAL/TRIO domain// Spectrin repeat// Extracellular link domain// RhoGEF domain// PH domain
 BRAWH20110960//PCI domain
 BRAWH20112940//Similarity to lectin domain of ricin beta-chain, 3 copies.
 50 BRAWH20114000//Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
 BRAWH20117950//Carboxylesterases
 BRAWH20118230//Transforming growth factor beta like domain
 BRAWH20121640//eubacterial secY protein// Transmembrane amino acid transporter protein
 BRAWH20132190//Acetyltransferase (GNAT) family
 55 BRAWH20137480//Villin headpiece domain
 BRAWH20138660//Adaptor complexes medium subunit family
 BRAWH20149340//IQ calmodulin-binding motif// RhoGEF domain
 BRAWH20164460//Sigma-54 interaction domain// ATPases associated with various cellular activities (AAA)

EP 1 347 046 A1

BRAWH20171030//Adenylate kinase// NB-ARC domain// ATPases associated with various cellu
 BRAWH20185060//Integrase core domain
 BRCAN10001490// chromo' (CHRromatin Organization MOfifier)
 BRCAN20003460//Thioredoxin
 5 BRCAN20071190//Ubiquitin family// UBX domain
 BRCAN20091560//Rieske [2Fe-2S] domain// Phosphoglucose isomerase// FAD binding domain// Pyridine nucle-
 ctide-disulphide oxidoreductase// Phytoene dehydrogenase related enzyme
 BRCAN20124080//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 10 comain: G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 WD domain, G-beta repeat// WD domain, G-beta repeat
 BRCAN20273550//FATC domain
 BRCAN20273640//Formin Homology 2 Domain
 BRCAN20280210//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 15 BRCAN20280360//PAP2 superfamily
 BRCOC20001860//FliP family// Glycosyl hydrolase family 47
 BRCOC20004040//7 transmembrane receptor (rhodopsin family)// Neurohypophysial hormones, C-terminal Do-
 main
 BRCOC20006370//Plexin repeat
 20 BRCOC20008160//Spectrin repeat// Spectrin repeat// Tropomyosins// Spectrin repeat// Adenylate cyclase// Spec-
 trin repeat// FF domain// Spectrin repeat// Spectrin repeat// Spectrin repeat
 BRCOC20008500//Vacuolar sorting protein 9 (VPS9) domain// Ras association (RalGDS/AF-6) domain
 BRCOC20023230//Reverse transcriptase (RNA-dependent DNA polymerase)
 BRCOC20026640//Gag P30 core shell protein
 25 BRCOC20027510//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 BRCOC20031250//Triosephosphate isomerase
 BRCOC20035130//14-3-3 proteins
 BRCOC20037320//Apolipoprotein A1/A4/E family
 30 BRCOC20055420//Helix-loop-helix DNA-binding domain// Myristoyl-CoA
 BRCOC20074760//Herpesvirus UL25 family// Beige/BEACH domain
 BRCOC20110100//Integrase core domain
 BRCOC20121720//PHD-finger
 BRCOC20144000//Helicases conserved C-terminal domain
 35 BRCOC20178270//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 BRCOC20178560//LIM domain containing proteins// LIM domain containing proteins// LIM domain containing pro-
 teins// Ribosomal protein L24e// LIM domain containing proteins
 40 BRHIP10001290//Ribosomal protein S3, C-terminal domain// Similarity to lectin domain of ricin b
 BRHIP20001630//Protein of unknown function DUF16
 BRHIP20003120//Dehydrins// Reticulon
 BRHIP20005530//ThiF family
 BRHIP20046850//ICE-like protease (caspase) p20 domain// Aminotransferases class-I
 45 BRHIP20*15080//PH domain
 BRHIP20*18410//Fibronectin type I domain
 BRHIP20*19330//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor
 50 S-II (TFIIS): Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc
 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRHIP20*32860//PDZ domain (Also known as DHR or GLGF).
 BRHIP20*43730//MYND finger
 55 BRHIP20*53600//RNA recognition motif. (a.k.a. RRM, RBD, or
 BRHIP20*74040//GAF domain// GAF domain// Transposase, Mutator family// 3'5'-cyclic nucleotide phosphodi-
 esterase
 BRHIP20*76420//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

EP 1 347 046 A1

BRHIP20183690//DEAD/DEAH box helicase// Integral membrane protein DUF6// Integral membrane protein DUF7
 BRHIP20189980//bZIP transcription factor
 BRHIP20191860//Helix-loop-helix DNA-binding domain
 BRHIP20207990//Phorbol esters/diacylglycerol binding dom// Zinc finger, C3HC4 type (RING finger)// PHD-finger
 5 BRHIP20222280//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin)
 10 BRHIP20238600//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD do-
 main, G-beta repeat
 BRHIP20238880//wnt family of developmental signaling protei
 BRHIP20249110//Hexokinase// Hexokinase
 BRHIP20252450//Spectrin repeat// Spectrin repeat// Spectrin repeat// Phosphoenolpyruvate carboxykinase//
 15 Spectrin repeat// Spectrin repeat// Spectrin repeat// eRF1-like proteins// Spectrin repeat
 BRHIP20253660//SH3 domain
 BRHIP20283030//Cadherin domain// Cadherin domain// Cadherin domain// Cadherin domain// Cadherin domain//
 Cadherin domain// Cadherin domain// Cadherin domain
 BRHIP20285830//Intermediate filament proteins
 20 BRHIP30004570//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi
 domain (SCR repeat)
 BRHIP30004880//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III domain// Fibronectin type III do-
 main
 25 BRSSN2C003120//7 transmembrane receptor (metabotropic gluta
 BRSSN2C013420//Histone deacetylase family// Zn-finger in ubiquitin-hydrolases and o
 BRSSN2C014260//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat
 BRSSN2C015790//Pyridoxal-dependent decarboxylase
 30 BRSSN2C021600//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif
 BRSSN2C038200//Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif// Initiator RepB
 protein RasGEF domain
 BRSSN2C039370//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 BRSSN2C046790//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 35 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type
 BRSSN2C101100//Cold-shock DNA-binding domain
 BRSSN2C105870//ATPases associated with various cellular activities (AAA)
 BRSSN2C117950//short chain dehydrogenase
 BRSSN2C120810//Trypsin
 40 BRSSN2C146100//Adenylate and Guanylate cyclase catalytic domain// Adenylate and Guanylate cyclase catalytic
 domain// Zinc finger, C4 type (two domains)// Adenylate and Guanylate cyclase catalytic domain
 BRSSN2C176820//Wiskott Aldrich syndrome homology region 2
 BRSSN2C177570//Phosducin
 BRSSN2C187310//Ank repeat// Ank repeat// Ank repeat// Ank repeat
 45 BRSTN10000830//Kelch motif// Kelch motif// Kelch motif// Kelch motif
 BRSTN20005360//TPR Domain// TPR Domain
 BRTHA20000570//Reverse transcriptase (RNA-dependent DNA pol
 BRTHA20004740//Phosphoglycerate kinases// lactate/malate dehydrogenase// Flavoprotein// short chain dehy-
 drogenase// Zinc-binding dehydrogenases
 50 BRTHA20046250//Transmembrane 4 family
 CD34C3004240//RhoGAP domain
 COLON10001350//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain
 CTONG10000220//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 55 CTONG10000620//Sec7 domain// PH domain// Josephin
 CTONG10000930//Armadillo/beta-catenin-like repeats
 CTONG10000940//Ank repeat// Ank repeat// Ank repeat
 CTONG10002770//Calponin homology (CH) domain// Calponin homology (CH) domain

CTONG20009770//Proteasome/cyclosome repeat// Proteasome/cyclosome repeat// Proteasome/cyclosome re-
 peat// Proteasome/cyclosome repeat// Proteasome/cyclosome repeat// Proteasome/cyclosome repeat// Proteas-
 ome/cyclosome repeat

5 CTONG20014280//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat

CTONG20050280//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

10 CTONG20075860//Ribulose biphosphate carboxylase, smal

CTONG20076130//Hepatitis C virus non-structural protein NS2

CTONG20085950//SCAN domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG20092570//Integral membrane protein DUF6// Uncharacterized protein family UPF0005

15 CTONG20092700//BTB/POZ domain

CTONG20093950//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

CTONG20095340//E1-E2 ATPase

CTONG20096750//Disintegrin

20 CTONG20098440//Acyltransferase

CTONG20099550//GGL domain

CTONG20105080//Integral membrane protein DUF6

CTONG20106520//Pyridoxal-phosphate dependent enzyme CTONG20114290//Apolipoprotein A1/A4/E family

25 CTONG20118150//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

CTONG20118250//Eukaryotic-type carbonic anhydrase

CTONG20121010//Zinc finger, C2H2 type// CONSTANS family zinc finger// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type

30 CTONG20121580//Kinesin motor domain// FHA domain// Histidine carboxylase PI chain

CTONG20124010//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

35 CTONG20125640//Ribosomal protein L10// 60s Acidic ribos-
 omal protein CTONG20128430//Beta/Gamma crystallin// Beta/Gamma crystallin// Beta/Gamma crystallin// Beta/
 Gamma crystallin// Beta/Gamma crystallin// Similarity to lectin domain of ricin b

CTONG20129960//F-box domain// UvrD/REP helicase// UvrD/REP helicase// Viral (Superfamily 1) RNA helicase

CTONG20131560//PDZ domain (Also known as DHR or GLGF).

CTONG20133390//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type

40 CTONG20133520//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type CTONG20139860//Ank repeat// Ank repeat// Ank repeat

45 CTONG20140580//Domain of unknown function DUF25// SNF2 and others N-terminal domain// SNF2 and others
 N-terminal domain// Small cytokines (interleukin/chemokine), inter

CTONG20143690//MYND finger

CTONG20146300//Reverse transcriptase (RNA-dependent DNA pol

50 CTONG20149460//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif// Domain of unknown function// Kelch
 motif// Kelch motif// Kelch motif

CTONG20153300//C. elegans Srg family integral membrane prote// TBC domain

CTONG20153580//F-box domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat// Leucine Rich Repeat

55 CTONG20155180//RNA helicase

CTONG20156780//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

CTONG20158040//UTP—glucose-1-phosphate uridylyltransferase

CTONG20158660//Latrophilin/CL-1-like GPS domain// 7 transmembrane receptor (Secretin family)

CTONG20159530//Glypican
 CTONG20160560//DNA binding domain with preference for A/T rich regions
 CTONG20161850//Immunoglobulin domain
 CTONG20165050//Keratin, high sulfur B2 protein
 5 CTONG20186320//Kelch motif// Kelch motif// Kelch motif// Kelch motif
 CTONG20200310//RNB-like proteins
 D3OST20006180//Dual specificity phosphatase, catalytic domain
 D3OST20036070//Leucine Rich Repeat
 D9OST20023970//Glycosyl hydrolases family 18// Glycosyl hydrolases family 18
 10 D9OST20026730//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 D9OST20033970//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 15 finger, C2H2 type// Zinc finger, C2H2 type// Putative zinc finger in N-recogin// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type
 D9OST20035940//Mitochondri carrier proteins// Mitochondrial carrier proteins
 D9OST20040180//7 transmembrane receptor (rhodopsin family) DFNES20037420//Elongation factor Tu family
 DFNES20071130//Phosphotriesterase family// Phosphotriesterase family// Phosphotriesterase family
 20 FCBBF10000240//Phosphoenolpyruvate carboxylase// Bacterial Cytochrome Ubiquinol Oxidas// Glycosyl trans-
 ferase
 FCBBF10000630//Molluscan rhodopsin C-terminal tail// WW domain FCBBF10001150//Cadherin domain// Cad-
 herin domain// Cadherin domain// Cadherin domain// Cadherin domain
 FCBBF10001210//Immunoglobulin domain// Immunoglobulin domain FCBBF10001550//Glutamate/Leucine/Phe-
 25 nylalanine/Valine dehydrogenase FCBBF10001710//DM DNA binding domain// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 FCBBF10002800//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain FCBBF10003670//Ubiquitin carboxyl-terminal hydrolases famil
 30 FCBBF10003770//PDZ domain (Also known as DHR or GLGF)// PDZ domain (Also known as DHR or GLGF)//
 pfkB family carbohydrate kinase// PDZ domain (Also known as DHR or GLGF)// ThiC family// PDZ domain (Also
 known as DHR or GLGF)// PDZ domain (Also known as DHR or GLGF)// PDZ domain (Also known as DHR or
 GLGF)// TIR domain
 FCBBF10004120//RNA recognition motif. (a.k.a. RRM, RBD, or FCBBF10004370//KRAB box// Zinc finger, C2H2
 35 type// Ribosomal protein L37e// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type FCBBF10005060//CRAL/TRIO domain.
 FCBBF10005460//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type
 III domain// Fibronectin type III domain FCBBF10005500//Keratin, high sulfur B2 protein
 40 FCBBF10005740//Mitochon carrier proteins// Mitochondrial carrier proteins
 PCBBF20014270//Acyl CoA binding protein
 FCBBF20042170//Fibrillar collagen C-terminal domain
 FCBBF20049300//Olfactomedin-like domain
 FCBBF20059090//Zinc finger, C2H2 type
 45 FCBBF20064520//RNA recognition motif. (a.k.a. RRM, RBD, or
 FCBBF20067810//Nerve growth factor family// GTP1/OBG family// GTP1/OBG family// GTPase of unknown func-
 tion// ADP-ribosylation factor family// Ras family
 FCBBF20068820//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 50 FCBBF30010810//KRAB box// Rieske [2Fe-2S] domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-
 finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type
 FCBBF30012350//Eukaryotic protein kinase domain
 FCBBF30012810//Ubiquitin carboxyl-terminal hydrolases famil
 55 FCBBF30015940//Methyl-accepting chemotaxis protein (MCP) signaling domain
 FCBBF30016320//SecA protein, amino terminal region
 FCBBF30018550//Oxysterol-binding protein
 FCBBF30025560//Prolyl oligopeptidase family// Pou domain - N-terminal to homeobox doma// Homeobox domain

FCBBF30033050//Sm protein
 FCBBF30039020//Herpesvirus UL6 like// Growth-Arrest-Specific Protein 2 Domain
 FCBBF30049550//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Glutamine ami-
 dotransferases class-I// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//
 5 Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//
 ZU5 domain
 FCBBF30054440//PLAT/LH2 domain
 FCBBF30057290//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 10 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 FCBBF30078290//DNA binding domain with preference for A/T r FCBBF30086440//Pilin (bacterial filament)
 FCBBF30090690//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 15 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat C-terminal domain
 FCBBF30095260//DHH zinc finger domain
 FCBBF30129630//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 20 FCBBF30175310//C1q domain// CDP-alcohol phosphatidyltransferase FCBBF30190850//Sushi domain (SCR re-
 peat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Keratin, high sulfur B2 protein// Sushi domain
 (SCR repeat)// Phosphate transporter family
 FCBBF30195640//PHD-finger// CONSTANS family zinc finger// PHD-finger// PHD-finger// Hsp20/alpha crystallin
 family
 FCBBF30225660//Ank repeat// Ank repeat// Ank repeat// K⁺ channel tetramerisation domain// BTB/POZ domain
 25 FCBBF30233680//G10 protein
 FCBBF30238870//Laminin G domain// Thrombospondin N-terminal -like domains// Laminin G domain// von Will-
 ebrand factor type C domain// von Willebrand factor type C domain// EGF-like domain// EB module// EGF-like
 domain// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// Metallothionein// EGF-like domain// EGF-
 like domain// EGF-like domain
 30 FCBBF30240960//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 FCBBF30246630//Leucine Rich Repeat// Leucine Rich Repeat FCBBF30247930//Uncharacterized protein family
 UPF0004
 35 FCBBF30262510//Ank repeat// Fibronectin type III domain FCBBF30281880//Regulator of G protein signaling do-
 main// PX domain FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family
 FCBBF40001730//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
 domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
 40 FEBRA10001880//Eukaryotic protein kinase domain// Eukaryotic protein kinase domain
 FEBRA10001900//Zinc finger, C2H2 type
 FEBRA20004620//Rap/ran-GAP
 FEBRA20007620//Bacterial type II secretion system protein// DEAD/DEAH box helicase// Helicases conserved
 C-terminal domain
 FEBRA20018690//Zinc finger, C2H2 type
 45 FEBRA20024100//Ank repeat// Ank repeat// Myosin head (motor domain)// Myosin head (motor domain)
 FEBRA20025270//Sulfotransferase proteins
 FEBRA20026110//Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Dictyostelium (slime mold) re-
 peats// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 50 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Dictyostelium (slime mold) repeats// Zinc finger, C2H2 type
 55 FEBRA20034680//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain
 (4 repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type
 FEBRA20040530//KRAB box// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Bacterial dnaA protein// Zinc finger, C2H2 type// Zinc finger, C2H2

EP 1 347 046 A1

type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 FEBRA20080810//POT family
 FEBRA20082010//KRAB box// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 5 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 FEBRA20086620//Olfactomedin-like domain
 FEBRA20088360//Alpha adaptin carboxyl-terminal domai
 FEBRA20090290//Zinc finger, C3HC4 type (RING finger)
 FEBRA20092890//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 10 domain// Immunoglobulin domain// Immunoglobulin domain// Fibronectin type III domain
 FEBRA20097310//SAP domain// RNA recognition motif. (a.k.a. RRM, RBD, or
 FEBRA20111460//Hemagglutinin
 FEBRA20130190//Galactosyltransferase// Fringe-like
 FEBRA20132740//PH domain
 15 FEBRA20144170//Eukaryotic protein kinase domain// Protein kinase C terminal domain// Eukaryotic protein kinase
 domain
 FEBRA20167390//Sialyltransferase family
 FEBRA20171380//KRAB box// wnt family of developmental signaling protei// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 20 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2
 type// Putative zinc finger in N-recogin// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 FEBRA20184330//PDZ domain (Also known as DHR or GLGF).
 FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 25 FEBRA20195820//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger//
 Zinc finger, C2H2 type
 FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 FEBRA20196630//DEAD/DEAH box helicase// Helicases conserved C-terminal domain
 30 FEBRA20214970//Reverse transcriptase (RNA-dependent DNA pol
 FEBRA20222040//bZIP transcription factor// K-box region
 FEBRA20223220//EGF-like domain// EGF-like domain// Cadherin domain
 FEBRA20229630//NADH-Ubiquinone/plastoquinone (complex I)
 FEBRA20235500//Sodium Bile acid symporter family// ABC 3 transport family
 35 FEBRA20237640//SAM domain (Sterile alpha motif)
 FEHRT20003250//Phosphatidylinositol 3- and 4-kinases
 HCASM10000500//Ribonucleotide reductases// Nucleotidyltransferase domain
 HCHON10001760//Histone deacetylase family
 HCHON20000380//Glucose-6-phosphate dehydrogenase
 40 HCHON20003220//Formyl transferase// Phosphopantetheine attachment site// Protein of unknown function
 DUF132// Aldehyde dehydrogenase family
 HCHON20007510//Phosphotyrosine interaction domain (PTB/PID)// TBC domain
 HCHON20008150//RNA recognition motif. (a.k.a. RRM, RBD, or
 HCHON20008320//Glutamine synthetase// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 45 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// PHD-finger// Zinc finger, C2H2 type
 HCHON20009560//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 HCHON20010990//TPR Domain
 50 HCHON20015350//FtsJ cell division protein
 HCHON20015980//FG-GAP repeat// von Willebrand factor type A domain
 HCHON20016040//Insulin-like growth factor binding proteins
 HCHON20016650//Leucine rich repeat C-terminal domain// Immunoglobulin domain// Latrophilin/CL-1-like GPS
 domain// 7 transmembrane receptor (Secretin family)
 55 HCHON20035130//Zinc finger, C2H2 type// Zinc finger, C2H2 type
 HCHON20036420//Death effector domain
 HCHON20040020//Syntaxin
 HCHON20059870//Bromodomain// Bromodomain

HCHON20064590//Alpha-2-macroglobulin family N-terminal regi// Alpha-2-macroglobulin family N-terminal regi
 HCHON20068410//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ
 calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 5 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding
 motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmod-
 ulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmod-
 ulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 10 calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding
 motif// IQ calmodulin-binding motif
 HCHON20086720//Insulin-like growth factor binding pr// Thyroglobulin type-1 repeat
 HCHON20100740//EGF-like domain// F5/8 type C domain// F5/8 type C domain
 HEART20003060//Immunoglobulin domain// Immunoglobulin domain
 HEART20005410//u-PAR/Ly-6 domain
 15 HEART20017730//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 HEART20025980//Calponin homology (CH) domain
 HEART20034320//Glycosyl hydrolase family 9// Glycosyl hydrolase family 9
 HEART20061950//PDZ domain (Also known as DHR or GLGF).
 HEART20077670//Protein phosphatase 2A regulatory B subunit
 20 HEART20083640//NAD-dependent DNA ligase
 HEART20090000//Inositol polyphosphate phosphatase family, c
 HHDP C10000830//Zinc finger, C3HC4 type (RING finger)
 HHDP C20014320//Reprolysin family propeptide
 HHDP C20031130//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 25 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 HHDP C20034390//Cereal trypsin/alpha-amylase inhibitor
 30 HHDP C20034720//Glutathione S-transferases.
 HHDP C20068620//Immunoglobulin domain// Immunoglobulin domain
 HHDP C20091780//CUB domain// F5/8 type C domain
 HHDP C20092080//Thyroglobulin type-1 repeat
 HLUNG20016330//Methyl-accepting chemotaxis protein (MCP) s// PH domain// PH domain// Methanol dehydro-
 35 genase beta subunit
 HLUNG20017120//Peptidyl-tRNA hydrolase domain
 HLUNG20023340//KH domain
 HLUNG20033780//Birnavirus VP3 protein// RhoGEF domain// PH domain// SH3 domain
 IMR3220002430//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD do-
 40 main, G-beta repeat// WD domain, G-beta repeat KIDNE20002520//tRNA synthetases class I (E and Q)// tRNA
 synthetases class I (K)// tRNA synthetases class I (E and Q)
 KIDNE20003940//Phosphotransferase system, EIIC// FecCD transport family// ABC 3 transport family
 KIDNE20007770//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
 KIDNE20008010//Dihydropyridine sensitive L-type calcium
 45 KIDNE20009470//G-patch domain// Peptidase family M1
 KIDNE20017130//MYND finger// DM DNA binding domain// Ribosomal protein L36 KIDNE20020150//Ribosomal
 protein S13/S18// Hsp70 protein
 KIDNE20021680//3-hydroxyacyl-CoA dehydrogenase
 KIDNE20022620//Glycosyl transferase family 8
 50 KIDNE20024830//C2 domain// C2 domain
 KIDNE20027250//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 KIDNE20027950//KRAB box
 KIDNE20028390//Galactose-1-phosphate uridyl transfer// Galactose-1-phosphate uridyl transfer
 KIDNE20028720//ATP synthase (C/AC39) subunit
 55 KIDNE20028830//K-box region
 KIDNE20100070//AMP-binding enzyme
 KIDNE20101510//EGF-like domain// Trypsin Inhibitor like cysteine rich d// EGF-like domain// Keratin, high sulfur
 B2 protein// Zona pellucida-like domain

EP 1 347 046 A1

KIDNE20102710//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat KIDNE20107390//Histone-like transcription factor (CBF// GHMP kinases putative ATP-binding prote
KIDNE20107620//Eukaryotic protein kinase domain// Dihydropyridine sensitive L-type calcium
KIDNE20109730//Sodium
5 KIDNE20109890//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD do-
main, G-beta repeat// WD domain, G-beta repeat// Zinc finger, C4 type (two domains)// WD domain, G-beta repeat//
WD domain, G-beta repeat
KIDNE20121880//PMP-22/EMP/MP20/Claudin family
KIDNE20125630//ATP1G1/PLM/MAT8 family
10 KIDNE20127100//Kelch motif// Kelch motif// Kelch motif
KIDNE20127750//Bacterial regulatory proteins, tetR family
KIDNE20137340//Uncharacterized membrane protein family UPFO
KIDNE20182690//BAH domain// ELM2 domain
LIVER10004790//EF hand
15 LIVER20002160//Hsp70 protein
LIVER20035680//UvrD/REP helicase
LIVER20055440//RhoGAP domain
LIVER20064690//Serpins (serine protease inhibitors)
LIVER20080530//Ank repeat// Ank repeat// Ank repeat// SAM domain (Sterile alpha motif)
20 LIVER20087060//Guanylate-binding protein
LIVER20087510//PHD-finger
MAMGL10000830//LysM domain
MESAN10001260//von Willebrand factor type C domain// von Willebrand factor type C domain// von Willebrand
factor type C domain// von Willebrand factor type C domain// TILa domain// von Willebrand factor type C domain//
25 Keratin, high sulfur B2 protein// PEP-utilizing enzymes// von Willebrand factor type D domain// Plant PEC family
metallothionein// Trypsin Inhibitor like cysteine rich
MESAN20029400//Zinc finger, C3HC4 type (RING finger)// RNA polymerases M/15 Kd subunits
MESAN20031900//Zinc finger, C3HC4 type (RING finger)// Peroxidase// Zinc finger, C3HC4 type (RING finger)//
B-box zinc finger// Fibronectin type III domain
30 MESAN20035290//FYVE zinc finger
MESAN20036460//Corticotropin-releasing factor family MESAN20038510//Oxidoreductase molybdopterin bind-
ing d
MESAN20101140//LIM domain containing proteins
MESAN20103120//Sodium/calcium exchanger protein
35 MESAN20125860//Transferrin
MESAN20127350//Zinc knuckle
MESAN20130220//'chromo' (CHRromatin Organization Modifier)// Enoyl-CoA hydratase/isomerase family
MESAN20136110//KH domain// KH domain// Zinc finger, C3HC4 type (RING finger)
MESAN20141920//Troponin// Tropomyosins// Borrelia ORF-A
40 MESAN20154010//Tryptophan synthase alpha chain// Ribulose-phosphate 3 epimerase family// Indole-3-glycerol
phosphate synthases
MESAN20171520//PH domain
MESAN20174170//Regulator of G protein signaling domain
MESAN20186700//Hepatitis C virus RNA dependent RNA polymerase
45 NOVAR10000150//Cytosolic long-chain acyl-CoA thioester hydrolase
NT2NE20010490//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DM DNA binding domain// Zinc
finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type
50 NT2NE20021620//Vacuolar sorting protein 9 (VPS9) domain
NT2NE20080170//CRAL/TRIO domain
NT2NE20089970//KRAB box
NT2NE20118960//Gram-negative pili assembly chaperone
NT2NE20125050//Ezrin/radixin/moesin family
55 NT2NE20130190//Zinc finger, C2H2 type
NT2NE20132170//GNS1/SUR4 family// Transmembrane amino acid transporter protein
NT2NE20142210//PAS domain// PAS domain
NT2NE20157470//von Willebrand factor type A domain// Trypsin

EP 1 347 046 A1

NT2NE20158600//Ank repeat// Ank repeat
 NT2NE20177520//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)
 NT2NE20181650//Src homology domain 2
 5 NT2NE20183760//Calcitonin / CGRP / IAPP family
 NT2NE20184900//FF domain
 NT2RI20001330//Ank repeat// Ank repeat
 NT2RI20003480//Glypican
 NT2RI20005750//Cell division protein// Sigma-54 interaction domain// ADP-ribosylation factor family// ABC trans-
 10 porter// Ras family
 NT2RI20009870//Fringe-like
 NT2RI20025640//Reverse transcriptase (RNA-dependent DNA pol
 NT2RI20040930//Mitochondrial carrier proteins// Mitochondrial carrier proteins
 NT2RI20040990//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 15 NT2RI20046080//recA bacterial DNA recombination proteins
 NT2RI20048840//ADP-ribosylation factor family// G-protein alpha subunit
 NT2RI20054050//HSF-type DNA-binding domain
 NT2RI20056700//Spectrin repeat// Apolipoprotein A1/A4/E family// Olfactomedin-like domain
 NT2RI20091730//Molluscan rhodopsin C-terminal tail
 20 NT2RI20240080//TPR Domain// TPR Domain// TPR Domain
 NT2RI20244600//PAP2 superfamily.
 NT2RI20273230//DEAD/DEAH box helicase
 NT2RP60000770//Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 25 NT2RP60000850//C2 domain
 NT2RP70027380//PX domain// SH3 domain// RhoGAP domain
 NT2RP70032610//Peptidase family M20/M25/M40// Enol-ase
 NT2RP70036880//TBC. domain
 NT2RP70043480//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 30 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type
 NT2RP70044280//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 35 NT2RP70062230//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Pancreatic hormone peptides// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 NT2RP70063950//RhoGEF domain// Extracellular link domain// PH domain
 NT2RP70078420//PH domain// Putative GTP-ase activating protein for Arf// Ank repeat// Ank repeat
 NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an
 40 NT2RP70102350//Viral methyltransferase// Helix-loop-helix DNA-binding domain
 NT2RP70105210//Myc amino-terminal region
 NT2RP70157890//KRAB box
 NT2RP70159960//PH domain
 NT2RP70179710//Zinc finger, C3HC4 type (RING finger)// PHD-finger
 45 NT2RP70188710//Yeast PIR proteins
 NT2RP70192730//alpha/beta hydrolase fold
 NT2RP70194450//Bacterial regulatory proteins, crp family
 NT2RP70195430//Zinc-binding dehydrogenases
 NT2RP70198350//PWWP domain
 50 NTONG20009770//Coronavirus S2 glycoprotein// Peptidase family M3
 NTONG20013620//Sulfotransferase proteins
 NTONG20015870//Transposase// Outer membrane efflux protein// Intermediate filament proteins
 NTONG20028070//von Willebrand factor type C domain
 NTONG20029480//NAD-dependent DNA ligase
 55 NTONG20029700//Laminin N-terminal (Domain VI)// Laminin EGF-like (Domains III and V)// Laminin EGF-like
 (Domains III and V)// Laminin EGF-like (Domains III and V)
 NTONG20046140//Eukaryotic protein kinase domain// Aminoglycoside phosphotransferase
 NTONG20051530//Mov34/MPN/PAD-1 family// Extracellular link domain// Adhesin lipoprotein// Lectin C-type do-

main

NTONG20056570//WD domain, G-beta repeat// WD domain, G-beta repeat
 NTONG20063010//EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like domain// EGF-like do-
 main// Keratin, high sulfur B2 protein// Chitin binding Peritrophin-A domain// Zona pellucida-like domain
 5 NTONG20064840//C2 domain// C2 domain
 NTONG20067830//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat
 NTONG20070200//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 10 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type
 NTONG20070340//Collagen triple helix repeat (20 copies)// Collagen triple helix repeat (20 copies)// Collagen
 triple helix repeat (20 copies)
 NTONG20075220//RyR domain
 NTONG20076930//Alpha-2-macroglobulin family
 15 NTONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR
 Domain
 NTONG20092290//Immunoglobulin domain// Immunoglobulin domain
 NTONG20092330//Putative membrane protein
 20 OCBBF2C001850//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// DM DNA binding
 domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// MYND finger// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 OCBBF2C019380//Sushi domain (SCR repeat)// CUB domain
 OCBBF2C019830//Fibronectin type III domain// Fibronectin type III domain// EGF-like domain// Metallothionein
 25 family 5
 OCBBF2C020830//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family
 RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka
 PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology do-
 main)// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Putative GTP-ase acti-
 30 vating protein for Arf// Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-
 family RNA binding domains (aka PUM-HD, Pumilio homology domain)// Pumilio-family RNA binding domains (aka
 PUM-HD, Pumilio homology domain)
 OCBBF2C022900//IQ calmodulin-binding motif// Dishevelled specific domain// Kunitz/Bovine pancreatic trypsin
 inhibitor domain
 35 OCBBF2C023050//Phorbol esters/diacylglycerol binding domain (C1 domain)// Zinc finger, C3HC4 type (RING
 finger)// PHD-finger
 OCBBF2C023650//Ank repeat// Ank repeat// Helicases conserved C-terminal domain
 OCBBF2C030280//Lipoprotein amino terminal region
 OCBBF2C035930//NSF attachment protein
 40 OCBBF2C037440//Zinc finger, C3HC4 type (RING finger)
 OCBBF2C046120//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type
 45 OCBBF2C047300//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Putative zinc finger in N-recognition// Zinc finger, C2H2 type// DM DNA binding domain//
 Zinc finger, C2H2 type
 50 OCBBF2C049840//PDZ domain (Also known as DHR or GLGF).
 OCBBF2C050770//Dehydrins// Carnitine acyltransferase
 OCBBF2C053430//Extracellular link domain// Eukaryotic protein kinase domain// Protein kinase C terminal domain
 OCBBF2C053730//Ank repeat// Ank repeat// Patatin OCBBF20054760//Death domain
 OCBBF2C059560//UvrB/uvrC motif
 55 OCBBF2C066390//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type
 OCBBF2C071210//Spectrin repeat
 OCBBF2C071840//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger,

[illegible]

EP 1 347 046 A1

PEBLM20078320//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain (4 repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PERIC10000250//Prokaryotic DNA topoisomerase

PERIC20003870//Ribosomal L32p protein family// NAC domain// TS-N domain

PERIC20004220//Domain of unknown function

PERIC20004780//bZIP transcription factor

PLACE60003480//Chorismate synthase

PLACE60060420//Ribosomal protein L44

PLACE60079250//Bacterial flagellin N-terminus// Spectrin repeat// Spectrin repeat// Spectrin repeat// Caulimovirus movement protein// Spectrin repeat// Spectrin repeat// Spectrin repeat// UvrB/uvrC motif// Spectrin repeat// Spectrin repeat// Flagellar hook-associated protein 2// Spectrin repeat// KE2 family protein

PLACE60136500//dUTPase

PLACE60136720//Porphyobilinogen deaminase// GHMP kinases putative ATP-binding prot

PLACE60177140//7 transmembrane receptor (rhodopsin family)

PROST20047270//CRAL/TRIO domain.

PROST20047390//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20050670//Endothelin family

PROST20066880//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20079500//Hepatitis C virus non-structural protein NS4b// Ras association (RalGDS/AF-6) domain

PROST20100460//Cystine-knot domain

PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif)

PROST20114390//Integrase DNA binding domain

PROST20161950//RasGEF domain

PROST20169800//Cytochrome P450

PROST20170980//Immunoglobulin domain// Adenovirus E3 region protein CR1

PROST20171280//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20176170//LIM domain containing proteins// LIM domain containing proteins// LIM domain containing proteins

PROST20185830//GATA zinc finger

PROST20189770//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST20191640//Zinc finger, C3HC4 type (RING finger)// IBR domain// Keratin, high sulfur B2 protein// Zinc finger, C3HC4 type (RING finger)

PUAEN10000850//Uncharacterized protein family UPF0025// SecI family

PUAEN20011880//ZAP domain// Piwi domain

PUAEN20015860//PDZ domain (Also known as DHR or GLGF).// Regulator of G protein signaling domain

PUAEN20018820//Sterile alpha motif (SAM)/Pointed domain// Ets-domain

PUAEN20030180//Eukaryotic-type carbonic anhydrase

PUAEN20040670//FERM domain (Band 4.1 family)// FERM domain (Band 4.1 family)

PUAEN20055020//PH domain// START domain

PUAEN20078980//PH domain// FYVE zinc finger// Domain of unknown function DUF123// PH domain

PUAEN20083140//EF hand// PH domain// Neuregulin family

PUAEN20108240//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat

SALGL10001710//ENV polyprotein (coat polyprotein)

SKMUS20001980//Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat

SKMUS20003610//Syndecan domain// Mitochondrial carrier proteins// Mitochondrial carrier proteins// Mitochondrial carrier proteins

SKMUS20007800//Matrix protein (MA), p15// Prenyltransferase and squalene oxidase re

SKMUS20016220//Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat

EP 1 347 046 A1

repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat
 SKMUS20018230//Ank repeat
 SKMUS20018500//Coronavirus S2 glycoprotein
 SKMUS20024750//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat//
 5 Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 SKMUS20029200//Ank repeat// Respiratory-chain NADH dehydrogenase, 4// Ank repeat// Ank repeat// Ank re-
 peat// Ank repeat
 SKMUS20048970//Actin// Actin
 SKMUS20049030//Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin repeat// Nebulin
 10 repeat
 SKMUS20084740//Syndecan domain
 SKNSH20008190//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// AN1-like Zinc finger// Zinc finger, C2H2 type// Zinc
 15 finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type
 SKNSH20020540//Arginase family
 SKNSH20063040//Transmembrane 4 family// Transmembrane 4 family
 SMINT20001760//PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 20 SMINT20009840//Immunoglobulin domain// Immunoglobulin domain
 SMINT20013480//Metallo-beta-lactamase superfamily
 SMINT20028820//Eukaryotic protein kinase domain
 SMINT20035690//Ribosomal L29 protein
 SMINT20046090//Eukaryotic protein kinase domain
 25 SMINT2005C750//Kazal-type serine protease inhibitor domain
 SMINT20068010//Kinesin motor domain
 SMINT20071400//NOL1/NOP2/sun family
 SMINT20073650//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain
 30 SMINT20102780//Quinolate phosphoribosyl transferase
 SMINT20106290//Formamidopyrimidine-DNA glycosylase
 SMINT20106720//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 SMINT20110330//pKID domain
 35 SMINT20112730//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain
 SMINT20115880//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 SMINT20121220//Myosin tail
 SMINT20121950//2Fe-2S iron-sulfur cluster binding domains
 40 SMINT20122910//START domain
 SMINT20127930//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain
 SMINT2013C320//NB-ARC domain// ATPases associated with various cellular act
 SMINT20131810//ENV polyprotein (coat polyprotein)
 45 SMINT2013e130//Immunoglobulin domain
 SMINT20138900//Hrl repeat motif// Apolipoprotein A1/A4/E family// Intermediate filament proteins
 SMINT20144430//Immunoglobulin domain
 SMINT20144800//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 50 finger, C2H2 type
 SMINT20152940//Sigma-54 interaction domain// ATPases associated with various cellular activities (AAA)
 SMINT20154540//Glutathione S-transferases.
 SMINT20163960//Immunoglobulin domain
 SMINT20168570//Fascin domain
 55 SMINT20174360//haloacid dehalogenase-like hydrolase
 SMINT20177360//RNA recognition motif. (a.k.a. RRM, RBD, or
 SMINT20179740//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain

EP 1 347 046 A1

[illegible]

EP 1 347 046 A1

5

EP 1 347 046 A1

SYNOV20004260//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20007000//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20008240//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20009230//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain// Immunoglobulin domain
SYNOV20010880//Immunoglobulin domain// Immunoglobulin-domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20011110//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20013000//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20013560//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20013900//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
SYNOV20017080//UBX domain
SYNOV30001840//Asparagine synthase// AMP-binding enzyme
TBAES20000590//Cytochrome P450// Cytochrome P450
TBAES20002550//Peptidase family M1// Sigma-70 factor (ECF subfamily)
TBAES20003150//Cytochrome P450
TESOP20004000//Papain family cysteine protease
TESOP20005270//Sulfotransferase proteins
TESTI20001000//Formamidopyrimidine-DNA glycosylase
TESTI20001170//HORMA domain
TESTI20002780//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// PEP-utilizing enzymes
TESTI20017950//Regulator of G protein signaling domain
TESTI20023510//Transcription termination factor nusG
TESTI20031810//Bacterial luciferase// Domain of unknown function DUF28
TESTI20035960//Coproporphyrinogen III oxidase// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
WD domain, G-beta repeat// WD domain, G-beta repeat
TESTI20036380//Sulfate transporter family// Sodium Bile acid symporter family// STAS domain
TESTI20041690//Zinc finger, C3HC4 type (RING finger)// PHD-finger// IBR domain// Zinc finger, C3HC4 type
(RING finger)// B-box zinc finger// lactate/malate dehydrogenase// Fibronectin type III domain
TESTI20044230//Nucleosome assembly protein (NAP)// Nucleosome assembly protein (NAP)// Nucleosome as-
sembly protein (NAP)
TESTI20044310//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Chor-
ismate synthase// UvrB/uvrC motif TESTI20046750//Respiratory-chain NADH dehydrogenase, 4
TESTI20057750//RNase H// Integrase Zinc binding domain
TESTI20061110//Heavy-metal-associated domain// ATPases associated with various cellular act
TESTI20063830//Transposase
TESTI20066670//Acyl-CoA dehydrogenase
TESTI20067200//K-box region// Homeobox domain
TESTI20082330//Tudor domain
TESTI20083200//Dual specificity phosphatase, catalytic doma
TESTI20083940//Progesterone receptor
TESTI20088220//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// BolA-like protein// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Snake toxin// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type
TESTI20094470//Ets-domain
TESTI20098350//VAT-Nn domain
TESTI20108720//Protein phosphatase 2C
TESTI20121550//Putative GTP-ase activating protein for Arf

EP 1 347 046 A1

TESTI20127760//Cyclin// Calcitonin / CGRP / IAPP family
 TESTI20130010//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 TESTI20136710//Glypican// PHD-finger
 5 TESTI20143390//Integral membrane protein DUF6// Integral membrane protein DUF6
 TESTI20148000//Thioredoxin// Calsequestrin// Thioredoxin
 TESTI20152460//Putative zinc finger in N-recognin// PHD-finger
 TESTI20156100//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain
 10 TESTI20168480//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// MAM domain//
 Immunoglobulin domain
 TESTI20170350//Cystine-knot domain
 TESTI20184620//PH domain// Oxysterol-binding protein
 TESTI20185650//AN1-like Zinc finger
 15 TESTI20189410//PHD-finger
 TESTI20192800//HCO3- transporter family// Ank repeat// Ank repeat// Ank repeat// Alpha-2-macroglobulin family
 TESTI20197940//Domain of unknown function DUF27// Aconitase family (aconitate hydratase)
 TESTI20200710//PHD-finger// LIM domain containing proteins
 TESTI20202650//Repeat in HS1/Cortactin
 20 TESTI20204450//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Homeobox domain
 TESTI20208400//NOL1/NOP2/sun family
 TESTI20208710//WD domain, G-beta repeat// WD domain, G-beta repeat
 TESTI20211160//Hydroxyethylthiazole kinase family
 TESTI20214250//Mitochondrial carrier proteins// Mitochondrial carrier proteins
 25 TESTI20215990//F-box domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine
 Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 TESTI20216370//Carboxylesterases
 TESTI20226230//Adenylate kinase// Pou domain - N-terminal to homeobox d
 TESTI20229600//EGF-like domain// Metallothionein family 5// Replication protein// Laminin G domain// EGF-like
 30 domain// Laminin G domain// Insulin-like growth factor binding prot// EGF-like domain// Laminin G domain
 TESTI20230850//PAS domain
 TESTI20231920//Gag P30 core shell protein
 TESTI20232140//Phosphatidylinositol-specific phospholipase// Phosphatidylinositol-specific phospholipase
 TESTI20234140//EF hand// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat//
 35 WD domain G-beta repeat
 TESTI20234360//WW domain// PPIC-type PPIASE domain.
 TESTI20238610//MAGE family// Uncharacterized protein family UPF0057
 TESTI20242830//E2 (early) protein, C terminal// Syndecan domain
 TESTI20244190//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 40 domain
 TESTI20254860//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Reeler domain// Fibronectin type III domain// Fibronectin type III domain
 TESTI20255820//FERM domain (Band 4.1 family)// FERM domain (Band 4.1 family)// Isocitrate lyase
 TESTI20258460//PH domain
 45 TESTI20265970//Guanylate-binding protein
 TESTI20266740//Nucleotidyltransferase domain
 TESTI20272960//Transmembrane receptor (rhodopsin family)
 TESTI20275030//WD domain, G-beta repeat// WD domain, G-beta repeat
 TESTI20288910//SH3 domain
 50 TESTI20291960//Rhomboid family
 TESTI20303220//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Fibronectin type III domain// Alphaherpesvirus glycoprotein E// Fibronectin type III domain// Fibronectin
 type III domain// Fibronectin type III domain
 TESTI20303360//ENV polyprotein (coat polyprotein)
 55 TESTI20305540//Hantavirus nucleocapsid protein// Troponin// Apolipoprotein A1/A4/E family
 TESTI20308600//Homeobox domain
 TESTI20309170//TPR Domain// Zinc finger, C3HC4 type (RING finger)// Aldo/keto reductase family// ATP-depend-
 ent protease La (LON) domain

EP 1 347 046 A1

TESTI20314180//Trypsin// Trypsin
 TESTI20317600//Terpene synthase family
 TESTI20318090//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 5 TESTI20320440//Thioredoxin
 TESTI20320670//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM,
 RBD, or RNP domain)
 TESTI20326810//RanBP1 domain.
 TESTI20327680//EF hand// EF hand
 10 TESTI20328280//KE2 family protein// Troponin
 TESTI20333000//Immunoglobulin domain// Immunoglobulin domain
 TESTI20334410//DEAD/DEAH box helicase// Helicases conserved C-terminal domain
 TESTI20335050//Zinc finger, C3HC4 type (RING finger)
 TESTI20335200//Immunoglobulin domain
 15 TESTI20343070//Transcription factor E2F/dimerisation partner (TDP)
 TESTI20351830//K-box region
 TESTI20352620//Saposin A-type domain
 TESTI20355020//Tudor domain
 TESTI20358980//Homeobox domain// Collagen triple helix repeat (20 copies)
 20 TESTI20366910//Pyridine nucleotide-disulphide oxidoreductase
 TESTI20368330//Rhodanese-like domain
 TESTI20369690//PHD-finger
 TESTI20370020//Bleomycin resistance protein
 TESTI20370810//Ion transport protein// Polysaccharide biosynthesis protein// Sugar (and other) transporter
 25 TESTI20371030//Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif
 TESTI20375340//Phosphatidylinositol-specific phospholipase// UvrD/REP helicase// Phosphatidylinositol-specific
 phospholipase// C2 domain TESTI20377230//Thymidylate synthase
 TESTI20378190//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2
 30 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI20381040//Putative zinc finger in N-recognition
 TESTI20382750//Kinesin motor domain
 TESTI20383880//DnaJ domain
 TESTI20385960//Zinc finger, C3HC4 type (RING finger)// SPRY domain
 35 TESTI20390410//Arsenical pump membrane protein
 TESTI20391210//IQ calmodulin-binding motif
 TESTI20391770//Domain of unknown function DUF19// Thioredoxin
 TESTI20392250//PH domain// Phorbol esters/diacylglycerol binding domain (C1 domain)
 TESTI20392270//Cyclin
 40 TESTI20392760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leu-
 cine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 TESTI20393530//Mitochondrial carrier proteins
 TESTI20397760//E1-E2 ATPase
 TESTI20400940//K-box region
 45 TESTI20401020//Mitochondrial carrier proteins// Mitochondrial carrier proteins
 TESTI20408150//Keratin, high sulfur B2 protein
 TESTI20416640//Choline/ethanolamine kinase
 TESTI20432750//Cytochrome C and Quinol oxidase polypeptide
 TESTI20432820//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
 50 Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TESTI20436560//Spectrin repeat// Intermediate filament proteins// Intermediate filament tail domain
 TESTI20442760//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 55 domain// Immunoglobulin domain
 TESTI20443090//SAP domain// Zinc knuckle// Zinc finger, C3HC4 type (RING finger)
 TESTI20444130//ENV polyprotein (coat polyprotein)
 TESTI20449200//7 transmembrane receptor (metabotropic gluta

EP 1 347 046 A1

TESTI20451990//SAP domain
TESTI20455090//Intermediate filament proteins
TESTI20455620//Hsp70 protein
TESTI20456110//B-box zinc finger// Spectrin repeat// SPRY domain
TESTI20463580//Ubiquitin carboxyl-terminal hydrolases famil// Immunoglobulin domain// Ubiquitin carboxyl-ter-
minal hydrolase family
TESTI20467320//Wiskott Aldrich syndrome homology region 2
TESTI20467970//Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Do-
main// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neu-
rohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophy-
sial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hor-
mones, N-terminal Domain
TESTI20471410//Protein phosphatase 2C
TESTI20478850//Herpesvirus Glycoprotein B
THYMU10005360//Immunoglobulin domain// Viral coat protein// Immunoglobulin domain
THYMU10005540//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
THYMU20023380//Copper/zinc superoxide dismutase (SODC)
THYMU20027560//Domain of unknown function
THYMU20039810//MAC/Perforin domain
THYMU20105190//Myosin head (motor domain)
THYMU20106710//Immunoglobulin domain
THYMU20111180//Domain of unknown function DUF27// Aconitase family (aconitate hydratase)
THYMU20115850//Reverse transcriptase (RNA-dependent DNA pol
THYMU20118520//Ubiquitin family
THYMU20122730//VHS domain
THYMU20126900//3-hydroxyacyl-CoA dehydrogenase// UDP-glucose/GDP-mannose dehydrogenase fa
THYMU20130890//Ribosomal protein S9/S16
THYMU20141670//Phorbol esters/diacylglycerol binding dom// PHD-finger// FYVE zinc finger
THYMU20142040//Wiskott Aldrich syndrome homology region 2
THYMU20143270//Cytochrome C oxidase subunit II
THYMU20147770//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain
THYMU20159430//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
domain// Immunoglobulin domain
THYMU20161640//PMP-22/EMP/MP20/Claudin family// Integral membrane protein DUF6
THYMU20169680//Ank repeat// Ank repeat
THYMU20172150//WD domain, G-beta repeat
THYMU20194360//Kelch motif
THYMU20201980//PH domain// Phorbol esters/diacylglycerol binding domain (C1 domain)// FYVE zinc finger//
PH domain
THYMU20202890//Eukaryotic protein kinase domain
THYMU20209590//PH domain// Dynamin GTPase effector domain
THYMU20216840//PHD-finger
THYMU20229220//Closterovirus coat protein
THYMU20239000//Collagen triple helix repeat (20 copies)
THYMU20240710//tRNA synthetases class I (E and-Q)
THYMU20241850//Class II histocompatibility antigen, beta// Immunoglobulin domain
THYMU20247480//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
THYMU20279750//Immunoglobulin domain
TKIDN10000010//Mitochondrial import inner membrane transloc
TKIDN20004640//GHMP kinases putative ATP-binding protei
TKIDN20047480//Eukaryotic protein kinase domain
TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat
TRACH20002870//PMP-22/EMP/MP20/Claudin family
TRACH20003590//Cytochrome P450
TRACH20005020//Ank repeat// MutT-like domain

EP 1 347 046 A1

TRACH20005400//ADP-ribosylation factor family// Ras family
 TRACH20016210//Fucosyl transferase
 TRACH20019960//Na+/K+ ATPase C-terminus
 TRACH20028030//DnaJ domain// DnaJ central domain (4 repeats)// DnaJ C terminal region
 5 TRACH20033230//Nucleoside transporter// Sugar (and other) transporter// Influenza RNA-dependent RNA
 polymerase subunit PB2
 TRACH20041830//Thioredoxin// Thioredoxin
 TRACH20042920//Glutamine synthetase
 TRACH20048450//Phospholipase D. Active site motif// Phospholipase D. Active site motif
 10 TRACH20050040//Plexin repeat
 TRACH20067620//Core-2/I-Branching enzyme
 TRACH20069180//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain
 TRACH20076740//Reduced folate carrier
 15 TRACH20076760//Keratin, high sulfur B2 protein
 TRACH20077540//Zinc finger, C2H2 type// G-patch domain
 TRACH20079690//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II
 (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 20 TRACH20084720//tRNA synthetases class I (C)// tRNA synthetases class I (I, L, M and V)
 TRACH20085400//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin
 domain// Immunoglobulin domain// Immunoglobulin domain
 TRACH20085830//Cytochrome P450
 TRACH20096610//Intermediate filament proteins// Intermediate filament tail domain
 25 TRACH20105870//Regulatory subunit of type II PKA R-subunit// eIF4-gamma/eIF5/eIF2-epsilon
 TRACH20121380//Raf-like Ras-binding domain// Leptin// Raf-like Ras-binding domain// LGN motif, putative GEF
 specific for G-alpha GTPase
 TRACH20128230//Immunoglobulin domain// Chitin synthase// Immunoglobulin domain// Immunoglobulin domain//
 Immunoglobulin domain
 30 TRACH20135520//TBC domain// Rhodanese-like domain
 TRACH20136710//Immunoglobulin domain
 TRACH20141240//Granulins
 TRACH20145440//von Willebrand factor type D domain
 TRACH20154860//Squash family of serine protease inhibitor// Zinc finger, C4 type (two domains)// T-box// Zinc
 35 finger, C4 type (two domains)// Ligand-binding domain of nuclear hormone
 TRACH20163170//Homeobox domain
 TRACH20164980//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Transcription factor S-II (TFIIS)// Zinc
 40 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
 TRACH20167220//wnt family of developmental signaling protein// PLAT/LH2 domain// Fibroblast growth factor
 TRACH20184490//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 finger, C2H2 type// Zinc finger, C2H2 type
 45 TRACH20190240//EGF-like domain// EGF-like domain// Trypsin Inhibitor like cysteine rich domain// EGF-like do-
 main
 TSTOM20005690//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif
 TUTER20002830//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 UMVEN10001860//PH domain// RhoGAP domain// bZIP transcription factor
 50 UMVEN20000690//F5/8 type C domain
 UTERU20030570//ABC 3 transport family// Voltage gated chloride channels// CBS domain// CBS domain
 UTERU20046640//Rotavirus NS26
 UTERU20046980//EB module// TNFR/NGFR cysteine-rich region// Furin-like cysteine rich region// Thrombospon-
 din type 1 domain
 55 UTERU20050690//Androgen receptor
 UTERU20055330//Reverse transcriptase (RNA-dependent DNA polymerase)
 UTERU20055480//AMP-binding enzyme
 UTERU20055930//Helper component proteinase

UTERU20064000//Peptidase family M1
 UTERU20065930//Hr1 repeat motif// PDZ domain (Also known as DHR or GLGF).
 UTERU20115740//KRAB box
 UTERU20116570//Villin headpiece domain
 5 UTERU20119060//ADP-ribosyl cyclase
 UTERU20144640//Cholesteryl glycolate hydrolase
 UTERU20145480//KRAB box// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type//
 TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// wnt family of developmental signaling
 proteins// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
 10 finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
 C2H2 type// Zinc finger, C2H2 type
 UTERU20146310//Diacylglycerol kinase accessory domain (pres
 UTERU20161570//7 transmembrane receptor (rhodopsin family)
 15 UTERU20168220//Cell division protein// Integrase Zinc binding domain// GTPase of unknown function
 UTERU20176130//Putative GTP-ase activating protein for Arf
 UTERU20176320//SMC domain N terminal domain// Tropomyosins
 UTERU20178100//Aminotransferases class-III pyridoxal-pho
 UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain
 20 UTERU20183640//Immunoglobulin domain
 UTERU20185230//DUP family of yeast membrane proteins

EXAMPLE 6

Functional categorization based on the full-length nucleotide sequences

[0230] The functional prediction and categorization of the proteins encoded by the clones were carried out based
 on the result of homology search of the databases of GenBank, Swiss-Prot, UniGene and nr (see the Homology Search
 Result Data) for the full-length nucleotide sequences and the result of domain search of the amino acid sequences
 30 deduced from the full-length nucleotide sequences (see Example 5).

[0231] The clone predicted to belong to the category of secretory protein/membrane protein means a clone having
 hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extra-
 cellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell ad-
 35 hesion, collagen, connective tissue, etc., suggesting that it is a secretory or membrane protein, or means a clone in
 which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested
 by the results of PSORT and SOSUI analyses for deduced ORF.

[0232] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data
 with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0233] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit
 40 data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain,
 etc., suggesting that the clone encodes a signal transduction-related protein.

[0234] The clone predicted to belong to the category of transcription-related protein means a clone having hit data
 with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes
 a transcription-related protein.

45 [0235] The clone predicted to belong to the category of disease-related protein means a clone having hit data with
 some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related
 protein, or means a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, or UniGene,
 where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance
 in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database.

50 [0236] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone
 having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No (Enzyme commission number),
 etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0237] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means
 a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth,
 55 apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0238] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data
 with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the
 clone encodes a cytoskeleton-related protein.

[0239] The clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0240] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0241] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0242] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0243] The clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0244] The clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0245] In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional category in this classification, and there is the possibility that other functions are newly assigned to the protein.

[0246] The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 652 clones

ADIPS10000640, ADRGL10001470, ADRGL20013520, ADRGL20018540, ADRGL20035850, ASTRO20001410, ASTRO20005330, ASTRO20033160, ASTRO20055750, ASTRO20058630, ASTRO20190390, BEAST20004540, BGGI110000240, BNGH420088500, BRACE20006400, BRACE20038000, BRACE20038470, BRACE20039040, BRACE20039540, BRACE20051380, BRACE20053630, BRACE20059370, BRACE20060550, BRACE20061050, BRACE20063530, BRACE20067430, BRACE20069090, BRACE20081720, BRACE20101700, BRACE20101710, BRACE20116110, BRACE20147800, BRACE20153680, BRACE20163350, BRACE20179340, BRACE20188470, BRACE20195100, BRACE20201570, BRACE20210140, BRACE20224480, BRACE20224500, BRACE20228480, BRACE20232340, BRACE20238000, BRACE20273890, BRACE20274080, BRALZ20013500, BRALZ20054710, BRALZ20054740, BRALZ20069760, BRALZ20073760, BRALZ20077930, BRAMY20000860, BRAMY20002770, BRAMY20025840, BRAMY20039260, BRAMY20060920, BRAMY20063970, BRAMY20111960, BRAMY20112800, BRAMY20124260, BRAMY20134140, BRAMY20135900, BRAMY20136210, BRAMY20144620, BRAMY20152110, BRAMY20174550, BRAMY20181220, BRAMY20195090, BRAMY20211390, BRAMY20211420, BRAMY20215230, BRAMY20218250, BRAMY20218670, BRAMY20229800, BRAMY20231720, BRAMY20247280, BRAMY20252180, BRAMY20273960, BRAMY20277170, BRAMY20284910, BRAMY20285160, BRAWH20015350, BRAWH20015890, BRAWH20016860, BRAWH20018730, BRAWH20030250, BRAWH20064050, BRAWH20110790, BRAWH20112940, BRAWH20117950, BRAWH20118230, BRAWH20121640, BRAWH20122580, BRAWH20132190, BRCAN20064010, BRCAN20071190, BRCAN20091560, BRCAN20103740, BRCAN20224720, BRCAN20273550, BRCAN20280360, BRCAN20285450, BRCOC10000870, BRCOC20004040, BRCOC20006370, BRCOC20041750, BRCOC20077690, BRCOC20078640, BRCOC20090520, BRCOC20101230, BRCOC20107300, BRCOC20114180, BRCOC20121720, BRCOC20134480, BRCOC20136750, BRHIP10001290, BRHIP20000870, BRHIP20003120, BRHIP20103090, BRHIP20111230, BRHIP20118380, BRHIP20118910, BRHIP20121410, BRHIP20135100, BRHIP20174040, BRHIP20174200, BRHIP20183690, BRHIP20191490, BRHIP20191770, BRHIP20198190, BRHIP20207430, BRHIP20208270, BRHIP20208590, BRHIP20217620, BRHIP20233090, BRHIP20234380, BRHIP20238880, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20043040, BRSSN20066110, BRSSN20120810, BRSSN20137320, BRSSN20142940, BRSSN20146100, BRSSN20151990, BRSSN20169050, BRSTN20002200, BRTHA20004740, BRTHA20046290, BRTHA20046420, COLON10001350, COLON20093370, CTONG10000100, CTONG10000940, CTONG10001650, CTONG20004690, CTONG20009770, CTONG20092570, CTONG20092580, CTONG20095340, CTONG20099380, CTONG20103480, CTONG20105080, CTONG20114740, CTONG20119200, CTONG20120770, CTONG20124730, CTONG20131490, CTONG20132220, CTONG20133480, CTONG20139340, CTONG20139950, CTONG20155400, CTONG20158660, CTONG20159530, CTONG20161850, CTONG20267700, D3OST10001090, D3OST20036070, D3OST20038560, D3OST30002580, D6OST20005070, D9OST20002780, D9OST20015470, D9OST20023970, D9OST20026730, D9OST20035940, D9OST20040180, DFNES20025880, FCBBF10000340, FCBBF10000380, FCBBF10001150, FCBBF10001210, FCBBF10001550, FCBBF10002430, FCBBF10002700, FCBBF10003220, FCBBF10003760, FCBBF10005460, FCBBF10005740, FCBBF20032970, FCBBF20042560, FCBBF20049300, FCBBF20051220, FCBBF30008470, FCBBF30024750, FCBBF30078290,

EP 1 347 046 A1

FCBBF30083620, FCBBF30086440, FCBBF30090690, FCBBF30095260, FCBBF30123470, FCBBF30172550,
 FCBBF30175310, FCBBF30190850, FCBBF30215060, FCBBF30238870, FCBBF30251420, FCBBF30279030,
 FEBRA20002100, FEBRA20004620, FEBRA20009090, FEBRA20029860, FEBRA20037260, FEBRA20080810,
 FEBRA20086620, FEBRA20092890, FEBRA20093520, FEBRA20095880, FEBRA20111460, FEBRA20125070,
 5 FEBRA20130190, FEBRA20140100, FEBRA20145780, FEBRA20211710, FEBRA20223220, FEBRA20229630,
 FEBRA20235500, HCHON20000380, HCHON20008180, HCHON20015980, HCHON20016040, HCHON20016650,
 HCHON20040020, HCHON20064590, HCHON20067700, HCHON20068710, HCHON20086720, HCHON20100740,
 HEART20003060, HEART20005410, HEART20034320, HEART20049410, HEART20049800, HEART20072310,
 HHDP20001040, HHDP20014320, HHDP20034720, HHDP20068620, HHDP20084140, HHDP20091780,
 10 HHDP20092080, HLUNG10000550, KIDNE20003940, KIDNE20007770, KIDNE20011400, KIDNE20021910,
 KIDNE20022620, KIDNE20100070, KIDNE20101510, KIDNE20109730, KIDNE20121880, KIDNE20125630,
 KIDNE20126010, KIDNE20126130, KIDNE20127450, KIDNE20130450, KIDNE20131580, KIDNE20137340,
 KIDNE20181660, LIVER20035110, LIVER20045650, LIVER20055200, LIVER20062510, LIVER20064690,
 LIVER20075680, LIVER20087060, LIVER20091180, MESAN10001260, MESAN20014500, MESAN20027090,
 15 MESAN20038510, MESAN20089360, MESAN20103120, MESAN20115970, MESAN20125860, MESAN20139360,
 MESAN20152770, MESAN20153910, MESAN20174170, NOVAR20000380, NT2NE20010050, NT2NE20021620,
 NT2NE20068130, NT2NE20118960, NT2NE20124480, NT2NE20131890, NT2NE20132170, NT2NE20155110,
 NT2NE20156260, NT2NE20157470, NT2NE20159740, NT2NE20177520, NT2NE20183760, NT2RI20003480,
 NT2RI20023910, NT2RI20025400, NT2RI20028470, NT2RI20040930, NT2RI20054050, NT2RI20056700,
 20 NT2RI20076290, NT2RI20086220, NT2RI20091940, NT2RI20244600, NT2RP70072690, NT2RP70081610,
 NT2RP70122910, NT2RP70125160, NT2RP70133740, NT2RP70134990, NT2RP70137290, NT2RP70179710,
 NT2RP70188020, NT2RP70192730, NT2RP70198350, NTONG20028070, NTONG20029700, NTONG20048060,
 NTONG20049910, NTONG20051530, NTONG20061870, NTONG20063010, NTONG20067830, NTONG20076930,
 NTONG20092330, OCBBF10001750, OCBBF20013890, OCBBF20019830, OCBBF20023570, OCBBF20026630,
 25 OCBBF20046690, OCBBF20050770, OCBBF20059560, OCBBF20063320, OCBBF20071210, OCBBF20072320,
 OCBBF20080050, OCBBF20086400, OCBBF20086910, OCBBF20087010, OCBBF20088140, OCBBF20091150,
 OCBBF20107090, OCBBF20108630, OCBBF20116850, OCBBF20120390, OCBBF20122620, OCBBF20130910,
 OCBBF20132850, OCBBF20145760, OCBBF20155060, OCBBF20178880, OCBBF20180120, OCBBF20180840,
 OCBBF20188730, PANCR10000910, PEBLM10000710, PEBLM20024320, PEBLM20040150, PEBLM20074370,
 30 PEBLM20075980, PERIC20004220, PLACE60086400, PLACE60121080, PLACE60161600, PLACE60177140,
 PROST20005050, PROST20005670, PROST20107820, PROST20116600, PROST20120160, PROST20127800,
 PROST20146010, PROST20164440, PROST20169800, PROST20170980, PROST20175290, PUAEN20003740,
 PUAEN20030180, SALGL10001710, SKMUS20003610, SKMUS20007800, SKMUS20011640, SKMUS20020840,
 SKMUS20028210, SKMUS20028400, SKMUS20077400, SKNSH20028660, SKNSH20031740, SKNSH20051940,
 35 SKNSH20063040, SMINT20009840, SMINT20011990, SMINT20022020, SMINT20029760, SMINT20040860,
 SMINT20050750, SMINT20053870, SMINT20073650, SMINT20095050, SMINT20100680, SMINT20105330,
 SMINT20106720, SMINT20121950, SMINT20127930, SMINT20144430, SMINT20144890, SMINT20153260,
 SMINT20154540, SMINT20157450, SMINT20173240, SMINT20178550, SMINT20191420, SMINT20192000,
 SPLEN20003070, SPLEN20021660, SPLEN20029310, SPLEN20079510, SPLEN20095810, SPLEN20097330,
 40 SPLEN20118300, SPLEN20141360, SPLEN20141990, SPLEN20142100, SPLEN20144520, SPLEN20152760,
 SPLEN20157880, SPLEN20165310, SPLEN20167200, SPLEN20169220, SPLEN20169720, SPLEN20171890,
 SPLEN20172120, SPLEN20179810, SPLEN20186430, SPLEN20211570, SPLEN20211940, SPLEN20213830,
 SPLEN20273950, SPLEN20292950, SPLEN20293800, SPLEN20304950, SPLEN20329240, STOMA20005390,
 STOMA20005670, STOMA20006400, STOMA20006780, STOMA20008880, STOMA20051200, STOMA20056640,
 45 STOMA20056670, STOMA20062130, STOMA20077450, STOMA20080500, STOMA20088380, STOMA20092530,
 SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790, SYNOV20002970, SYNOV20004260,
 SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000,
 SYNOV20013560, SYNOV20013900, SYNOV30001840, TBAES20003150, TESOP20004000, TESOP20005690,
 TESTI20001720, TESTI20036380, TESTI20037560, TESTI20094120, TESTI20110280, TESTI20123080,
 50 TESTI20123560, TESTI20128350, TESTI20136100, TESTI20136710, TESTI20143390, TESTI20148000,
 TESTI20164100, TESTI20193360, TESTI20209810, TESTI20209990, TESTI20211220, TESTI20214250,
 TESTI20216370, TESTI20230250, TESTI20231940, TESTI20242990, TESTI20244190, TESTI20254220,
 TESTI20254860, TESTI20265970, TESTI20271850, TESTI20272960, TESTI20284880, TESTI20291310,
 TESTI20291960, TESTI20303220, TESTI20303360, TESTI20303420, TESTI20307700, TESTI20309170,
 55 TESTI20314180, TESTI20316870, TESTI20333000, TESTI20335200, TESTI20347180, TESTI20347300,
 TESTI20352620, TESTI20357960, TESTI20370810, TESTI20373820, TESTI20383880, TESTI20390260,
 TESTI20390410, TESTI20391770, TESTI20393530, TESTI20396130, TESTI20397760, TESTI20401020,
 TESTI20401280, TESTI20415170, TESTI20421490, TESTI20422640, TESTI20441940, TESTI20442760,

EP 1 347 046 A1

TESTI20444130, TESTI20444180, TESTI20449200, TESTI20463520, TESTI20463580, TESTI20465350, THYMU10005360, THYMU10005540, THYMU20027560, THYMU20032870, THYMU20039810, THYMU20066100, THYMU20081490, THYMU20100410, THYMU20106710, THYMU20111830, THYMU20141670, THYMU20147770, THYMU20159430, THYMU20161640, THYMU20162190, THYMU20173980, THYMU20194420, THYMU20208300, THYMU20216840, THYMU20222890, THYMU20229220, THYMU20241850, THYMU20277390, TKIDN20005210, TRACH20002870, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20029540, TRACH20033230, TRACH20034840, TRACH20042920, TRACH20050040, TRACH20067620, TRACH20068660, TRACH20069180, TRACH20076740, TRACH20085400, TRACH20085830, TRACH20109650, TRACH20111130, TRACH20121380, TRACH20128110, TRACH20128230, TRACH20134950, TRACH20136710, TRACH20139820, TRACH20140820, TRACH20145440, TRACH20168350, TRACH20180840, TRACH20190240, UMVEN20000690, UTERU20030570, UTERU20040610, UTERU20046980, UTERU20055480, UTERU20064860, UTERU20076390, UTERU20094350, UTERU20135860, UTERU20144640, UTERU20158300, UTERU20158800, UTERU20161570, UTERU20178100, UTERU20183640, UTERU20186740

[0247] The clones predicted to belong to the category of glycoprotein-related protein are the following 128 clones.

ADIPS10000640, BRACE20059370, BRACE20163350, BRAMY20277170, BRAMY20285160, BRAWH20064050, BRAWH20112940, BRAWH20117950, BRAWH20118230, BRCAN20103740, BRCOC20004040, BRCOC20006370, BRHIP10001290, BRHIP20103090, BRHIP20283030, BRHIP30004570, BRSSN20003120, BRSSN20146100, BRTHA20046290, COLON10001350, CTONG20159530, D9OST20023970, D9OST20040180, FCBBF10001150, FCBBF20049300, FCBBF30024750, FCBBF30083620, FCBBF30190850, FCBBF30238870, FEBRA20086620, FEBRA20092890, HCHON20015980, HCHON20016040, HCHON20064590, HCHON20086720, HCHON20100740, HEART20003060, HHDP20014320, HHDP20068620, HHDP20092080, KIDNE20003940, KIDNE20007770, KIDNE20101510, LIVER20064690, MESAN20125860, NT2NE20118960, NT2NE20157470, NT2NE20177520, NT2RI20003480, NT2RI20056700, NT2RP70192730, NTONG20051530, NTONG20076930, OCBBF20107090, OCBBF20108630, OCBBF20120390, OCBBF20145760, OCBBF20155060, PLACE60177140, SMINT20050750, SMINT20073650, SMINT20105330, SMINT20106720, SMINT20112730, SMINT20127930, SMINT20153260, SMINT20179740, SMINT20190170, SPLEN20021660, SPLEN20142100, SPLEN20157880, SPLEN20165310, SPLEN20179810, SPLEN20186430, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400, STOMA20008880, STOMA20034770, STOMA20056640, STOMA20056670, STOMA20083610, STOMA20088380, STOMA20092530, SYNOV20001520, SYNOV20001730, SYNOV20002510, SYNOV20002790, SYNOV20002970, SYNOV20004260, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, SYNOV20013000, SYNOV20013560, SYNOV20013900, TESOP20004000, TESTI20136100, TESTI20216370, TESTI20244190, TESTI20254860, TESTI20303220, TESTI20335200, TESTI20352620, TESTI20358980, TESTI20442760, TESTI20449200, TESTI20455090, THYMU10005360, THYMU10005540, THYMU20147770, THYMU20159430, THYMU20241850, TRACH20016210, TRACH20050040, TRACH20067620, TRACH20069180, TRACH20076740, TRACH20128230, UTERU20046980, UTERU20064860, UTERU20144640, UTERU20158800, UTERU20161570, UTERU20183640

[0248] The clones predicted to belong to the category of signal transduction-related protein are the following 84 clones.

ASTRO20108190, BRACE20115920, BRACE20154120, BRACE20177200, BRACE20237270, BRAMY20104640, BRAMY20242470, BRAMY20271400, BRAWH20016620, BRAWH20103290, BRAWH20149340, BRCOC20021550, BRCOC20091960, BRHIP20189980, BRHIP20218580, BRHIP20238600, BRSSN20038200, CD34C30004240, CTONG20118150, CTONG20127450, CTONG20200310, FCBBF30012350, FCBBF40001730, FEBRA10001880, FEBRA20004620, FEBRA20132740, FEBRA20144170, FEHRT20003250, HCHON20007510, HLUNG20033780, IMR3220002430, KIDNE20008010, KIDNE20102710, KIDNE20107620, NT2NE20080170, NT2NE20181650, NT2RP70027380, NT2RP70036880, NT2RP70063950, NT2RP70078420, NT2RP70159960, NTONG20046140, NTONG20056570, OCBBF20028050, OCBBF20053430, OCBBF20054760, OCBBF20124360, OCBBF20127140, OCBBF20149280, OCBBF20173980, PEBLM20013120, PEBLM20085760, PROST20161950, PUAEN20015260, PUAEN20015860, PUAEN20083140, SMINT20028820, SMINT20049090, SMINT20110660, SPLEN20011410, SPLEN20121750, SPLEN20170310, SPLEN20181810, SPLEN20222270, SPLEN20250170, SPLEN20283650, TESTI20035960, TESTI20288910, TESTI20305540, TESTI20326810, TESTI20369650, TESTI20392250, TESTI20416640, TESTI20432750, TESTI20467320, THYMU20169680, THYMU20172150, THYMU20201980, THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20057690, UMVEN10001860, UTERU20146310

[0249] The clones predicted to belong to the category of transcription-related protein are the following 144 clones.

3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20060890, BRACE20068590, BRACE20257100, BRAMY20210400, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700, BRAWH20096780, BRCAN20280210, BRCOC20144000, BRCOC20178270, BRHIP20005340, BRHIP20096170, BRHIP20119330, BRHIP20191860, BRHIP20195890, BRHIP20222280, BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950,

EP 1 347 046 A1

CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20133390, CTONG20133520, D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20068820, FCBBF30007680, FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630, FCBBF30240960, FCBBF30246230, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20171380, FEBRA20195820, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130, HHDP20000830, HHDP20030490, HHDP20031130, KIDNE20027250, KIDNE20027950, KIDNE20182690, LIVER20055440, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900, NT2RP60000770, NT2RP70043480, NT2RP70063950, NT2RP70102350, NT2RP70157890, NTONG20070200, OCB3F10001850, OCB3F20020830, OCB3F20037440, OCB3F20046120, OCB3F20049300, OCB3F20054200, OCB3F20066390, OCB3F20071840, OCB3F20080410, OCB3F20108190, OCB3F20125530, OCB3F20148280, OCB3F20060360, PEBLM20078320, PERIC20003870, PROST10003220, PROST20047390, PROST20066880, PROST20185830, PROST20189770, PROST20191640, SKNSH20008190, SMINT20001760, SMINT20028820, SMINT20130320, SMINT20144800, SPLEN20026950, SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20117660, SPLEN20140800, SPLEN20147390, SPLEN20160450, SPLEN20162680, SPLEN20243830, SPLEN20250170, SPLEN20252190, SPLEN20267650, STOMA20032890, STOMA20063250, TESTI20039400, TESTI20041690, TESTI20067200, TESTI20088220, TESTI20130010, TESTI20156100, TESTI20230850, TESTI20318090, TESTI20320670, TESTI20378190, TESTI20385960, TESTI20409890, TESTI20420620, TESTI20432820, TESTI20456110, THYMU20247480, TRACH20079690, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130

[0250] The clones predicted to belong to the category of disease-related protein are the following 387 clones.

ADIPS20004250, ADRGL10001470, ADRGL20011190, ADRGL20018300, ADRGL20035850, ADRGL20078100, ASTRO10001550, ASTRO20008010, ASTRO20027430, ASTRO20106150, ASTRO20108190, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20038480, BRACE20039540, BRACE20059370, BRACE20108130, BRACE20108380, BRACE20115920, BRACE20116460, BRACE20232840, BRACE20248260, BRACE20253330, BRACE20284100, BRALZ20013500, BRALZ20017430, BRALZ20018340, BRAMY20000520, BRAMY20025840, BRAMY20020910, BRAMY20134140, BRAMY20135900, BRAMY20162510, BRAMY20174550, BRAMY20210400, BRAMY20211390, BRAMY20242470, BRAMY20245300, BRAMY20266850, BRAMY20285160, BRAWH20016620, BRAWH20028110, BRAWH20064050, BRAWH20096780, BRAWH20110960, BRAWH20113430, BRAWH20114000, BRAWH20118230, BRAWH20121640, BRAWH20128270, BRAWH20137480, BRCAN20103740, BRCAN20224720, BRCAN20279700, BRCAN20280210, BRCAN20283190, BRCOC20001860, BRCOC20006370, BRCOC20027510, BRCOC20055420, BRCOC20099370, BRCOC20178270, BRCOC20178560, BRHIP20003120, BRHIP20005340, BRHIP20174040, BRHIP20176420, BRHIP20191490, BRHIP20191860, BRHIP20194940, BRHIP20195890, BRHIP20222280, BRHIP20249110, BRHIP20285930, BRHIP30004880, BRSSN20013420, BRSSN20038200, BRSSN20039370, BRSSN20046790, BRSSN20066110, BRSSN20101100, BRSSN20120810, BRSSN20187310, BRTHA20046290, CD34C30004240, COLON10001350, CTONG20004690, CTONG20052650, CTONG20099550, CTONG20124220, CTONG20125640, CTONG20128430, CTONG20131560, CTONG20133390, CTONG20153300, CTONG20153580, CTONG20158040, CTONG20159530, D6OST20003580, D9OST20023970, DFNES20001530, DFNES20037420, FCBBF10001210, FCBBF10001710, FCBBF10003770, FCBBF20059090, FCBBF20064520, FCBBF20068820, FCBBF30010810, FCBBF30024750, FCBBF30025560, FCBBF30039020, FCBBF30049550, FCBBF30057290, FCBBF30083620, FCBBF30129630, FCBBF30190850, FCBBF30238870, FCBBF30240960, FCBBF30243640, FCBBF30279030, FCBBF30281880, FCBBF40001730, FEBRA10001880, FEBRA20004620, FEBRA20010120, FEBRA20018690, FEBRA20082010, FEBRA20097310, FEBRA20130190, FEBRA20132740, FEBRA20144170, FEBRA20195820, FEBRA20223220, FEBRA20233770, FEBRA20235500, FEHRT20003250, HCHON10001760, HCHON20007380, HCHON20008320, HCHON20009560, HCHON20015230, HCHON20015980, HCHON20016040, HCHON20035130, HCHON20036420, HCHON20064590, HCHON20067700, HCHON20086720, HCHON20100740, HEART20003060, HEART20017730, HEART20025980, HEART20049410, HHDP20014320, HHDP20030490, HHDP20084140, HHDP20091140, HHDP20091780, HHDP20092080, HLUNG20033780, IMR3220002430, KIDNE20007770, KIDNE20020150, KIDNE20021680, KIDNE20022620, KIDNE20024830, KIDNE20027950, KIDNE20101370, KIDNE20101510, KIDNE20182690, LIVER20002160, LIVER20055200, LIVER20055440, LIVER20059810, LIVER20064690, MESAN20101140, MESAN20125860, MESAN20130220, MESAN20154010, MESAN20174170, NOVAR10000910, NT2NE20010490, NT2NE20118960, NT2NE20157470, NT2RI20040930, NT2RI20041880, NT2RI20048840, NT2RI20050960, NT2RI20240080, NT2RP60000770, NT2RP70027380, NT2RP70032610, NT2RP70037240, NT2RP70192730, NT2RP70198350, NTONG20013620, NTONG20015870, NTONG20028070, NTONG20067830, NTONG20070200, NTONG20090600, NTONG20092330, OCB3F20006770, OCB3F20037440, OCB3F20046120, OCB3F20049300, OCB3F20053490, OCB3F20053730, OCB3F20054760, OCB3F20071840, OCB3F20072240, OCB3F20078920, OCB3F20108430, OCB3F20108580, OCB3F20127140, OCB3F20129360, OCB3F20145760, OCB3F20153350, OCB3F20173980, OCB3F20178880, PEBLM10000710, PEBLM20013120, PERIC10000250, PLACE60060420, PLACE60177140, PROST20100460,

EP 1 347 046 A1

PROST20159240, PROST20169800, PROST20176170, PUAEN20018820, PUAEN20030180, PUAEN20055020, PUAEN20083140, SKMUS20018230, SKMUS20018500, SKMUS20021530, SKMUS20024750, SKMUS20029200, SKMUS20048970, SKMUS20049030, SKNSH20008190, SKNSH20089400, SMINT20001760, SMINT20026890, SMINT20028820, SMINT20050750, SMINT20073650, SMINT20105330, SMINT20112730, SMINT20121220, SMINT20127350, SMINT20127930, SMINT20136130, SMINT20138900, SMINT20153260, SMINT20155180, SMINT20179740, SMINT20190170, SMINT20191420, SPLEN20006070, SPLEN20011410, SPLEN20026950, SPLEN20027440, SPLEN20039240, SPLEN20079260, SPLEN20095410, SPLEN20146450, SPLEN20147390, SPLEN20151210, SPLEN20160450, SPLEN20170310, SPLEN20179180, SPLEN20186430, SPLEN20212730, SPLEN20243830, SPLEN20245300, SPLEN20250390, SPLEN20252190, SPLEN20267650, SPLEN20305620, STOMA20001830, STOMA20005390, STOMA20008880, STOMA20010250, STOMA20034770, STOMA20046680, STOMA20056670, STOMA20064470, STOMA20077450, STOMA20080500, STOMA20083610, STOMA20088380, SYNOV20001520, SYNOV20001730, SYNOV20002790, SYNOV20002970, SYNOV20007000, SYNOV20008240, SYNOV20009230, SYNOV20010880, SYNOV20011110, TBAES20003770, TESOP20004000, TESOP20005270, TESTI20031270, TESTI20036380, TESTI20044310, TESTI20067200, TESTI20116830, TESTI20121550, TESTI20156100, TESTI20168480, TESTI20208400, TESTI20215990, TESTI20231940, TESTI20234360, TESTI20237520, TESTI20238610, TESTI20239510, TESTI20249990, TESTI20266740, TESTI20316870, TESTI20318090, TESTI20335050, TESTI20335200, TESTI20343570, TESTI20352620, TESTI20368330, TESTI20369650, TESTI20385960, TESTI20392250, TESTI20400940, TESTI20404240, TESTI20420620, TESTI20436560, TESTI20438570, TESTI20441940, TESTI20442760, TESTI20443090, TESTI20449200, TESTI20455090, TESTI20455620, TESTI20456110, TESTI20463580, TESTI20465350, TESTI20465690, TESTI20467210, THYMU20122730, THYMU20126900, THYMU20130890, THYMU20159430, THYMU20169680, THYMU20172150, THYMU20180280, THYMU20193640, THYMU20209590, THYMU20232090, THYMU20247480, TKIDN1000010, TKIDN20004640, TKIDN20047480, TRACH20016210, TRACH20019960, TRACH20050040, TRACH20057590, TRACH20067620, TRACH20077540, TRACH20079690, TRACH20096610, TRACH20105870, TRACH20121380, TRACH20154860, TRACH20162860, TRACH20163170, TRACH20164980, TRACH20190240, TSTOM20005590, TUTER20002830, UTERU20030570, UTERU20116570, UTERU20144640, UTERU20151980, UTERU20158800, UTERU20183640, UTERU20185230

[0251] In particular hit data of the following 386 clones for Swiss-Prot, or GenBank, UniGene, or nr corresponded to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human gene and disease database, (the OMIM Number is shown in the parenthesis after the Clone Name).

ADIPS20004250 (601505), ADRGL10001470 (202010;103900), ADRGL20011190 (182790), ADRGL20018300 (600025), ADRGL20035850 (202110), ADRGL20078100 (103270), ASTRO10001650 (126660), ASTRO20008010 (603899), ASTRO20027430 (179555), ASTRO20106150 (602537), ASTRO20108190 (191092), ASTRO20168470 (604077), BLADE20003400 (601276), BLADE20003890 (604077), BRACE20038480 (601504), BRACE20039540 (600169), BRACE20059370 (130500;266140), BRACE20108130 (605413), BRACE20108880 (603758), BRACE20115920 (300023), BRACE20116460 (603150), BRACE20232840 (601213), BRACE20248260 (600813), BRACE20253330 (604990), BRACE20284100 (602415), BRALZ20013500 (602470), BRALZ20017430 (600658), BRALZ20018340 (600547), BRAMY20000520 (164020), BRAMY20025840 (602327), BRAMY20120910 (600188), BRAMY20134140 (603931), BRAMY20135900 (601342), BRAMY20162510 (300098), BRAMY20174550 (605464), BRAMY20210400 (603809), BRAMY20211390 (602212), BRAMY20242470 (605000), BRAMY20245300 (605367), BRAMY20266850 (605609), BRAWH20096780 (602277), BRAWH20110960 (603481), BRAWH20113430 (602649), BRAWH20114000 (138130), BRAWH20118230 (112267), BRAWH20121640 (604437), BRAWH20128270 (601997), BRAWH20137480 (602330), BRCAN20103740 (602566), BRCAN20224720 (600923;176200), BRCAN20279700 (604205), BRCAN20280210 (134538), BRCAN20283190 (602118), BRCOC20001860 (604346), BRCOC20006370 (603784), BRCOC20027510 (179555), BRCOC20055420 (603801), BRCOC20099370 (606045), BRCOC20178270 (194558), BRCOC20178560 (602567), BRHIP20003120 (604249), BRHIP20005340 (147586), BRHIP20174040 (602658), BRHIP20176420 (154020), BRHIP20191490 (600009), BRHIP20191860 (602272), BRHIP20194940 (604696), BRHIP20195890 (602211), BRHIP20222280 (603899), BRHIP20249110 (142600), BRHIP20285930 (602626), BRHIP30004880 (188840), BRSSN20013420 (300272), BRSSN20038200 (602306), BRSSN20039370 (194531), BRSSN20046790 (604077), BRSSN20066110 (605248), BRSSN20101100 (600188), BRSSN20120810 (142440), BRSSN20187310 (182900), BRTHA20046290 (602644), COLON10001350 (146900), CTONG20004690 (600019), CTONG20052650 (603871), CTONG20099550 (190370), CTONG20124220 (184756), CTONG20125640 (180510), CTONG20128430 (601797), CTONG20131560 (103390), CTONG20133390 (604077), CTONG20153300 (604334), CTONG20153580 (605652), CTONG20158040 (602862), CTONG20159530 (600395), D6OST20003580 (602443), D9OST20023970 (601525), DFNES20001530 (164500), DFNES20037420 (139259), FCBBF10001210 (602461), FCBBF10001710 (194558), FCBBF10003770 (604597), FCBBF20059090 (194542), FCBBF20064520 (164020), FCBBF20068820

EP 1 347 046 A1

(194558), FCBBF30010810 (603899), FCBBF30024750 (603706), FCBBF30025560 (600494), FCBBF30039020 (602835), FCBBF30049550 (106410), FCBBF30057290 (194556), FCBBF30083620 (300022), FCBBF30129630 (603899), FCBBF30190850 (131210), FCBBF30238870 (602320), FCBBF30240960 (604078), FCBBF30243640 (601961), FCBBF30279030 (605208), FCBBF30281880 (602517), FCBBF40001730 (176981), FEBRA10001880 (605451), FEBRA20004620 (600278), FEBRA20010120 (600368), FEBRA20018690 (194542), FEBRA20082010 (602187), FEBRA20097310 (602895), FEBRA20130190 (605863), FEBRA20132740 (602654), FEBRA20144170 (601685), FEBRA20195820 (604074), FEBRA20223220 (604633), FEBRA20233770 (603347), FEBRA20235500 (312090), FEHRT20003250 (600286), HCHON10001760 (605315), HCHON20007380 (600833), HCHON20008320 (604077), HCHON20009560 (194548), HCHON20015230 (604646), HCHON20015980 (604789), HCHON20016040 (146732), HCHON20035130 (194529), HCHON20036420 (603434), HCHON20064590 (103950), HCHON20067700 (603054), HCHON20086720 (146732), HCHON200100740 (602281), HEART20003060 (109480), HEART20017730 (106410), HEART20025980 (602127), HEART20049410 (603777), HHDP20014320 (602714), HHDP20030490 (603795), HHDP20084140 (605184), HHDP20091140 (603054), HHDP20091780 (227400), HHDP20092080 (146732), HLUNG20033780 (600888), IMR3220002430 (602923), KIDNE20007770 (114890), KIDNE20020150 (140550;603012), KIDNE20021680 (601609), KIDNE20022620 (603590), KIDNE20024830 (604205), KIDNE20027950 (194531), KIDNE20101370 (602580), KIDNE20101510 (191845), KIDNE20182690 (605226), LIVER20002160 (600816), LIVER20055200 (604814), LIVER20055440 (605277), LIVER20059810 (230350), LIVER20064690 (601841), MESAN20101140 (602567), MESAN20125860 (155750), MESAN20130220 (603778), MESAN20154010 (180480), MESAN20174170 (602516), NOVAR10000910 (159350), NT2NE20010490 (603899), NT2NE20118960 (180490), NT2NE20157470 (217000), NT2RI20040990 (106410), NT2RI20041880 (160775), NT2RI20048840 (139360), NT2RI20050960 (606103), NT2RI20240080 (603419), NT2RP60000770 (603044), NT2RP70027380 (118423), NT2RP70032610 (172430), NT2RP70037240 (604108), NT2RP70192730 (278000), NT2RP70198350 (300043), NTONG20013620 (604125), NTONG20015870 (123940), NTONG20028070 (602369), NTONG20067830 (182900), NTONG20070200 (194558), NTONG20090600 (313440), NTONG20092330 (153700), OCBBF20006770 (154500), OCBBF20037440 (602290), OCBBF20046120 (601262), OCBBF20049300 (602277), OCBBF20053490 (154550;602579), OCBBF20053730 (603604), OCBBF20054760 (603453), OCBBF20071840 (604077), OCBBF20072240 (604331), OCBBF20078920 (602120), OCBBF20108430 (139360), OCBBF20108580 (300103), OCBBF20127140 (139380), OCBBF20129360 (602142), OCBBF20145760 (600395), OCBBF20153350 (601935), OCBBF20173980 (603524), OCBBF20178880 (601617), PEBLM10000710 (601007), PEBLM20013120 (602288), PERIC10000250 (603582), PLACE60060420 (180469), PLACE60177140 (600022), PROST20100460 (158374), PROST20159240 (606019), PROST20169800 (604426), PROST20176170 (605903), PUAEN20018820 (164740), PUAEN20030180 (603263), PUAEN20055020 (604677), PUAEN20083140 (604762), SKMUS20018230 (603768), SKMUS20018500 (601402), SKMUS20021530 (606045), SKMUS20024750 (179555), SKMUS20029200 (605758), SKMUS20048970 (102610), SKMUS20049030 (161650), SKNSH20008190 (604075), SKNSH20089400 (603070), SMINT20001760 (194558), SMINT20026890 (602127), SMINT20028820 (604719), SMINT20050750 (182120), SMINT20073650 (146900), SMINT20105330 (230500;230600;230650;253010), SMINT20112730 (146900), SMINT20121220 (160776), SMINT20127350 (180740), SMINT20127930 (146900), SMINT20136130 (147220), SMINT20138900 (125660;601419), SMINT20153260 (602201), SMINT20155180 (603004), SMINT20179740 (147020), SMINT20190170 (146900), SMINT20191420 (102770), SPLEN20006070 (182900), SPLEN20011410 (602732), SPLEN20026950 (600014), SPLEN20027440 (106410), SPLEN20039240 (140550;603012), SPLEN20079260 (604074), SPLEN20095410 (602277), SPLEN20146450 (602861), SPLEN20147390 (604078), SPLEN20151210 (600267), SPLEN20160450 (604375), SPLEN20170310 (605216), SPLEN20179180 (605890), SPLEN20186430 (600052), SPLEN20212730 (114230), SPLEN20243830 (601796), SPLEN20245300 (606004), SPLEN20250390 (114220), SPLEN20252190 (604077), SPLEN20267650 (602277), SPLEN20305620 (126064), STOMA20001830 (146900), STOMA20005390 (146900), STOMA20008880 (601652;137750), STOMA20010250 (605786), STOMA20034770 (146900), STOMA20046680 (164772), STOMA20056670 (146900), STOMA20064470 (173320), STOMA20077450 (314370), STOMA20080500 (605414), STOMA20083610 (146900), STOMA20088380 (146900), SYNOV20001520 (147200), SYNOV20001730 (147120), SYNOV20002790 (147120), SYNOV20002970 (147120), SYNOV20007000 (147120), SYNOV20008240 (147120), SYNOV20009230 (146900), SYNOV20010880 (147120), SYNOV20011110 (147120), TBAES20003770 (118990), TESOP20004000 (116810), TESOP20005270 (600641), TESTI20031270 (191161), TESTI20036380 (126650; 214700), TESTI20044310 (179555), TESTI20067200 (176312), TESTI20116830 (603142), TESTI20121550 (600862), TESTI20156100 (602253), TESTI20168480 (188840), TESTI20208400 (164031), TESTI20215990 (605652), TESTI20231940 (604200), TESTI20234360 (601052), TESTI20237520 (604212), TESTI20238610 (300097), TESTI20239510 (604334), TESTI20249990 (164500), TESTI20266740 (605198), TESTI20316870 (605497), TESTI20318090 (604077), TESTI20335050 (605209), TESTI20335200 (109770), TESTI20343570 (190470), TESTI20352620 (176801;249900), TESTI20368330 (157680), TESTI20369650 (602052), TESTI20385960 (605970), TESTI20392250 (605541),

EP 1 347 046 A1

TESTI20400940 (117143), TESTI20404240 (602725), TESTI20420620 (602955), TESTI20436560 (150330), TESTI20438570 (603577), TESTI20441940 (604119), TESTI20442760 (603491), TESTI20443090 (602954), TESTI20449200 (604101).

TESTI20455090 (148070), TESTI20455620 (140560), TESTI20456110 (109092), TESTI20463580 (603486), TESTI20465350 (123830), TESTI20465690 (605468), TESTI20467210 (600833), THYMU20122730 (604700), THYMU20126900 (603370), THYMU20130890 (603675), THYMU20159430 (146900), THYMU20169680 (601441), THYMU20172150 (605000), THYMU20180280 (600549), THYMU20193640 (603083;164021), THYMU20209590 (602378), THYMU20232090 (601717), THYMU20247480 (604077), TKIDN10000010 (605034), TKIDN20004640 (137028), TKIDN20047480 (602399), TRACH20016210 (136836), TRACH20019960 (182310), TRACH20050040 (603784), TRACH20057690 (164731), TRACH20067620 (600429;110800), TRACH20077540 (300080), TRACH20079690 (604078), TRACH20096610 (150330), TRACH20105870 (600495), TRACH20121380 (602513), TRACH20154860 (180240), TRACH20162860 (603845), TRACH20163170 (601739), TRACH20164980 (602277), TRACH20190240 (604633), TSTOM20005690 (605775), UTERU20002830 (602719), UTERU20030570 (602023; 241200), UTERU20116570 (602330),

UTERU20144640 (228000), UTERU20151980 (602038), UTERU20158800 (600738), UTERU20183640 (601281), UTERU20185230 (605333)

[0252] The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following 206 clones.

3NB6910001910, ADRGL10001470, ADRGL20035850, ADRGL20078100, ASTRO20105820, ASTRO20106150, ASTRO20130500, ASTRO20145760, BRACE20027620, BRACE20038000, BRACE20062640, BRACE20096200, BRACE20107530, BRACE20108130, BRACE20108880, BRACE20116460, BRACE20148240, BRACE20185680, BRACE20253160, BRALZ20017430, BRALZ20018340, BRAMY20104640, BRAMY20134140, BRAMY20153110, BRAMY20213100, BRAMY20252720, BRAWH20016620, BRAWH20105840, BRAWH20112940, BRAWH20114000, BRAWH20117950, BRAWH20125380, BRAWH20132190, BRAWH20171030, BRCAN20054490, BRCAN20224720, BRCAN20280360, BRCAN20283190, BRCAN20283380, BRCOC20001860, BRCOC20031250, BRCOC20055420, BRCOC20091960, BRCOC20144000, BRHIP10001290, BRHIP20005530, BRHIP20096850, BRHIP20103090, BRHIP20174040, BRHIP20249110, BRSSN20013420, BRSSN20015790, BRSSN20120810, BRSSN20146100, CTONG20095340, CTONG20106520, CTONG20118250, CTONG20127450, CTONG20140580, CTONG20153300, CTONG20158040, D3OST20006180, D6OST20003580, DFNES20031920, DFNES20071130, FCBBF10001820, FCBBF10003670, FCBBF30012350, FCBBF30012810, FCBBF30175310, FCBBF30243640, FEBRA10001880, FEBRA20007620, FEBRA20130190, FEBRA20144170, FEBRA20167390, FEBRA20196630, FEHRT20003250, HCHON10001760, HCHON20003220, HCHON20015350, HEART20034320, HEART20090000, HHDP20014320, KIDNE20002520, KIDNE20008010, KIDNE20021680, KIDNE20022620, KIDNE20028390, KIDNE20028720, KIDNE20107620, LIVER20059810, MESAN20154010, NT2NE20118960, NT2NE20157470, NT2RI20005750, NT2RI20244600, NT2RI20273230, NT2RP70032610, NT2RP70045590, NT2RP70192730, NT2RP70195430, NTONG20009770, NTONG20013620, NTONG20046140, OCBBF20028650, OCBBF20030910, OCBBF20046690, OCBBF20050770, OCBBF20053430, OCBBF20053490, OCBBF20053730, OCBBF20054760, OCBBF20078920, OCBBF20124360, OCBBF20129360, OCBBF20178880, PEBLM20044520, PEBLM20052820, PEBLM20060490, PERIC10000250, PLACE50000660, PROST20083600, PROST20169800, PUAEN20015260, PUAEN20030180, SKMUS20018230, SMINT20028820, SMINT20049090, SMINT20102780, SMINT20105330, SMINT20106290, SMINT20110660, SMINT20152940, SMINT20191420, SMINT20191530, SPLEN20021660, SPLEN20026950, SPLEN20121750, SPLEN20145720, SPLEN20149240, SPLEN20150940, SPLEN20151210, SPLEN20173510, SPLEN20212730, SPLEN20250390, SPLEN20305620, STOMA20006860, STOMA20077450, TBAES20002550, TBAES20003150, TESOP20004000, TESOP20005270, TESTI20001000, TESTI20002720, TESTI20002780, TESTI20060400, TESTI20066670, TESTI20082330, TESTI20083200, TESTI20108720, TESTI20116830, TESTI20143390, TESTI20148000, TESTI20216370, TESTI20232140, TESTI20234360, TESTI20237520, TESTI20239510, TESTI20266740, TESTI20314180, TESTI20334410, TESTI20343570, TESTI20352620, TESTI20355020, TESTI20366910, TESTI20368330, TESTI20369650, TESTI20375340, TESTI20397760, TESTI20416640, TESTI20432750, TESTI20463580, TESTI20465350, TESTI20471410, TESTI20473830, THYMU20023380, THYMU20111830, THYMU20126900, THYMU20169680, THYMU20202890, TKIDN20004640, TKIDN20047480, TRACH20003590, TRACH20016210, TRACH20019960, TRACH20041830, TRACH20057690, TRACH20067620, TRACH20084720, TRACH20085830, TRACH20162860, UTERU20064860, UTERU20144640, UTERU20146310, UTERU20151980

[0253] The clones predicted to belong to the category of cytoskeleton-related protein are the following 75 clones.

ADRGL20011190, ADRGL20018300, ASTRO10001650, ASTRO20055750, BRACE20003070, BRACE20059370, BRACE20163350, BRAMY20121620, BRAMY20157820, BRAMY20242470, BRAWH20028110, BRAWH20137480, BRCAN20003460, BRCOC20008160, BRCOC20059510, BRHIP20115080, BRHIP20137230, BRHIP20167880, BRHIP20283030, BRHIP20285830, BRSSN20187310, CTONG10002770, CTONG20052900, CTONG20121580,

EP 1 347 046 A1

FCBBF10001150, FCBBF30013770, FCBBF30015940, FCBBF30049550, FEBRA20024100, FEBRA20237640, HCHON20015980, HCHON20068410, HEART20017730, HEART20025980, HEART20061950, HEART20077670, HLUNG20016330, KIDNE20118580, MESAN20004570, NT2RI20040990, NT2RI20041880, NT2RP70037240, NT2RP70062230, NTONG20015870, NTONG20056570, NTONG20067830, NTONG20090600, OCBBF20107090, OCBBF20155060, PLACE60079250, PUAEN20040670, SKMUS20001980, SKMUS20016220, SKMUS20048970, SKMUS20049030, SMINT20024570, SMINT20026890, SMINT20121220, SMINT20138900, SPLEN20006070, SPLEN20027440, SPLEN20142100, TESTI20063830, TESTI20094230, TESTI20278400, TESTI20371030, TESTI20417300, TESTI20436560, TESTI20455090, THYMU20105190, THYMU20172150, THYMU20209590, TRACH20096610, UMVEN10001560, UTERU20116570

[0254] The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 65 clones.

BRACE20057190, BRACE20064880, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20120910, BRAWH20113430, BRAWH20171030, BRCAN10001490, BRCAN20283190, BRCOC20037320, BRCOC20178560, BRHIP20106100, BRHIP20176420, BRHIP20243470, BRSSN20101100, CTONG20114290, CTONG20125540, CTONG20131560, CTONG20140580, DFNES20001530, FCBBF20064520, FEBRA20007620, FEBRA20010120, FEBRA20097310, FEBRA20144170, FEBRA20174410, FEBRA20215500, IMR3220002430, MESAN20101140, NT2RI20273230, OCBBF20028650, OCBBF20030910, OCBBF20078920, PROST20104000, PUAEN20018820, SKMUS20007010, SMINT20127350, SMINT20177360, SMINT20191530, SPLEN20008740, SPLEN20146450, STOMA20046680, TESTI20082330, TESTI20094470, TESTI20121550, TESTI20208400, TESTI20234360, TESTI20237520, TESTI20249990, TESTI20334410, TESTI20355020, TESTI20368330, TESTI20392760, TESTI20408970, TESTI20436560, TESTI20438570, TESTI20443090, THYMU20193640, THYMU20202890, THYMU20241210, TRACH20096610, TATER20002830, UTERU20151980, UTERU20176320

[0255] The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 62 clones.

3NB6910001910, ASTRO20106150, ASTRO20130500, ASTRO20141350, BRACE20038480, BRACE20052160, BRACE20057620, BRACE20106840, BRACE20172980, BRACE20192440, BRAWH20110960, BRCOC20037320, BRHIP20005530, BRSSN20120810, BRSTN20005360, CTONG20009770, CTONG20114290, CTONG20125640, CTONG20153300, D6OST20003580, DFNES20037420, FCBBF30012810, FEBRA20080810, HCHON20064590, HHDPC20014320, HHDPC20084140, HLUNG200017120, LIVER20064690, NT2NE20132170, NT2NE20157470, NT2RP70133740, NTONG20009770, NTONG20075220, NTONG20076930, OCBBF20030910, OCBBF20035930, OCBBF20153340, PLACE60060420, SMINT20152940, SPLEN20008740, SPLEN20103950, SPLEN20118300, SPLEN2012730, SPLEN20250390, STOMA20077450, TBAES20002550, TESOP20004000, TESTI20239510, TESTI20278400, TESTI20314180, TESTI20463580, THYMU20111830, THYMU20122730, THYMU20130890, THYMU20232090, TKIDN10000010, TRACH20084720, TRACH20105870, TRACH20139820, TRACH20149970, UTERU20120310, UTERU20188110

[0256] The clones predicted to belong to the category of cellular defense-related protein are the following 15 clones. BRCOC20144000, CTONG20092680, KIDNE20020150, LIVER20002160, NT2RI20050960, NT2RP70045590, OCBBF20128120, PLACE60003480, SKNSH20089400, SMINT20106290, SPLEN20039240, TESTI20001000, TESTI20455620, TRACH20028030, UTERU20176320

[0257] The clones predicted to belong to the category of development and/or differentiation-related protein are the following 13 clones.

3NB6920014590, BRAMY20211390, CTONG20091080, CTONG20121010, FCBBF30024750, KIDNE20027250, NT2NE20142210, OCBBF20054200, PROST10003220, SKMUS20007010, SPLEN20179810, STOMA20063250, TESTI20291960

[0258] The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 174 clones

3NB6920014590, ADIPS20004250, ASTRO20008010, ASTRO20168470, BLADE20003400, BLADE20003890, BRACE20057620, BRACE20060890, BRACE20064880, BRACE20068590, BRACE20248260, BRACE20253160, BRAMY20000520, BRAMY20213100, BRAMY20260910, BRAMY20270730, BRAWH20028110, BRAWH20075700, BRAWH20096780, BRAWH20113430, BRCAN10001490, BRCAN20280210, BRCAN20283190, BRCOC20144000, BRCOC20178270, BRCOC20178560, BRHIP20005340, BRHIP20106100, BRHIP20119330, BRHIP20153600, BRHIP20176420, BRHIP20191860, BRHIP20195890, BRHIP20222280, BRSSN20039370, BRSSN20046790, BRSSN20176820, CTONG20050280, CTONG20075860, CTONG20085950, CTONG20091080, CTONG20092700, CTONG20121010, CTONG20124220, CTONG20125540, CTONG20133390, CTONG20133520, CTONG20140580, CTONG20156780, D9OST20033970, FCBBF10001710, FCBBF10004370, FCBBF20059090, FCBBF20064520, FCBBF20068820, FCBBF30007680, FCBBF30010810, FCBBF30018550, FCBBF30025560, FCBBF30057290, FCBBF30083820, FCBBF30129630, FCBBF30240960, FCBBF30246230, FEBRA20010120, FEBRA20018690, FEBRA20026110, FEBRA20034680, FEBRA20040530, FEBRA20082010, FEBRA20097310, FEBRA20171380,

EP 1 347 046 A1

FEBRA20195820, FEBRA20196630, FEBRA20233770, HCHON20008320, HCHON20009560, HCHON20035130, HHDP20000830, HHDP20031130, KIDNE20017130, KIDNE20027250, KIDNE20027950, KIDNE20107390, KIDNE20182690, LIVER20055440, MESAN20101140, NT2NE20010490, NT2NE20089970, NT2NE20142210, NT2NE20184900, NT2RP60000770, NT2RP70044280, NT2RP70102350, NT2RP70157890, NTONG20070200, OCBFF10001850, OCBFF20020830, OCBFF20037440, OCBFF20046120, OCBFF20049300, OCBFF20066390, OCBFF20071840, OCBFF20078920, OCBFF20080410, OCBFF20108190, OCBFF20125530, OCBFF20148280, PEBLM20060360, PEBLM20060490, PEBLM20078320, PERIC10000250, PROST10003220, PROST20047390, PROST20066880, PROST20185830, PROST20189770, PROST20191640, PUAEN20018820, SKNSH20008190, SKNSH20089400, SMINT20001760, SMINT20127350, SMINT20144800, SMINT20177360, SMINT20191530, SPLEN20054290, SPLEN20079260, SPLEN20095410, SPLEN20140800, SPLEN20147390, SPLEN20160450, SPLEN20252190, SPLEN20267650, STOMA20010250, STOMA20032890, STOMA20046680, STOMA20063250, TESTI20039400, TESTI20067200, TESTI20088220, TESTI20094470, TESTI20121550, TESTI20130010, TESTI20156100, TESTI20204450, TESTI20230850, TESTI20237520, TESTI20266740, TESTI20318090, TESTI20320670, TESTI20334410, TESTI20355020, TESTI20378190, TESTI20385960, TESTI20432820, TESTI20443090, TESTI20456110, THYMU20193640, THYMU20241210, THYMU20247480, TRACH20079690, TRACH20105870, TRACH20139820, TRACH20154860, TRACH20163170, TRACH20164980, TRACH20184490, TUTER20002830, UTERU20099720, UTERU20116570, UTERU20145480, UTERU20176130, UTERU20185230

[0259] The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 68 clones.

3NB6910001910, BRACE20108130, BRACE20148240, BRAMY20134140, BRAMY20157820, BRAMY20174550, BRAWH20164460, BRCAN20003460, BRCAN20054490, BRCAN20283190, BRCOC20059510, BRCOC20144000, BRHIP20103090, BRHIP20115080, BRHIP20167880, BRSTN20005360, CD34C30004240, CTONG20095340, CTONG20121580, CTONG20200310, DFNES20037420, FCBBF20067810, FCBBF30012350, FCBBF30015940, FEBRA20007620, FEBRA20024100, FEBRA20144170, KIDNE20020150, KIDNE20028720, LIVER20002160, LIVER20087060, NT2RI20005750, NT2RI20041880, NT2RI20048840, NT2RI20273230, OCBFF20028650, OCBFF20046690, OCBFF20054760, OCBFF20108430, OCBFF20108630, SMINT20121220, SMINT20183530, SMINT20191530, SPLEN20026950, SPLEN20039240, SPLEN20099700, SPLEN20145720, SPLEN20179180, STOMA20006860, TESTI20035960, TESTI20355020, TESTI20397760, TESTI20400940, TESTI20417300, TESTI20443090, TESTI20455620, THYMU20105190, THYMU20202890, THYMU20209590, TKIDN20004640, TKIDN20047480, TRACH20005400, TRACH20019960, TRACH20057690, TRACH20084720, UTERU20168220, UTERU20176320, UTERU20185230

[0260] Among the clones other than the ones shown above, BRAMY20248490, FCBBF10002800, NTONG20092290, OCBFF20127040, SMINT20163960, THYMU20279750, TRACH20167220, are clones which were predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

FCBBF10002800, NTONG20092290, OCBFF20127040, SMINT20163960, TESTI20478850, THYMU20279750

[0261] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20060720, BRACE20223330, BRALZ20058880, BRAMY20148130, BRAWH20101360, BRCAN20124080, BRHIP20253660, CTONG10000620, CTONG20014280, CTONG20124010, KIDNE20109890, MESAN20171520, OCBFF20109310, OCBFF20140640, PROST20079500, PUAEN20078980, SPLEN20077500, SPLEN20143180, TESTI20017950, TESTI20184620, TESTI20208710, TESTI20211160, TESTI20226230, TESTI20234140, TESTI20258460, TESTI20275030

[0262] The 26 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

ADRGL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRALZ20058880, BRHIP20207990, CTONG20093950, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, KIDNE20109890, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, NT2NE20130190, PEBLM20060310, PERIC20004780, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, TESTI20023510, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, UTERU20050690

[0263] The 36 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BGGI120006160, BRACE20053480, BRACE20190040, BRACE20223330, BRAWH20101360, BRAWH20185060, BRCOC20023230, BRHIP20252450, BRSSN20105870, BRSSN20117990, BRTHA20000570, CTONG20098440, CTONG20129960, CTONG20146300, CTONG20155180, FEBRA20025270, HEART20083640, KIDNE20009470, LIVER20035680, MESAN20029400, MESAN20031900, MESAN20186700, NOVAR10000150, NTONG20029480,

EP 1 347 046 A1

OCBBF20079310, OCBBF20082830, PEBLM20042900, PLACE60136500, PLACE60136720, PROST20114390, SKNSH20020540, SMINT20013480, SMINT20174360, SPLEN20077500, SPLEN20119810, SPLEN20126190, SPLEN20174260, SPLEN20211220, TESTI20046750, TESTI20057750, TESTI20061110, TESTI20197940, TESTI20211160, TESTI20226230, TESTI20255820, TESTI20317600, TESTI20377230, THYMU20111180, THYMU20115850, THYMU20143270, THYMU20240710, UTERU20055330, UTERU20055930, UTERU20064000, UTERU20119060

[0264] The 55 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.
TESTI20127760, TESTI20392270

[0265] The 2 clones shown above are clones which were predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

FCBBF30262510, MESAN20031900, NT2NE20125050, SMINT20068010, SPLEN20163560, STOMA20092890, TESTI20382750

[0266] The 7 clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

THYMU20118520

[0267] The clone shown above is clone which were predicted to highly possibly belong to the category of nuclear protein and/or RNA synthesis-related protein based on the result of domain search by Pfam.

BRACE20053480, BRACE20240740, KIDNE20009470, OCBBF20140890, SMINT20035690, UTERU20064000

[0268] The 6 clones shown above are clones which were predicted to highly possibly belong to the category of protein synthesis and/or transport-related protein based on the result of domain search by Pfam.

ADRL20048330, ASTRO20064750, ASTRO20084250, BRACE20151320, BRACE20190040, BRACE20223330, BRALZ20058880, BRAMY20103570, BRCOC20023230, BRHIP20207990, BRTHA20000570, CTONG20093950, CTONG20129960, CTONG20146300, CTONG20155180, CTONG20160560, FCBBF10004120, FCBBF30195640, FEBRA10001900, FEBRA20090290, FEBRA20214970, FEBRA20222040, HCHON20008150, HEART20083640, KIDNE20109890, LIVER20035680, LIVER20087510, MESAN20029400, MESAN20031900, MESAN20035290, MESAN20136110, MESAN20186700, NT2NE20130190, NT2RI20025640, NTONG20029480, PEBLM20060310, PERIC20004780, PROST20114390, PROST20171280, PUAEN20078980, SMINT20115880, SPLEN20095550, SPLEN20119810, TESTI20023510, TESTI20057750, TESTI20083940, TESTI20152460, TESTI20185650, TESTI20189410, TESTI20200710, TESTI20308600, TESTI20343070, TESTI20369690, TESTI20381040, THYMU20115850, UTERU20050690, UTERU20055330

[0269] The 57 clones shown above are clones which were predicted to highly possibly belong to the category of DNA-binding and/or RNA-binding protein based on the result of domain search by Pfam.

PLACE60136720

[0270] The clone shown above is a clone which was predicted to highly possibly belong to the category of ATP-binding and/or GTP-binding protein based on the result of domain search by Pfam.

[0271] The 213 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search for their full-length nucleotide sequences and motif search in their deduced ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (//), are shown below.

ADRL20028570//Rattus norvegicus MG87 mRNA, complete cds.

ADRL20061930//transposon-derived Buster1 transposase-like protein

ASTRO20012490//Eukaryotic initiation factor 1A

ASTRO20072210//PERIAXIN.

ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds.

ASTRO20125520//dnaj protein [Schizosaccharomyces pombe]

ASTRO20143630//KH domain// Bacterial regulatory proteins, crp family

ASTRO20155290//TPR Domain// TPR Domain// TPR Domain

ASTRO20181690//oocyte-specific protein P100

BGGI110001930//UBX domain

BRACE20011070//Mus musculus F-box protein FBX15 mRNA, partial cds.

BRACE20039440//Drosophila melanogaster CHARYBDE (charybde) mRNA, complete cds.

BRACE20050900//TPR Domain// TPR Domain// TPR Domain

BRACE20053280//Mus musculus PdZ-containing protein (PdZx) mRNA, complete cds.

BRACE20057730//toxin sensitivity protein KTI12 homolog

BRACE20058580//Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds.

BRACE20063780//NOL1/NOP2/sun family

EP 1 347 046 A1

BRACE20269200//Heat-labile enterotoxin alpha chain
 BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds.
 BRACE20286360//Alpha adaptin carboxyl-terminal domain
 BRAMY10001300//Homo sapiens MAGE-E1b mRNA, complete cds.
 5 BRAMY20045240//Flagellar L-ring protein
 BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.
 BRAMY20167060//Collagen triple helix repeat (20 copies)
 BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds.
 10 BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete
 cds, alternatively spliced.
 BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds.
 BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, com-
 plete cds.
 15 BRAWH20004600//Mus musculus mRNA for NAKAP95. complete cds.
 BRAWH20011710//cytoplasmic linker 2
 BRAWH20012390//Trichomonas vaginalis mRNA for centrin (ce1 gene).
 BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds.
 BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds.
 BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds.
 20 BRCOC20008500//Human ras inhibitor mRNA, 3' end.
 BRCOC20026640//Gag P30 core shell protein
 BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION FACTOR L SUBU-
 NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E).
 BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT).
 25 BRCOC20110100//Integrase core domain
 BRCOC20176520//Rattus norvegicus mRNA for type-II brain 4.1. complete cds.
 BRHIP20001630//Protein of unknown function DUF16
 BRHIP20132860//Homo sapiens rhophilin-like protein mRNA, complete cds.
 BRHIP20143730//MYND finger
 30 BRHIP20175420//Mus musculus partial mRNA for stretch responsive protein 278 (sr278 gene).
 BRHIP20236950//Outer Capsid protein VP4 (Hemagglutinin)
 BRSSN20014260//RIBONUCLEASE INHIBITOR.
 BRSSN20018690//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
 BRSSN20021600//RING CANAL PROTEIN (KELCH PROTEIN).
 35 BRSSN20177570//Phosducin
 BRSTN10000830//Kelch motif// Kelch motif// Kelch motif// Kelch motif
 CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds.
 CTONG10000930//Armadillo/beta-catenin-like repeats
 CTONG20027090//Glypican// Leucine Rich Repeat// Leucine Rich Repeat
 40 CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A).
 CTONG20096750//Disintegrin
 CTONG20100240//Mus musculus radial spokehead-L protein (Rshl1) mRNA, complete cds.
 CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.
 CTONG20143690//MYND finger
 45 CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN).
 CTONG20165050//Keratin, high sulfur B2 protein
 CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN).
 D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC).
 D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds.
 50 D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene).
 DFNES20014040//TRICHOHYALIN.
 FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds.
 FCBBF10000770//Homo sapiens REC8 mRNA, partial cds.
 FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).
 55 FCBBF10005500//Keratin, high sulfur B2 protein
 FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-
 DOZEPINE) (EP).
 FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds.

EP 1 347 046 A1

FCBBF30016320//SecA protein, amino terminal region
 FCBBF30033050//Sm protein
 FCBBF30054440//PLAT/LH2 domain
 FCBBF30225660//Ank repeat// Ank repeat// Ank repeat// K+ channel tetramerisation domain// BTB/POZ domain
 5 FCBBP30233680//G10 protein
 FCBBF30246630//H. sapiens mRNA for ZYG homologue.
 FCBBF30250730//TRICHOHYALIN.
 FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds.
 FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING
 10 AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN
 CAP43).
 FCBBF30252850//Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA, complete
 cds.
 FCBBF30285280//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family
 15 FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE
 CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-
 PHA C SUBUNIT).
 FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds.
 FEBRA20192420//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 20 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 FEBRA20196370//Cyclin-dependent kinase inhibitor// IQ calmodulin-binding motif// IQ calmodulin-binding motif//
 IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
 FEBRA20225040//high-glucose-regulated protein 8
 HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4.
 25 HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.
 HCHON20010990//TPR Domain
 HCHON20059870//Hypothetical protein.
 HHDP20034390//Cereal trypsin/alpha-amylase inhibitor
 HHDP20057420//Mus musculus proline-rich protein (Bprp) mRNA, complete cds.
 30 HHDP20064600//SUPPRESSOR PROTEIN SRP40.
 HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds.
 KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene).
 KIDNE20028830//K-box region
 KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds.
 35 KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds.
 KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds.
 KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (TTS-2.1 gene).
 KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds.
 LIVER10004790//EF hand
 40 LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds.
 LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds.
 LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds.
 MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds.
 MESAN20036460//Corticotropin-releasing factor family
 45 MESAN20127350//myelin expression factor-3
 MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds.
 NT2NE20010400//Homo sapiens GL013 mRNA, complete cds.
 NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN.
 50 NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803).
 NT2RI20001330//Homo sapiens KE03 protein mRNA, partial cds.
 NT2RI20009870//lunatic fringe precursor [Mus musculus]
 NT2RI20046080//recA bacterial DNA recombination proteins
 NT2RI20091730//Molluscan rhodopsin C-terminal tail
 55 NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds.
 NT2RP70080850//SPRY domain// Adenovirus EB1 55K protein / large t-an
 NT2RP70105210//Myc amino-terminal region
 NT2RP70188710//Yeast PIR proteins

EP 1 347 046 A1

NT2RP70194450//Bacterial regulatory proteins, crp family
 NTONG20052650//Gallus gallus Xin mRNA, complete cds.
 NTONG20064400//REPETIN.
 NTONG20064840//Mus musculus s1p1 mRNA for synaptotagmin-like protein 1, complete cds.
 5 NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds.
 NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds.
 NTONG20070340//collagen alpha 1(IX) chain
 NTONG20083650//TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain// PPR repeat// TPR
 Domain
 10 NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds.
 OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds.
 OCBBF20019380//seizure related gene 6
 OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds.
 OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds.
 15 OCBBF20046470//ARFAPTIN 1.
 OCBBF20049840//Homo sapiens mRNA for neurabin II protein.
 OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds.
 OCBBF20071960//Coturnix coturnix japonica qMEF2D gene.
 OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds.
 20 OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN).
 OCBBF20127550//Outer Capsid protein VP4 (Hemagglutinin)
 OCBBF20148730//RING CANAL PROTEIN (KELCH PROTEIN).
 OCBBF20178150//Plasmodium falciparum ADA2-like protein gene, partial cds.
 PEBLM10000240//Domain found in Dishevelled, Eg1-10, and Plc
 25 PROST20047270//CRAL/TRIO domain.
 PROST20112970//Sterile alpha motif (SAM)/Pointed domain// SAM domain (Sterile alpha motif)
 PUAEN10000850//Uncharacterized protein family UPF0025// SecI family
 PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds.
 PUAEN20051100//Mus musculus otogelin mRNA, complete cds.
 30 PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds.
 SKMUS20084740//Syndecan domain
 SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.
 SMINT20071400//NOL1/NOP2/sun family
 SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds.
 35 SMINT20110330//pKID domain
 SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds.
 SMINT20131810//ENV polyprotein (coat polyprotein)
 SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene).
 SPLEN20008390//Human placenta (Diff48) mRNA, complete cds.
 40 SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN).
 SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds.
 SPLEN20149110//Dishevelled specific domain
 SPLEN20171470//Keratin, high sulfur B2 protein
 SPLEN20194050//Homo sapiens HOTTL protein mRNA, complete cds.
 45 SPLEN20214580//Mus musculus mdg1-1 mRNA, complete cds.
 STOMA20057820//Uncharacterized protein family UPF0024
 STOMA20063980//Collagen triple helix repeat (20 copies)
 STOMA20069040//Keratin, high sulfur B2 protein
 SYNOV20017080//UBX domain
 50 TBAES20000590//Cytochrome P450// Cytochrome P450
 TESTI20001170//HORMA domain
 TESTI20031810//Bacterial luciferase// Domain of unknown function DUF28
 TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspsyl1) mRNA, complete cds.
 TESTI20098350//VAT-Nn domain
 55 TESTI20157520//K+ channel tetramerisation domain// K+ channel tetramerisation domain
 TESTI20170350//Cystine-knot domain
 TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.
 TESTI20199750//TRICHOHYALIN.

EP 1 347 046 A1

TESTI20202650//Repeat in HS1/Cortactin
 TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds.
 TESTI20231920//Gag P30 core shell protein
 TESTI20242830//E2 (early) protein, C terminal// Syndecan domain
 5 TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.
 TESTI20320440//THIOREDOXIN.
 TESTI20327680//EF hand// EF hand
 TESTI20328280//KE2 family protein// Troponin
 TESTI20351830//K-box region
 10 TESTI20370020//Bleomycin resistance protein
 TESTI20391210//IQ calmodulin-binding motif
 TESTI20408150//Keratin, high sulfur B2 protein
 TESTI20451990//SAP domain
 TESTI20467970//Neurohypophysial hormones. N-terminal Domain// Neurohypophysial hormones, N-terminal Do-
 15 main// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neu-
 rohypophysial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophy-
 sial hormones, N-terminal Domain// Neurohypophysial hormones, N-terminal Domain// Neurohypophysial hor-
 mones, N-terminal Domain
 THYMU20108310//Mouse NCBP-29 mRNA for PW29, complete cds.
 20 THYMU20142040//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).
 THYMU20194360//Kelch motif
 THYMU20239000//collagen alpha 1(XI) chain
 TOVAR20004760//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat
 TRACH20005020//Ank repeat// MutT-like domain
 25 TRACH20007020//TRICHOHYALIN.
 TRACH20048450//PROTEIN K4 (PROTEIN K3).
 TPACH20068700//Homo sapiens adaptor protein CIKS mRNA, complete cds.
 TRACH20076760//Keratin, high sulfur B2 protein
 TRACH20135520//TBC domain// Rhodanese-like domain
 30 TRACH20141240//Mus musculus G21 protein mRNA, complete cds.
 TRACH20183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA. complete cds.
 UTERU20000740//Human fusion protein mRNA, complete cds.
 UTERU20004240//CGI-96 protein
 UTERU20006960//endoplasmic reticulum resident protein 58
 35 UTERU20022940//Human (p23) mRNA, complete cds.
 UTERU20046640//Mus musculus IdIBp (LDLB) mRNA, complete cds.
 UTERU20065930//GTP-RHO BINDING PROTEIN 1 (RHOPHILIN).
 UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.
 UTERU20179880//TPR Domain// TPR Domain// TPR Domain// TPR Domain
 40

[0272] With respect to the remaining 882 clones, there are so far no information available for estimating their func-
 tions. However, there is the possibility that the functions of these clones will be revealed in future. Their Clone Names
 are indicated below.

3NB6920014080, ADRGL20000640, ADRGL20012870, ADRGL20013010, ADRGL20044590, ADRGL20067670,
 45 ADRGL20068170, ADRGL20068460, ADRGL20073570, ADRGL20076360, ADRGL20083310, ASTRO20032120,
 ASTRO20100720, ASTRO20111490, ASTRO20114G10, ASTRO20136710, ASTRO20138020, ASTRO20152140,
 ASTRO20166810, ASTRO20173480, BLADE20004630, BRACE20019540, BRACE20037660, BRACE20038850,
 BRACE20051690, BRACE20054500, BRACE20055180, BRACE20056810, BRACE20057420, BRACE20058810,
 50 BRACE20060840, BRACE20061740, BRACE20062400, BRACE20062740, BRACE20063800, BRACE20063930,
 BRACE20082950, BRACE20090440, BRACE20096540, BRACE20097320, BRACE20099570, BRACE20106690,
 BRACE20109370, BRACE20109830, BRACE20111830, BRACE20114780, BRACE20115450, BRACE20118380,
 BRACE20121850, BRACE20136240, BRACE20141080, BRACE20142320, BRACE20142570, BRACE20148210,
 BRACE20150310, BRACE20152870, BRACE20163150, BRACE20165830, BRACE20171240, BRACE20175870,
 BRACE20190440, BRACE20220300, BRACE20223280, BRACE20229280, BRACE20230700, BRACE20235400,
 55 BRACE20262930, BRACE20262940, BRACE20266750, BRACE20267250, BRACE20269710, BRACE20283920,
 BRACE20287410, BRALZ20014450, BRALZ20019660, BRALZ20059500, BRALZ20065600, BRALZ20075450,
 BRALZ20075760, BRALZ20080310, BRALZ20088690, BRAMY10001570, BRAMY20004110, BRAMY20011140,
 BRAMY20071850, BRAMY20102080, BRAMY20110640, BRAMY20116790, BRAMY20121190, BRAMY20137560.

EP 1 347 046 A1

BRAMY20147540, BRAMY20160700, BRAMY20163250, BRAMY20163270, BRAMY20167710, BRAMY20168920,
 BRAMY20170140, BRAMY20178640, BRAMY20182730, BRAMY20183080, BRAMY20196000, BRAMY20204450,
 BRAMY20205740, BRAMY20229840, BRAMY20230600, BRAMY20250240, BRAMY20250320, BRAMY20261680,
 BRAMY20267130, BRAMY20268990, BRAMY20277140, BRAMY20280720, BRAMY20285930, BRAMY20286820,
 5 BRAWH10000930, BRAWH20012410, BRAWH20014920, BRAWH20016660, BRAWH20100690, BRAWH20103180,
 BRAWH20106180, BRAWH20107540, BRAWH20110660, BRAWH20111550, BRAWH20122770, BRAWH20126190,
 BRAWH20126980, BRAWH20139410, BRAWH20142340, BRAWH20147290, BRAWH20155950, BRAWH20158530,
 BRAWH20160280, BRAWH20162690, BRAWH20166790, BRAWH20173050, BRAWH20182060, BRCAN20006200,
 BRCAN20006390, BRCAN20060190, BRCAN20126130, BRCAN20143700, BRCAN20147880, BRCAN20216690,
 10 BRCAN20237240, BRCAN20263400, BRCAN20273100, BRCAN20273340, BRCAN20275130, BRCAN20280400,
 BRCAN20284600, BRCOC20004870, BRCOC20020850, BRCOC20031000, BRCOC20031870, BRCOC20037400,
 BRCOC20093800, BRCOC20105100, BRCOC20117690, BRCOC20119960, BRCOC20122290, BRCOC20128130,
 BRCOC20135730, BRCOC20147480, BRCOC20148330, BRCOC20155970, BRCOC20158240, BRHIP10001740,
 BRHIP20104440, BRHIP20105710, BRHIP20107440, BRHIP20110800, BRHIP20115760, BRHIP20123140,
 15 BRHIP20129720, BRHIP20139720, BRHIP20140630, BRHIP20142850, BRHIP20143860, BRHIP20149540,
 BRHIP20153560, BRHIP20169680, BRHIP20169900, BRHIP20170100, BRHIP20173150, BRHIP20180140,
 BRHIP20186120, BRHIP20186500, BRHIP20190070, BRHIP20196410, BRHIP20205090, BRHIP20208420,
 BRHIP20214950, BRHIP20227080, BRHIP20230710, BRHIP20232290, BRHIP20238690, BRHIP20240460,
 BRHIP20254480, BRHIP20277620, BRHIP20284800, BRHIP30001110, BRSSN10000920, BRSSN20006340,
 20 BRSSN20015030, BRSSN20028570, BRSSN20038410, BRSSN20046570, BRSSN20046860, BRSSN20097020,
 BRSSN20105960, BRSSN20108300, BRSSN20121030, BRSSN20152380, BRSSN20159070, BRSSN20159820,
 BRSTN20000580, BRTHA20046390, CD34C30001250, CD34C30003140, CD34C30004940, COLON20043180,
 CTONG20002180, CTONG20028410, CTONG20038890, CTONG20049410, CTONG20077790, CTONG20082690,
 CTONG20091320, CTONG20095270, CTONG20095290, CTONG20096430, CTONG20097660, CTONG20099630,
 25 CTONG20101480, CTONG20105660, CTONG20106230, CTONG20108210, CTONG20124470, CTONG20126070,
 CTONG20128470, CTONG20136300, CTONG20138030, CTONG20139070, CTONG20140320, CTONG20141650,
 CTONG20146970, CTONG20147050, CTONG20150910, CTONG20158150, CTONG20162170, CTONG20163550,
 CTONG20164990, CTONG20265130, CTONG20273610, D3OST10002670, D3OST10002700, D3OST20006540,
 D3OST20007340, D3OST20024170, D3OST20024520, D3OST20037970, D3OST30002910, D6OST20004450,
 30 D9OST20000310, D9OST20035800, DFNES10000030, DFNES10001850, DFNES20010910, DFNES20055270,
 DFNES20082800, FCBBF10003740, FCBBF20006780, FCBBF20023700, FCBBF20035280, FCBBF20054280,
 FCBBF20056370, FCBBF20071860, FCBBF20072650, FCBBF20075560, FCBBF20076330, FCBBF30001840,
 FCBBF30016570, FCBBF30019120, FCBBF30028180, FCBBF30052180, FCBBF30062880, FCBBF30070770,
 FCBBF30071520, FCBBF30170590, FCBBF30178730, FCBBF30189490, FCBBF30199610, FCBBF30240020,
 35 FCBBF30242250, FCBBF30262360, FCBBF30266780, FCBBF30266920, FCBBF30278630, FCBBF30284720,
 FCBBF40001420, FCBBF40005480, FEBRA20003210, FEBRA20017050, FEBRA20018280, FEBRA20025520,
 FEBRA20026280, FEBRA20027810, FEBRA20034360, FEBRA20037500, FEBRA20042190, FEBRA20052910,
 FEBRA20060610, FEBRA20072120, FEBRA20079310, FEBRA20082100, FEBRA20095140, FEBRA20098460,
 FEBRA20161120, FEBRA20166540, FEBRA20176800, FEBRA20197110, FEBRA20204000, FEBRA20204060,
 40 FEBRA20216360, FEBRA20226010, FEBRA20229560, FEBRA20232850, FELNG20002410, HCHON20002260,
 HCHON20008980, HCHON20009350, HCHON20011160, HCHON20014970, HCHON20022470, HCHON20036760,
 HCHON20043590, HCHON20067220, HCHON20074820, HCHON20076500, HEART20021840, HEART20037810,
 HEART20049400, HEART20063340, HEART20067870, HEART20067890, HEART20074430, HEART20089940,
 HEART20095990, HHDP20000650, HHDP20006920, HHDP20057940, HHDP20095280, HLUNG20016770,
 45 HLUNG20084390, KIDNE20006780, KIDNE20011170, KIDNE20013730, KIDNE20018730, KIDNE20018970,
 KIDNE20021980, KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280, KIDNE20096470,
 KIDNE20100840, KIDNE20102650, KIDNE20104300, KIDNE20106740, KIDNE20107500, KIDNE20112000,
 KIDNE20120090, KIDNE20122910, KIDNE20132180, KIDNE20138010, KIDNE20141190, KIDNE20144890,
 KIDNE20148900, KIDNE20163880, KIDNE20180710, KIDNE20186780, LIVER10001260, LIVER20011910,
 50 LIVER20028420, LIVER20038540, LIVER20084730, LIVER20085800, MESAN20106640, MESAN20121130,
 MESAN20132110, MESAN20138450, MESAN20157080, MESAN20161590, MESAN20164090, MESAN20182090,
 NESOP10001080, NOVAR10001020, NOVAR20003520, NT2NE20003740, NT2NE20010210, NT2NE20015240,
 NT2NE20043780, NT2NE20053580, NT2NE20072200, NT2NE20074250, NT2NE20089610, NT2NE20108540,
 NT2NE20110360, NT2NE20146810, NT2NE20152750, NT2NE20172590, NT2NE20174800, NT2NE20174920,
 55 NT2NE20187390, NT2RI20022600, NT2RI20023160, NT2RI20023590, NT2RI20036670, NT2RI20055790,
 NT2RI20069730, NT2RI20198260, NT2RI20203900, NT2RI20207030, NT2RI20216250, NT2RI20244960,
 NT2RI20250750, NT2RI20252550, NT2RP70010740, NT2RP70056750, NT2RP70075240, NT2RP70077660,
 NT2RP70085440, NT2RP70110860, NT2RP70111320, NT2RP70130020, NT2RP70137640, NT2RP70143480,

EP 1 347 046 A1

NT2RP70147210, NT2RP70150800, NT2RP70169110, NT2RP70175670, NT2RP70181970, NT2RP70190640,
 NT2RP70203790, NTONG20050620, NTONG20050860, NTONG20065010, NTONG20077560, NTONG20090680,
 OCB3F20C05230, OCBBF20020150, OCBBF20029800, OCBBF20032460, OCBBF20041680, OCBBF20045330,
 OCB3F20C47570, OCBBF20048660, OCBBF20051610, OCBBF20060300, OCBBF20061720, OCBBF20062140,
 5 OCB3F20C62410, OCBBF20074140, OCBBF20076220, OCBBF20079460, OCBBF20081380, OCBBF20084660,
 OCB3F20C85200, OCBBF20088220, OCBBF20094240, OCBBF20097720, OCBBF20100400, OCBBF20103130,
 OCB3F20104340, OCBBF20105570, OCBBF20107920, OCBBF20111770, OCBBF20118970, OCBBF20126780,
 OCB3F2013011C, OCBBF20139260, OCBBF20151150, OCBBF20164050, OCBBF20164670, OCBBF20170690,
 OCB3F20173360, OCBBF20173250, OCBBF20178990, OCBBF20186870, OCBBF20189560, PEBLM20024550,
 10 PEBLM20C71880, PEBLM20072960, PERIC20002140, PERIC20003860, PLACE60004630, PLACE60119750,
 PLACE60138830, PLACE60153220, PLACE60155130, PLACE60169420, PLACE60181070, PLACE60187690,
 PLACE60188340, PROST10004800, PROST20005670, PROST20021010, PROST20024890, PROST20029270,
 PROST20C52280, PROST20057930, PROST20059040, PROST20087700, PROST20097950, PROST20111050,
 PROST20120350, PROST20121900, PROST20123530, PROST20127400, PROST20130530, PROST20132600,
 15 PHOSI20133270, PROST20144220, PROST20149160, PROST20149250, PROST20151240, PROST20152460,
 PHOSI20153320, PROST20166680, PROST20168290, PROST20178360, PUAEN20025680, PUAEN20027580,
 PUAEN20C44300, PUAEN20045110, PUAEN20045250, PUAEN20052470, PUAEN20081230, PUAEN20085150,
 RECTM10001410, RECTM20003490, RECTM20005100, SKMUS20012010, SKMUS20031680, SKMUS20046670,
 20 SKNMC20006220, SKNSH20034660, SKNSH20062340, SKNSH20080430, SKNSH20087770, SKNSH20091970,
 SMINT20005410, SMINT20008240, SMINT20011140, SMINT20011580, SMINT20014580, SMINT20015590,
 SMINT20023280, SMINT20033170, SMINT20033400, SMINT20042990, SMINT20047810, SMINT20056210,
 SMINT20058C00, SMINT20060780, SMINT20065960, SMINT20076470, SMINT20080540, SMINT20089170,
 SMINT20092330, SMINT20092720, SMINT20098320, SMINT20103690, SMINT20105000, SMINT20108530,
 SMINT20109670, SMINT20122850, SMINT20132280, SMINT20153530, SMINT20158100, SMINT20161220,
 25 SMINT20162660, SMINT20164400, SMINT20164770, SMINT20173190, SPLEN10000830, SPLEN20000640,
 SPLEN20002220, SPLEN20008820, SPLEN20013540, SPLEN20016260, SPLEN20019450, SPLEN20020070,
 SPLEN20022230, SPLEN20023140, SPLEN20031600, SPLEN20032040, SPLEN20032190, SPLEN20033960,
 SPLEN20040600, SPLEN20076530, SPLEN20101190, SPLEN20106250, SPLEN20129610, SPLEN20146690,
 SPLEN20149490, SPLEN20152610, SPLEN20157300, SPLEN20158900, SPLEN20158990, SPLEN20160690,
 30 SPLEN20150980, SPLEN20166270, SPLEN20171210, SPLEN20176200, SPLEN20193110, SPLEN20198110,
 SPLEN20204770, SPLEN20212950, SPLEN20214400, SPLEN20225220, SPLEN20242320, SPLEN20242730,
 SPLEN20249560, SPLEN20261440, SPLEN20264110, SPLEN20279950, SPLEN20280660, SPLEN20303970,
 STOMA20013890, STOMA20026880, STOMA20036460, STOMA20048520, STOMA20048840, STOMA20062290,
 STOMA20067800, STOMA20072690, STOMA20076800, STOMA20086140, STOMA20092560, SYNOV20003970,
 35 TCOLN20C0139C, TESOP20000900, TESOP20003120, TESTI10000940, TESTI20004890, TESTI20011200,
 TESTI20018230, TESTI20029930, TESTI20030310, TESTI20030890, TESTI20038270, TESTI20066770,
 TESTI20076850, TESTI20086210, TESTI20087620, TESTI20094020, TESTI20098530, TESTI20102800,
 TESTI20105720, TESTI20112940, TESTI20114070, TESTI20116650, TESTI20122310, TESTI20129150,
 TESTI20129220, TESTI20130120, TESTI20135660, TESTI20136990, TESTI20137370, TESTI20137670,
 40 TESTI20143240, TESTI20143620, TESTI20155900, TESTI20157100, TESTI20159140, TESTI20161970,
 TESTI20168630, TESTI20168960, TESTI20169960, TESTI20171020, TESTI20178160, TESTI20179320,
 TESTI20183370, TESTI20185810, TESTI20192280, TESTI20194300, TESTI20194810, TESTI20199170,
 TESTI20200260, TESTI20203440, TESTI20209460, TESTI20211240, TESTI20213150, TESTI20213580,
 TESTI20220100, TESTI20220650, TESTI20224620, TESTI20226490, TESTI20234270, TESTI20238000,
 45 TESTI20234470, TESTI20240090, TESTI20241530, TESTI20241920, TESTI20244760, TESTI20262330,
 TESTI20262910, TESTI20265250, TESTI20265370, TESTI20269570, TESTI20272060, TESTI20272390,
 TESTI20275620, TESTI20277360, TESTI20278200, TESTI20280980, TESTI20282540, TESTI20285830,
 TESTI20288110, TESTI20289850, TESTI20291620, TESTI20294700, TESTI20297850, TESTI20301360,
 TESTI20305560, TESTI20307540, TESTI20310070, TESTI20311290, TESTI20319190, TESTI20327740,
 50 TESTI20330310, TESTI20333950, TESTI20336410, TESTI20337100, TESTI20342430, TESTI20345060,
 TESTI20347740, TESTI20347770, TESTI20357750, TESTI20357930, TESTI20361140, TESTI20367360,
 TESTI20369130, TESTI20369220, TESTI20370550, TESTI20371060, TESTI20378450, TESTI20380650,
 TESTI20386230, TESTI20386440, TESTI20388580, TESTI20391130, TESTI20392090, TESTI20401430,
 TESTI20406420, TESTI20409440, TESTI20413300, TESTI20415640, TESTI20419560, TESTI20423020,
 55 TESTI20424000, TESTI20424730, TESTI20425070, TESTI20427830, TESTI20428060, TESTI20429280,
 TESTI20429580, TESTI20433130, TESTI20438660, TESTI20447540, TESTI20451710, TESTI20458190,
 TESTI20465520, TESTI20468630, TESTI20471470, TESTI20471530, TESTI20472120, TESTI20473420,
 TESTI20477920, TESTI20478010, TESTI20478180, TESTI20479300, THYMU20000570, THYMU20011950,

THYMU20015210, THYMU20018190, THYMU20029100, THYMU20045120, THYMU20058070, THYMU20061700, THYMU20070360, THYMU20075320, THYMU20095960, THYMU20101610, THYMU20101920, THYMU20111420, THYMU20114470, THYMU20118060, THYMU20119390, THYMU20128070, THYMU20128260, THYMU20142970, THYMU20153160, THYMU20158250, THYMU20186390, THYMU20186730, THYMU20187720, THYMU20195990, THYMU20204160, THYMU20204990, THYMU20215090, THYMU20215970, THYMU20226600, THYMU20228540, THYMU20235760, THYMU20239430, THYMU20246840, THYMU20250420, THYMU20251890, THYMU20253250, THYMU20255570, THYMU20255720, THYMU20259090, THYMU20265300, THYMU20271250, THYMU20272490, THYMU20283790, THYMU20284120, THYMU20286290, THYMU20286320, TKIDN20030590, TKIDN20030620, TOVAR20005750, TRACH20027840, TRACH20032720, TRACH20037360, TRACH20056980, TRACH20060150, TRACH20082780, TRACH20091230, TRACH20092680, TRACH20099340, TRACH20107710, TRACH20115740, TRACH20118940, TRACH20147250, TRACH20153810, TRACH20169800, TRACH20187180, TSTOM10001860, TSTOM20001390, TSTOM20003150, UMVEN20003540, UTERU20006290, UTERU20020010, UTERU20054460, UTERU20056010, UTERU20059050, UTERU20061030, UTERU20067050, UTERU20068990, UTERU20070040, UTERU20070810, UTERU20081300, UTERU20084260, UTERU20095380, UTERU20095400, UTERU20101240, UTERU20114100, UTERU20118110, UTERU20118970, UTERU20119680, UTERU20124070, UTERU20126880, UTERU20134910, UTERU20143980, UTERU20146680, UTERU20150870, UTERU20164260, UTERU20188810

EXAMPLE 7

Expression frequency analysis *in silico*

[0273] The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 1,402,070 clones, and thus the population of the database is large enough for the analysis.

[0274] Then clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search. The number of clones belonging to each cluster was determined and normalized for every library; thus, the ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

[0275] Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 3 to 51 shown below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0276] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38, 642-648, (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0277] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38, 642-648, (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D3OST, D6OST or D9OST) showed that the genes whose expression levels were different between the two were the following clones (Table 3).

ASTRO20001410, D3OST10001090, D3OST20036070, THYMU20039810, KIDNE20028720, BRAWH10000930, BRHIP20005340, CTONG20141650, D9OST20000310, D9OST20002780, D9OST20023970, D9OST20026730, D9OST20031370, D9OST20033970, D9OST20035800, D9OST20035940, D9OST20040180, FCBBF30018550, FCBBF30233680, KIDNE20102650, NT2RI20023160, PROST20107820, SKNSH20089400, SMINT20033400, CTONG20108210, D6OST20003580, D6OST20005070, ASTRO20155290, D3OST10002670, D3OST10002700, D3OST20006180, D3OST20006540, D3OST20007340, D3OST20013280, D3OST20024170, D3OST20024360,

D3OST20037970, D3OST30002580, D3OST30002910, FCBBF10004120, NT2RI20001330, NTONG20009770, SPLEN20084600, SPLEN20140800, THYMU20169680, TRACH20141240, CD34C30001250, CD34C30003140, CD34C30004240, CD34C30004940, DFNES10001850, HHDPC20034390, NT2RI20091730, SKMUS20003610, SPLEN20225220, BRCOC20101230

[0278] These genes are involved in osteoporosis.

Genes involved in neural cell differentiation

[0279] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0280] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following clones (Table 4).

CTONG20027090, CTONG20160560, NT2RP70032610, OCBBF20188730, SPLEN20162680, BRCOC20101230, BRHIP20005340, BRHIP20238880, FCBBF30016320, FEBRA20080810, FEBRA20225040, HCHON20008320, HHDPC20034390, HLUNG10000550, NT2RI20028470, NT2RI20054050, NT2RI20091730, NT2RP70078420, PUAEN20003740, THYMU20271250, BRACE20003070, BRACE20039040, BRAWH20004600, BRAWH20011710, BRCOC20121720, BRHIP20005530, D3OST10002700, HCHON20007380, HEART20072310, KIDNE20121880, MESAN20121130, NT2RI20022600, NT2RI20023160, NT2RI20086220, NT2RI20216250, NT2RP60000850, NT2RP70036880, NT2RP70043480, NT2RP70062230, NT2RP70081610, NT2RP70102350, NT2RP70130020, NT2RP70190640, OCBBF10001850, OCBBF20097720, OCBBF20173980, PEBLM20044520, SPLEN20173510, TRACH20007020, UTERU20065930, HCHON20022470, NT2NE20010490, NT2NE20174800, NT2NE20177520, PROST20087700, PROST20107820, SMINT20028820, TESTI20063830, ASTRO20125520, BRHIP30001110, HCHON20002260, HCHON20008150, KIDNE20002520, NT2NE20130190, NT2NE20158600, NT2RI20001330, NT2RI20025400, NT2RI20036670, NT2RI20048840, SKMUS20020840, BRACE20057190, BRACE20060550, BRACE20267250, BRAWH20107540, BRAWH20118230, CTONG20075860, CTONG20095290, FEBRA20086620, FEBRA20144170, FEBRA20196370, HLUNG20023340, NT2NE20003740, NT2NE20010050, NT2NE20010210, NT2NE20010400, NT2NE20015240, NT2NE20021620, NT2NE20043780, NT2NE20053580, NT2NE20068130, NT2NE20072200, NT2NE20074250, NT2NE20080170, NT2NE20089610, NT2NE20089970, NT2NE20108540, NT2NE20110360, NT2NE20118960, NT2NE20122430, NT2NE20124480, NT2NE20125050, NT2NE20131890, NT2NE20132170, NT2NE20142210, NT2NE20146810, NT2NE20152750, NT2NE20155110, NT2NE20156260, NT2NE20157470, NT2NE20159740, NT2NE20172590, NT2NE20174920, NT2NE20181650, NT2NE20183760, NT2NE20184900, NT2NE20187390, OCBBF20108430, RECTM20005100, SMINT20001760, SPLEN20169720, TESTI20265250, ASTRO10001650, ASTRO20033160, BRACE20011070, BRACE20039440, BRACE20151320, BRAMY20104640, BRAMY20137560, BRAMY20167060, BRAWH20028110, BRCAN20280360, BRCOC20004870, BRHIP20207990, BRHIP20217320, BRHIP20249110, BRSTN10000830, CTONG10000940, CTONG20004690, CTONG20050280, CTONG20105660, CTONG20125640, CTONG20133520, CTONG20186320, FCBBF10000770, FCBBF10002800, FCBBF10003770, FCBBF30018550, FCBBF30123470, FCBBF30246230, FEBRA20018280, FEBRA20095140, FEBRA20192420, HCHON20064590, HHDPC10000830, HLUNG20016770, HLUNG20033780, IMR3220002430, KIDNE20104300, MESAN20004570, MESAN20089360, NOVAR10000910, NT2RI20003480, NT2RI20005750, NT2RI20009870, NT2RI20023590, NT2RI20023910, NT2RI20025640, NT2RI20040930, NT2RI20041880, NT2RI20046080, NT2RI20050960, NT2RI20055790, NT2RI20056700, NT2RI20069730, NT2RI20076290, NT2RI20091940, NT2RI20198260, NT2RI20203900, NT2RI20207030, NT2RI20240080, NT2RI20244600, NT2RI20244960, NT2RI20250750, NT2RI20252550, NT2RI20273230, NTONG20067090, OCBBF10001750, OCBBF20047570, OCBBF20054760, OCBBF20059560, OCBBF20073540, OCBBF20125530, OCBBF20126780, OCBBF20127040, OCBBF20140890, SKMUS20003610, SKNSH20008190, SKNSH20080430, SMINT20144800, SPLEN20027440, SPLEN20095550, SPLEN20140800, TESTI20094020, TESTI20369690, TESTI20391770, TESTI20442760, TRACH20084720, TRACH20107710, TRACH20118940, UTERU20022940, ASTRO20108190, BGGI120006160, BRAMY20136210, BRAWH20016620, BRAWH20164460, BRCOC20144000, BRHIP20132860, BRSSN20146100, CTONG10000100, CTONG20103480, CTONG20108210, CTONG20139070, FCBBF10000240, FCBBF10000630, FCBBF20067810, FCBBF30010810, FCBBF30012810, FCBBF30013770, FCBBF30039020, FCBBF40001420, FEBRA10001880, FEBRA20082010, HHDPC20001040, KIDNE20021910, NT2RP60000770, NT2RP70010740, NT2RP70027380, NT2RP70037240, NT2RP70044280, NT2RP70045590, NT2RP70056750, NT2RP70063950, NT2RP70072690, NT2RP70077660, NT2RP70085440, NT2RP70105210, NT2RP70110860, NT2RP70111320, NT2RP70122910, NT2RP70125160, NT2RP70133740, NT2RP70134990.

NT2RP70137290, NT2RP70137640, NT2RP70143480, NT2RP70147210, NT2RP70150800, NT2RP70157890, NT2RP70159960, NT2RP70169110, NT2RP70175670, NT2RP70179710, NT2RP70181970, NT2RP70188020, NT2RP70188710, NT2RP70192730, NT2RP70194450, NT2RP70195430, NT2RP70198350, NT2RP70203790, OCBBF20039250, OCBBF20080410, OCBBF20108190, OCBBF20108580, OCBBF20122620, OCBBF20130110, OCBBF20151150, OCBBF20189560, PROST10003220, TESTI20001720, TESTI20121550, TESTI20152460, TESTI20211240, TESTI20234140, UMVEN20003540, UTERU20006960, UTERU20094350, UTERU20164260

[0281] These genes are neurological disease-related genes. Cancer-related genes

[0282] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression can contribute to the carcinogenesis in tissues and cells. Thus, the genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0283] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were the following clones (Table 5).

BRACE20039040, BRAMY20163250, BRCOC20031250, BRHIP20005340, BRHIP20217620, BRHIP30001110, FCBBF10000770, FCBBF30010810, FEBRA20080810, FEBRA20144170, FEBRA20196630, FEBRA20197110, HCHON20002260, HCHON20040020, HHDP20034390, HLUNG10000550, NOVAR10000910, NT2RI20023160, NT2RI20054050, NT2RI20091730, OCBBF20188730, SMINT20144800, SPLEN20128000, SPLEN20171210, SPLEN20264110, TBAES20000590, TBAES20002550, TBAES20003150, TESTI20334410, TESTI20432750, TRACH20003590, TRACH20084720, UTERU20046640, BEAST20004540, SPLEN20008740

[0284] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were the following clones (Table 6).

BGGI120006160, BRAMY20063970, BRHIP20218580, FEBRA20002100, SPLEN20162680, TESTI20214250, CTONG20105080, HCHON20015980, PROST20175290, TESTI20254220, THYMU20279750

[0285] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were the following clones (Table 7).

ASTRO20001410, BRAWH20162690, CTONG20132220, HCHON20002260, NT2RI20001330, TCOLN20001390, 3NB6910001910, BRAMY20120910, BRAWH20004600, BRCOC20031250, BRCOC20031870, COLON10001350, COLON20043180, COLON20093370, FEBRA20002100, FEBRA20082010, FEBRA20197110, KIDNE20007770, KIDNE20013730, NT2RP70045590, OCBBF20078920, PROST20083600, SPLEN20011410, TRACH20084720, THYMU20271250

[0286] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were the following clones (Table 8).

ASTRO20033160, ASTRO20125520, BRAMY20266850, BRAWH20164460, BRHIP20005340, BRHIP20191490, CTONG20095290, CTONG20143690, CTONG20161850, DFNES20001530, DFNES20071130, FCBBF30123470, FCBBF30175310, FEBRA20095140, HCHON20016650, MESAN20025190, NT2RI20028470, NT2RI20054050, NT2RP70036880, NTONG20009770, NTONG20064840, NTONG20076930, SMINT20042990, SPLEN20008820, SPLEN20128000, SPLEN20149110, STOMA20013890, TESOP20000900, TESOP20003120, TESOP20004000, TESOP20005270, TESOP20005690, TESTI20334410, THYMU20271250, TRACH20141240, UTERU20022940, NESOP10001080, NT2RI20023160, NTONG20013620, TRACH20077540, NTONG20015870

[0287] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 9).

ASTRO20008010, ASTRO20181690, BRACE20111830, BRACE20152870, BRACE20237270, BRAMY20147540, BRAMY20286820, BRAWH20015350, BRAWH20096780, BRAWH20132190, BRAWH20182060, BRCAN20060190, BRCOC20004870, BRCOC20176520, BRHIP20000870, BRHIP20198190, BRHIP20233090, BRHIP30001110, BRSSN20015790, BRSTN20000580, CTONG10000940, CTONG20098440, CTONG20150910, CTONG20165050, DFNES20014040, DFNES20037420, FCBBF10000770, FCBBF30083820, FCBBF30247930, FEBRA20037500, FEBRA20072120, FEBRA20080810, FEBRA20086620, FEBRA20140100, FEBRA20144170, FEBRA20176800, HCHON20008320, HCHON20059870, HLUNG10000550, MESAN20106640, NT2RI20025400, NT2RI20076290, NT2RI20091940, OCBBF20019830, OCBBF20022900, OCBBF20039250, OCBBF20080050, OCBBF20097720, OCBBF20125530, OCBBF20130110, OCBBF20140640, OCBBF20173980, PANCR10000910, PROST20087700, PUAEN20044000, SPLEN20144520, SPLEN20160980, TKIDN10000010, TKIDN20004640, TKIDN20005210, TKIDN20030590, TKIDN20030620, TKIDN20047480, TRACH20003590, TRACH20028030, TRACH20183170, TRACH20184490, UMVEN20003540, UTERU20004240, UTERU20055930, ASTRO10001650, ASTRO20108190,

BGGI120006160, BRACE20039040, BRAMY20102080, BRAWH20004600, BRAWH20125380, BRAWH20162690, BRHIP20115760, BRHIP20205090, CTONG20052650, CTONG20108210, CTONG20128470, CTONG20133480, CTONG20139070, D9OST20000310, DFNES20001530, FCBBF10001820, FEBRA20002100, HCHON20008980, HCHON20016650, HLUNG20033780, KIDNE20002520, KIDNE20003940, KIDNE20006780, KIDNE20007210, KIDNE20007770, KIDNE20008010, KIDNE20009470, KIDNE20011170, KIDNE20011400, KIDNE20013730, KIDNE20017130, KIDNE20018730, KIDNE20018970, KIDNE20020150, KIDNE20021680, KIDNE20021910, KIDNE20021980, KIDNE20022620, KIDNE20024830, KIDNE20027250, KIDNE20027950, KIDNE20028390, KIDNE20028720, KIDNE20028830, KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280, KIDNE20096470, KIDNE20100070, KIDNE20100840, KIDNE20101370, KIDNE20101510, KIDNE20102650, KIDNE20102710, KIDNE20104300, KIDNE20106740, KIDNE20107390, KIDNE20107500, KIDNE20107620, KIDNE20109730, KIDNE20109890, KIDNE20112000, KIDNE20115080, KIDNE20118580, KIDNE20120090, KIDNE20121880, KIDNE20122910, KIDNE20124400, KIDNE20125630, KIDNE20126010, KIDNE20126130, KIDNE20127100, KIDNE20127450, KIDNE20127750, KIDNE20130450, KIDNE20131580, KIDNE20132180, KIDNE20137340, KIDNE20138010, KIDNE20141190, KIDNE20144890, KIDNE20148900, KIDNE20163880, KIDNE20180710, KIDNE20181660, KIDNE20182690, KIDNE20186780, KIDNE20190740, LIVER20035110, MESAN20025190, NT2RP70043480, PROST20107820, PROST20123530, PROST20161950, PUAEN20030180, SKMUS20003610, SMINT20033400, TBAES20000590, TESTI20044310, TESTI20082330, TRACH20032720, UTERU20099720

[0288] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were the following clones (Table 10). BRAWH20166790, CTONG20103480, HEART20005410, LIVER10001260, LIVER10004790, LIVER20002160, LIVER20011130, LIVER20011910, LIVER20028420, LIVER20035110, LIVER20035680, LIVER20038540, LIVER20045650, LIVER20055200, LIVER20055440, LIVER20059810, LIVER20062510, LIVER20064100, LIVER20064630, LIVER20075680, LIVER20080530, LIVER20084730, LIVER20085800, LIVER20087510, LIVER20091180, NTONG20063010, PROST20087700, PROST20107820, TRACH20005400, ASTRO20001410, ASTRO20125520, BRACE20152870, BRAMY20167060, BRAMY20181220, BRAMY20285160, BRCOC20001860, FEBRA20144170, HLUNG10000550, OCBFF20073540, OCBFF20088220, PLACE60169420, SMINT20152940, SPFN20242320, THYMU20000570, TRACH20077540, UTERU20055930, UTERU20065930

[0289] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (LUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 11)

BRACE20096200, BRAWH20004600, BRAWH20030250, BRCAN20006390, BRCAN20280360, BRHIP20238880, CTONG10000940, CTONG20103480, CTONG20129960, CTONG20155180, FCBBF10001210, FEBRA20144170, FEBRA20197110, HCHON20002260, HHDPC20034390, HLUNG10000550, HLUNG20016330, HLUNG20016770, HLUNG20017120, HLUNG20023340, HLUNG20033780, HLUNG20084390, IMR3220002430, LIVER20028420, NOVAR20000380, NT2RI20023910, NT2RI20054050, NT2RI20091730, NT2RP70044280, OCBFF20020830, OCBFF20125530, PLACE60004630, PROST20057930, PROST20107820, PROST20185830, PUAEN20030180, SMINT20121220, SPLEN20002220, SPLEN20008740, SPLEN20054290, SPLEN20128000, SPLEN20157300, SPLEN20176200, SPLEN20179180, SPLEN20211940, STOMA20013890, TBAES20000590, TESTI20094230, TESTI20184620, TESTI20334410, THYMU20000570, THYMU20039810, TRACH20007020, TRACH20141240, TRACH20183170, ASTRO20108190, ASTRO20155290, BRHIP20096850, FEBRA20080810, MESAN20014500, SMINT20028820, SPLEN20162680

[0290] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were the following clones (Table 12)

BGGI120006160, BRHIP20005340, BRHIP20191860, HHDPC20001040, NOVAR10000150, NOVAR10000910, NOVAR10001020, NOVAR20000380, NOVAR20003520, THYMU20271250, ASTRO20141350, BRAMY20157820, BRCOC20001860, HLUNG20016770, NT2RI20054050, NTONG20090600, PROST20087700, PUAEN20015860, SPLEN20029310, TOVAR20004760, TOVAR20005750, TRACH20079690, UTERU20004240

[0291] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were the following clones (Table 13).

BRACE20060840, FEBRA20052910, HCHON20002260, HLUNG10000550, NTONG20009770, PROST20107820, THYMU20039810, TSTOM10001860, TSTOM20001390, TSTOM20003150, TSTOM20005690, ASTRO20125520, BRACE20039040, BRAMY20124260, BRCOC20031870, BRHIP20191860, CTONG20128470, FEBRA20037500, HCHON20040020, HHDPC10000830, IMR3220002430, KIDNE20007770, NOVAR20000380, NT2RI20054050, NT2RI20091730, PROST20130530, SPLEN20149110, SPLEN20157880, STOMA20001830, STOMA20005390, STOMA20005670, STOMA20006400, STOMA20006780, STOMA20006860, STOMA20008880, STOMA20010250,

STOMA20013890, STOMA20026880, STOMA20032890, STOMA20034770, STOMA20036460, STOMA20046680, STOMA20048520, STOMA20048840, STOMA20051200, STOMA20056640, STOMA20056670, STOMA20057820, STOMA20062130, STOMA20062290, STOMA20063250, STOMA20063980, STOMA20064470, STOMA20067800, STOMA20069040, STOMA20072690, STOMA20076800, STOMA20077450, STOMA20080500, STOMA20083610, STOMA20086140, STOMA20088380, STOMA20092530, STOMA20092560, STOMA20092890, TESTI20184620, TRACH20003590, TRACH20183170, PROST20083600, TRACH20068660

[0292] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were the following clones (Table 14).

DFNES10001850, NT2RI20023910, SMINT20144800, SPLEN20162680, TOVAR20004760, TUTER20002830, ASTRO20008010, ASTRO20033160, ASTRO20058630, ASTRO20105820, ASTRO20108190, BRACE20039040, BRACE20057190, BRACE20060840, BRACE20111830, BRACE20223330, BRAMY20266850, BRAWH20113430, BRAWH20126980, BRCOC20031870, BRCOC20107300, BRCOC20121720, BRCOC20155970, BRHIP20105710, BRHIP20191490, BRHIP20207990, BRHIP20217620, BRHIP20222280, BRHIP20238880, BRHIP20249110, BRSSN20018690, BRTHA20000570, CTONG10000940, CTONG10002770, CTONG20095290, CTONG20099380, CTONG20103480, CTONG20108210, CTONG20118250, CTONG20129960, CTONG20131560, CTONG20139070, CTONG20139340, CTONG20143690, CTONG20160560, D3OST30002580, FCBBF10000240, FCBBF10001820, FCBBF10003670, FCBBF10004120, FCBBF10005740, FCBBF30175310, FCBBF30240020, FCBBF30246230, FCBBF40001420, FEBRA20002100, FEBRA20004620, FEBRA20018280, FEBRA20025270, FEBRA20034360, FEBRA20037500, FEBRA20080810, FEBRA20082100, FEBRA20144170, FEBRA20225040, HCHON20002260, HCHON20007380, HCHON20015980, HCHON20016650, HCHON20022470, HCHON20040020, HCHON20076500, HEART20072310, HHDP20034390, HLUNG10000550, HLUNG20016770, KIDNE20131580, LIVER20028420, MAMGL10000830, MESAN20171520, NOVAR10000150, NOVAR10000910, NT2NE20053580, NT2NE20159740, NT2NE20174920, NT2RI20023160, NT2RI20041880, NT2RI20054050, NT2RI20076290, NT2RI20273230, NT2RP60000770, NT2RP60000850, NT2RP70036880, NT2RP70043480, NT2RP70045590, NT2RP70056750, NT2RP70062230, NT2RP70081610, OCBBF10001750, OCBBF20006770, OCBBF20032460, OCBBF20039250, OCBBF20047570, OCBBF20054760, OCBBF20059560, OCBBF20068490, OCBBF20080050, OCBBF20094240, OCBBF20097720, OCBBF20103130, OCBBF20105570, OCBBF20140640, OCBBF20173980, OCBBF20180120, OCBBF20188730, OCBBF20189560, PEBLM20044520, PLACE60060420, PROST20087700, PROST20107820, PROST20149160, PROST20159240, PROST20176170, PROST20189770, PUAEN20003740, PUAEN20015860, SKMUS20003610, SKNSH20008190, SKNSH20080430, SMINT20026890, SMINT20029760, SMINT20068010, SMINT20110330, SMINT20121220, SPLEN20008390, SPLEN20011410, SPLEN20054290, SPLEN20128000, SPLEN20140800, SPLEN20145720, SPLEN20169720, SPLEN20179180, SPLEN20193110, SPLEN20194050, SPLEN20211940, SPLEN20212730, SPLEN20225220, TBAES20000590, TESTI20061110, TESTI20116830, TESTI20184620, TESTI20208710, TESTI20211240, TESTI20213580, TESTI20214250, TESTI20334410, TESTI20369130, TESTI20369690, TESTI20391770, THYMU20039810, THYMU20216840, THYMU20240710, TRACH20003590, TRACH20032720, TRACH20033230, TRACH20141240, TRACH20149970, UMVEN10001860, UTERU20000740, UTERU20004240, UTERU20006290, UTERU20020010, UTERU20022940, UTERU20030570, UTERU20040610, UTERU20046640, UTERU20046980, UTERU20050690, UTERU20054460, UTERU20055330, UTERU20055930, UTERU20056010, UTERU20059050, UTERU20061030, UTERU20064000, UTERU20064860, UTERU20065930, UTERU20067050, UTERU20068990, UTERU20070040, UTERU20070810, UTERU20076390, UTERU20081300, UTERU20084260, UTERU20094350, UTERU20095380, UTERU20095400, UTERU20097760, UTERU20099720, UTERU20101240, UTERU20114100, UTERU20115740, UTERU20116570, UTERU20118110, UTERU20118970, UTERU20119060, UTERU20119680, UTERU20120310, UTERU20124070, UTERU20126880, UTERU20134910, UTERU20135860, UTERU20143980, UTERU20144640, UTERU20145480, UTERU20146310, UTERU20146680, UTERU20150870, UTERU20151980, UTERU20158300, UTERU20158800, UTERU20161570, UTERU20164260, UTERU20168220, UTERU20176130, UTERU20176320, UTERU20178100, UTERU20179880, UTERU20183640, UTERU20185230, UTERU20186740, UTERU20188110, UTERU20188810, BRAWH10000930, CTONG20128470, UTERU20006960

[0293] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were the following clones (Table 15).

ADRLGL20018300, ASTRO20058630, ASTRO20072210, ASTRO20108190, BRACE20003070, BRACE20039040, BRACE20060720, BRACE20061050, BRACE20210140, BRACE20276430, BRAMY20152110, BRAMY20266850, BRAMY20271400, BRAWH10000930, BRAWH20004600, BRCAN20280360, BRCOC20004870, BRHIP20005340, BRHIP20005530, BRHIP20238880, BRSSN20146100, CTONG10000100, CTONG10000220, CTONG10000620, CTONG10000930, CTONG10000940, CTONG10001650, CTONG10002770, CTONG20002180, CTONG20004690, CTONG20009770, CTONG20014280, CTONG20027090, CTONG20028410, CTONG20038890, CTONG20049410,

CTONG20050280, CTONG20052650, CTONG20052900, CTONG20075860, CTONG20076130, CTONG20077790,
 CTONG20082690, CTONG20085950, CTONG20091080, CTONG20091320, CTONG20092570, CTONG20092580,
 CTONG20092680, CTONG20092700, CTONG20093950, CTONG20095270, CTONG20095290, CTONG20095340,
 CTONG20096430, CTONG20096750, CTONG20097660, CTONG20098440, CTONG20099380, CTONG20099550,
 5 CTONG20099630, CTONG20100240, CTONG20101480, CTONG20103480, CTONG20105080, CTONG20105660,
 CTONG20106230, CTONG20106520, CTONG20108210, CTONG20114290, CTONG20114740, CTONG20118150,
 CTONG20118250, CTONG20119200, CTONG20120770, CTONG20121010, CTONG20121580, CTONG20124010,
 CTONG20124220, CTONG20124470, CTONG20124730, CTONG20125540, CTONG20125640, CTONG20126070,
 CTONG20127450, CTONG20128470, CTONG20129960, CTONG20131490, CTONG20131560, CTONG20132220,
 10 CTONG20133390, CTONG20133480, CTONG20133520, CTONG20136300, CTONG20138030, CTONG20139070,
 CTONG20139340, CTONG20139860, CTONG20140320, CTONG20140580, CTONG20141650, CTONG20146300,
 CTONG20147050, CTONG20149460, CTONG20149950, CTONG20153300, CTONG20153580, CTONG20155180,
 CTONG20155400, CTONG20156780, CTONG20158040, CTONG20158150, CTONG20158660, CTONG20159530,
 CTONG20160560, CTONG20161850, CTONG20162170, CTONG20163550, CTONG20164990, CTONG20165050,
 15 CTONG20186320, CTONG20200310, CTONG20265130, CTONG20267700, CTONG20273610, FCBBF10000240,
 FCBBF10005740, FCBBF30123470, FCBBF30233680, FEBRA20025270, FEBRA20037500, HCHON20002260,
 HCHON20007380, HCHON20007510, HCHON20015350, HCHON20040020, HHDPC20034390, HLUNG10000550,
 KIDNE20002520, KIDNE20009470, KIDNE20115080, KIDNE20127100, LIVER20028420, MESAN20029400,
 NT2RI20023160, NT2RI20023910, NT2RI20091730, NT2RP70043480, NT2RP70078420, NT2RP70081610,
 20 OCBBF20006770, OCBBF20059560, OCBBF20073540, OCBBF20094240, OCBBF20108580, PEBLM20044520,
 PEBLM20071880, PROST20107820, PUAEN20030180, SKNSH20008190, SMINT20023280, SMINT20089170,
 SPLEN20179180, TESTI20094020, TESTI20094230, TESTI20152460, TESTI20184620, TESTI20211240,
 TESTI20442760, THYMU20039810, TRACH20028030, TRACH20141240, TSTOM20003150, UTERU20004240,
 UTERU20055930, UTERU20065930, UTERU20119060, UTERU20124070, BRACE20039440, BRACE20068590,
 25 FCBBF30018550, IMR3220002430, KIDNE20028830, NT2RI20028470, NT2RI20054050, NT2RI20086220,
 NTONG20009770, NTONG20013620, NTONG20028070, NTONG20029480, NTONG20029700, NTONG20046140,
 NTONG20048060, NTONG20049910, NTONG20050620, NTONG20050860, NTONG20051530, NTONG20052650,
 NTONG20056570, NTONG20061870, NTONG20063010, NTONG20064400, NTONG20064840, NTONG20065010,
 NTONG20066460, NTONG20067090, NTONG20067830, NTONG20070200, NTONG20070340, NTONG20075220,
 30 NTONG20076930, NTONG20077560, NTONG20083650, NTONG20088620, NTONG20090600, NTONG20090680,
 NTONG20092290, NTONG20092330, OCBBF20068490, SKMUS20001980, SMINT20138900, SPLEN20008390,
 SPLEN20162680, UTERU20134910, ASTRO20155290, FEBRA20080810, NT2RP70032610, NT2RP70036880,
 NTONG20015870, OCBBF20188730, SMINT20122910, SPLEN20099700

[0294] These genes are involved in cancers.

35 [0295] Further, there is a method to search for genes involved in development and differentiation: the expression frequency analysis in which the expression levels of genes are compared between developing or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for re-

40 [0296] Search was carried out for the genes whose expression frequencies were different between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, by using the information of gene expression frequency based on the database of the nucleotide sequences of 1,402,070 clones shown above.

[0297] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that

45 the genes whose expression levels were different between the two were the following clones (Tables 16 to 48).
 3NB6910001910, ADRGL20018300, ASTRO20001410, ASTRO20033160, ASTRO20058630, ASTRO20064750,
 ASTRO20100720, ASTRO20141350, ASTRO20145760, ASTRO20181690, BGGI120006160, BRACE20006400,
 BRACE20011070, BRACE20019540, BRACE20027620, BRACE20037660, BRACE20038000, BRACE20038470,
 BRACE20038480, BRACE20038850, BRACE20039440, BRACE20039540, BRACE20050900, BRACE20051380,
 50 BRACE20051690, BRACE20052160, BRACE20053280, BRACE20053480, BRACE20053630, BRACE20054500,
 BRACE20055180, BRACE20057420, BRACE20057620, BRACE20057730, BRACE20058580, BRACE20058810,
 BRACE20060840, BRACE20060890, BRACE20061050, BRACE20061740, BRACE20062400, BRACE20062740,
 BRACE20063630, BRACE20063780, BRACE20063800, BRACE20063930, BRACE20064880, BRACE20068590,
 BRACE20069090, BRACE20081720, BRACE20082950, BRACE20096200, BRACE20096540, BRACE20097320,
 55 BRACE20101700, BRACE20101710, BRACE20106840, BRACE20107530, BRACE20108130, BRACE20108880,
 BRACE20109370, BRACE20109830, BRACE20114780, BRACE20115450, BRACE20115920, BRACE20116110,
 BRACE20116460, BRACE20118380, BRACE20121850, BRACE20141080, BRACE20142320, BRACE20147800,
 BRACE20148210, BRACE20148240, BRACE20150310, BRACE20151320, BRACE20152870, BRACE20153680,

EP 1 347 046 A1

BRACE20154120, BRACE20163150, BRACE20163350, BRACE20165830, BRACE20171240, BRACE20172980,
 BRACE20175870, BRACE20177200, BRACE20179340, BRACE20185680, BRACE20188470, BRACE20190040,
 BRACE20190440, BRACE20192440, BRACE20195100, BRACE20201570, BRACE20220300, BRACE20223280,
 BRACE20223330, BRACE20224480, BRACE20224500, BRACE20228480, BRACE20229280, BRACE20230700,
 5 BRACE20232840, BRACE20235400, BRACE20237270, BRACE20238000, BRACE20240740, BRACE20248260,
 BRACE20253160, BRACE20253330, BRACE20257100, BRACE20262930, BRACE20262940, BRACE20266750,
 BRACE20267250, BRACE20269200, BRACE20269710, BRACE20273890, BRACE20274080, BRACE20283920,
 BRACE20284100, BRACE20286360, BRACE20287410, BRALZ20013500, BRALZ20014450, BRALZ20017430,
 BRALZ20018340, BRALZ20054710, BRALZ20058880, BRALZ20059500, BRALZ20064740, BRALZ20065600,
 10 BRALZ20069760, BRALZ20073760, BRALZ20075450, BRALZ20075760, BRALZ20077900, BRALZ20077930,
 BRALZ20080310, BRALZ20088690, BRAMY10001300, BRAMY10001570, BRAMY20000520, BRAMY20000860,
 BRAMY20002770, BRAMY20004110, BRAMY20011140, BRAMY20025840, BRAMY20039260, BRAMY20045240,
 BRAMY20054880, BRAMY20060920, BRAMY20063970, BRAMY20071850, BRAMY20102080, BRAMY20104640,
 BRAMY20110640, BRAMY20111960, BRAMY20116790, BRAMY20121190, BRAMY20121620, BRAMY20124260,
 15 BRAMY20134140, BRAMY20135900, BRAMY20136210, BRAMY20137560, BRAMY20144620, BRAMY20147540,
 BRAMY20148130, BRAMY20152110, BRAMY20153110, BRAMY20157820, BRAMY20160700, BRAMY20163250,
 BRAMY20163270, BRAMY20167060, BRAMY20167710, BRAMY20168920, BRAMY20170140, BRAMY20174550,
 BRAMY20178640, BRAMY20181220, BRAMY20182730, BRAMY20183080, BRAMY20184670, BRAMY20195090,
 BRAMY20204450, BRAMY20205740, BRAMY20210400, BRAMY20211390, BRAMY20211420, BRAMY20213100,
 20 BRAMY20215230, BRAMY20217460, BRAMY20218250, BRAMY20218670, BRAMY20229800, BRAMY20229840,
 BRAMY20230600, BRAMY20231720, BRAMY20240040, BRAMY20245300, BRAMY20247110, BRAMY20247280,
 BRAMY20248490, BRAMY20250240, BRAMY20250320, BRAMY20252180, BRAMY20252720, BRAMY20260910,
 BRAMY20261680, BRAMY20266850, BRAMY20267130, BRAMY20268990, BRAMY20270730, BRAMY20271400,
 BRAMY20273960, BRAMY20277140, BRAMY20277170, BRAMY20280720, BRAMY20284910, BRAMY20285160,
 25 BRAMY20285930, BRAMY20286820, BRAWH20002320, BRAWH20012390, BRAWH20014920, BRAWH20015350,
 BRAWH20015890, BRAWH20016660, BRAWH20016860, BRAWH20017010, BRAWH20018730, BRAWH20028110,
 BRAWH20029630, BRAWH20064050, BRAWH20075700, BRAWH20096780, BRAWH20100690, BRAWH20101360,
 BRAWH20103180, BRAWH20105840, BRAWH20106180, BRAWH20107540, BRAWH20110660, BRAWH20110790,
 BRAWH20110960, BRAWH20111550, BRAWH20112940, BRAWH20114000, BRAWH20117950, BRAWH20118230,
 30 BRAWH20122580, BRAWH20125380, BRAWH20126190, BRAWH20126980, BRAWH20132190, BRAWH20137480,
 BRAWH20138660, BRAWH20139410, BRAWH20142340, BRAWH20147290, BRAWH20149340, BRAWH20155950,
 BRAWH20158530, BRAWH20160280, BRAWH20162690, BRAWH20166790, BRAWH20171030, BRAWH20173050,
 BRAWH20182060, BRAWH20185060, BRCAN10001490, BRCAN20003460, BRCAN20006200, BRCAN20006390,
 BRCAN20054490, BRCAN20060190, BRCAN20064010, BRCAN20071190, BRCAN20091560, BRCAN20103740,
 35 BRCAN20124080, BRCAN20126130, BRCAN20143700, BRCAN20147880, BRCAN20216690, BRCAN20224720,
 BRCAN20237240, BRCAN20263400, BRCAN20273100, BRCAN20273340, BRCAN20273550, BRCAN20275130,
 BRCAN20279700, BRCAN20280210, BRCAN20280400, BRCAN20283190, BRCAN20283380, BRCAN20284600,
 BRCAN20285450, BRCOC10000870, BRCOC20001860, BRCOC20004040, BRCOC20004870, BRCOC20006370,
 BRCOC20008160, BRCOC20008500, BRCOC20020850, BRCOC20021550, BRCOC20023230, BRCOC20026640,
 40 BRCOC20027510, BRCOC20031000, BRCOC20031250, BRCOC20031870, BRCOC20035130, BRCOC20037320,
 BRCOC20037400, BRCOC20041750, BRCOC20055420, BRCOC20059510, BRCOC20077690, BRCOC20090520,
 BRCOC20091960, BRCOC20093800, BRCOC20099370, BRCOC20101230, BRCOC20107300, BRCOC20110100,
 BRCOC20114180, BRCOC20117690, BRCOC20119960, BRCOC20121720, BRCOC20122290, BRCOC20128130,
 BRCOC20134480, BRCOC20135730, BRCOC20136750, BRCOC20144000, BRCOC20147480, BRCOC20148330,
 45 BRCOC20155970, BRCOC20158240, BRCOC20176520, BRCOC20178560, BRHIP10001290, BRHIP20000870,
 BRHIP20001630, BRHIP20096170, BRHIP20096850, BRHIP20103090, BRHIP20104440, BRHIP20105710,
 BRHIP20106100, BRHIP20107440, BRHIP20111200, BRHIP20115080, BRHIP20115760, BRHIP20118380,
 BRHIP20118910, BRHIP20119330, BRHIP20121410, BRHIP20123140, BRHIP20129720, BRHIP20132860,
 BRHIP20135100, BRHIP20137230, BRHIP20139720, BRHIP20140630, BRHIP20142850, BRHIP20143730,
 50 BRHIP20143860, BRHIP20149540, BRHIP20153560, BRHIP20153600, BRHIP20167880, BRHIP20169680,
 BRHIP20169900, BRHIP20170100, BRHIP20173150, BRHIP20174040, BRHIP20175420, BRHIP20180140,
 BRHIP20183690, BRHIP20186120, BRHIP20186500, BRHIP20189980, BRHIP20190070, BRHIP20191490,
 BRHIP20191770, BRHIP20194940, BRHIP20195890, BRHIP20196410, BRHIP20205090, BRHIP20207430,
 BRHIP20207990, BRHIP20208420, BRHIP20208590, BRHIP20227080, BRHIP20230710, BRHIP20232290,
 55 BRHIP20233090, BRHIP20234380, BRHIP20236950, BRHIP20238600, BRHIP20238690, BRHIP20240460,
 BRHIP20243470, BRHIP20249110, BRHIP20252450, BRHIP20253660, BRHIP20277620, BRHIP20283030,
 BRHIP20284800, BRHIP20285830, BRHIP20285930, BRHIP30004880, BRSSN10000920, BRSSN20013420,
 BRSSN20014260, BRSSN20015030, BRSSN20015790, BRSSN20018690, BRSSN20028570, BRSSN20038200,

EP 1 347 046 A1

BRSSN20038410, BRSSN20039370, BRSSN20043040, BRSSN20046570, BRSSN20046790, BRSSN20046860,
BRSSN20066110, BRSSN20097020, BRSSN20101100, BRSSN20105870, BRSSN20105960, BRSSN20108300,
BRSSN20120810, BRSSN20121030, BRSSN20137020, BRSSN20142940, BRSSN20146100, BRSSN20151990,
BRSSN20159070, BRSSN20159820, BRSSN20169050, BRSSN20176820, BRSSN20177570, BRSSN20187310,
5 BRSTN20000580, BRSTN20005360, BRTHA20000570, BRTHA20004740, BRTHA20046290, BRTHA20046390,
BRTHA20046420, CD34C30001250, CD34C30004240, CTONG10000100, CTONG20004690, CTONG20027090,
CTONG20050280, CTONG20076130, CTONG20077790, CTONG20095290, CTONG20095340, CTONG20099380,
CTONG20106520, CTONG20118250, CTONG20121010, CTONG20127450, CTONG20128470, CTONG20141650,
CTONG20143690, CTONG20153300, CTONG20155180, CTONG20158150, CTONG20161850, CTONG20164990,
10 CTONG20186320, D3OST10002700, D6OST20003580, D9OST20000310, D9OST20035800, DFNES20010910,
DFNES20071130, HCHON20002260, HCHON20003220, HCHON20010990, HCHON20015350, HCHON20022470,
HCHON20067220, HCHON20067700, HEART20003060, HEART20005410, HEART20061950, HEART20090000,
HHDPC10000650, HHDPC20057940, HLUNG20033780, KIDNE20011170, KIDNE20027250, KIDNE20104300,
KIDNE20107500, KIDNE20122910, KIDNE20127100, KIDNE20180710, LIVER10001260, LIVER20064100,
15 LIVER20087510, MAMGL10000830, MESAN20031900, MESAN20036460, MESAN20106640, MESAN20164090,
NOVAR10000150, NOVAR20000380, NT2NE20010400, NT2NE20010490, NT2NE20021620, NT2NE20122430,
NT2NE20125050, NT2NE20174920, NT2RI20001330, NT2RI20023590, NT2RI20041880, NT2RI20046080,
NT2RI20216250, NT2RI20252550, NT2RP60000770, NT2RP70045590, NT2RP70063950, NT2RP70195430,
NT2RP70198350, NTONG20028070, NTONG20046140, NTONG20064840, NTONG20067830, NTONG20077560,
20 PANCR10000910, PEBLM20024550, PEBLM20052820, PEBLM20074370, PERIC20004780, PLACE50000660,
PLACE60079250, PLACE60136720, PLACE60138830, PROST20005670, PROST20050670, PROST20107820,
PROST20111050, PROST20116600, PROST20120160, PROST20123530, PROST20161950, PROST20171280,
PROST20175290, PROST20185830, PROST20191640, PUAEN20015860, PUAEN20030180, PUAEN20044000,
PUAEN20078980, PUAEN20085150, PUAEN20108240, SKMUS20012010, SKNSH20062340, SMINT20013480,
25 SMINT20042990, SMINT20053300, SMINT20076470, SMINT20092330, SMINT20101440, SMINT20121220,
SMINT20121950, SMINT20122910, SMINT20130320, SMINT20131810, SMINT20144800, SMINT20163960,
SPLEN20002220, SPLEN20008740, SPLEN20011410, SPLEN20016260, SPLEN20027440, SPLEN20029310,
SPLEN20033960, SPLEN20054290, SPLEN20126190, SPLEN20128000, SPLEN20145720, SPLEN20146450,
SPLEN20147110, SPLEN20149110, SPLEN20157880, SPLEN20158900, SPLEN20171210, SPLEN20179180,
30 SPLEN20186430, SPLEN20204170, SPLEN20212730, SPLEN20214580, SPLEN20250390, STOMA20051200,
STOMA20062290, STOMA20092890, SYNOV20003970, TESOP20005270, TESTI10000940, TESTI20001720,
TESTI20002720, TESTI20004890, TESTI20011200, TESTI20035960, TESTI20037560, TESTI20044310,
TESTI20061110, TESTI20063830, TESTI20086210, TESTI20152460, TESTI20168960, TESTI20170350,
TESTI20208400, TESTI20213580, TESTI20214250, TESTI20254220, TESTI20258460, TESTI20330310,
35 TESTI20334410, TESTI20366910, TESTI20391770, TESTI20432750, TESTI20455620, THYMU20000570,
THYMU20058070, THYMU20066100, THYMU20075320, THYMU20081490, THYMU20100410, THYMU20101920,
THYMU20108310, THYMU20119390, THYMU20126900, THYMU20128260, THYMU20169680, THYMU20193640,
THYMU20209590, THYMU20235760, THYMU20239430, THYMU20240710, THYMU20253250, THYMU20286290,
TKIDN10000010, TKIDN20005210, TKIDN20030590, TRACH20005020, TRACH20005400, TRACH20007020,
40 TRACH20019960, TRACH20034840, TRACH20079690, TRACH20128110, TRACH20149970, TRACH20183170,
UMVEN10001860, UMVEN20003540, UTERU20000740, UTERU20030570, UTERU20054460, UTERU20055930,
UTERU20056010, UTERU20064860, UTERU20065930, UTERU20070040, UTERU20081300, UTERU20084260,
UTERU20094350, UTERU20120310, UTERU20124070, UTERU20164260, UTERU20168220, UTERU20183640,
ASTRO20032120, ASTRO20125520, BRACE20039040, BRACE20060720, BRACE20062640, BRACE20090440,
45 BRACE20099570, BRACE20111830, BRACE20142570, BRAWH20128270, BRCAN20280360, BRHIP20110800,
BRHIP20176420, BRSSN20003120, CTONG20105660, CTONG20124010, CTONG20133480, CTONG20139070,
CTONG20160560, FCBBF10001210, FCBBF10001550, FCBBF10001710, FCBBF10001820, FCBBF10002430,
FCBBF10002700, FCBBF10002800, FCBBF10003220, FCBBF10003740, FCBBF10003760, FCBBF10005060,
FCBBF10005460, FCBBF10005500, FCBBF20006780, FCBBF20014270, FCBBF20023700, FCBBF20032970,
50 FCBBF20035280, FCBBF20042170, FCBBF20042560, FCBBF20051220, FCBBF20054280, FCBBF20056370,
FCBBF20064520, FCBBF20067810, FCBBF20071860, FCBBF20072650, FCBBF20076330, FCBBF30008470,
FCBBF30010810, FCBBF30012350, FCBBF30012810, FCBBF30015940, FCBBF30019120, FCBBF30024750,
FCBBF30028180, FCBBF30033050, FCBBF30039020, FCBBF30052180, FCBBF30054440, FCBBF30057290,
FCBBF30062880, FCBBF30070770, FCBBF30071520, FCBBF30078290, FCBBF30083620, FCBBF30123470,
55 FCBBF30170590, FCBBF30172550, FCBBF30175310, FCBBF30178730, FCBBF30190850, FCBBF30195640,
FCBBF30199610, FCBBF30215060, FCBBF30225660, FCBBF30240960, FCBBF30242250, FCBBF30243640,
FCBBF30247930, FCBBF30252520, FCBBF30252800, FCBBF30252850, FCBBF30262510, FCBBF30266780,
FCBBF30266920, FCBBF30278630, FCBBF30279030, FCBBF30281880, FCBBF30284720, FCBBF30285280,

EP 1 347 046 A1

FCBBF40001730, FCBBF40005480, HCHON20007380, HEART20072310, HHDP20068620, HLUNG20023340, KIDNE20017130, KIDNE20028830, MESAN20014500, NT2RP70072690, NT2RP70137640, NTONG20067090, PLACE60004630, PROST20083600, PROST20189770, RECTM20003490, SKNSH20008190, SMINT20115880, SPLEN20169720, SPLEN20194050, SPLEN20284240, TESTI20083940, TESTI20213150, TESTI20254540, 5 TESTI20265250, TRACH20118940, UTERU20145480, UTERU20146680, ASTRO20155290, BRAWH20030250, BRAWH20113430, BRAWH20122770, BRHIP20005340, BRHIP30001110, BRSTN20002200, CTONG20052900, CTONG20108210, DFNES20031920, FEBRA10001900, FEBRA20003210, FEBRA20007620, FEBRA20009090, FEBRA20010120, FEBRA20017050, FEBRA20018280, FEBRA20025270, FEBRA20025520, FEBRA20026110, FEBRA20026280, FEBRA20029860, FEBRA20034680, FEBRA20037260, FEBRA20040530, FEBRA20042190, 10 FEBRA20052910, FEBRA20060610, FEBRA20072120, FEBRA20079310, FEBRA20082010, FEBRA20088360, FEBRA20090290, FEBRA20092890, FEBRA20093520, FEBRA20097310, FEBRA20113560, FEBRA20125070, FEBRA20132740, FEBRA20140100, FEBRA20161120, FEBRA20166540, FEBRA20167390, FEBRA20171380, FEBRA20176800, FEBRA20184330, FEBRA20192420, FEBRA20195820, FEBRA20196370, FEBRA20196630, FEBRA20197110, FEBRA20211710, FEBRA20214970, FEBRA20215500, FEBRA20216360, FEBRA20222040, 15 FEBRA20223220, FEBRA20225040, FEBRA20226010, FEBRA20229560, FEBRA20229630, FEBRA20232850, FEBRA20235500, HCHON20040020, KIDNE20102650, NT2RP70037240, PEBLM20072960, PLACE60169420, SKMUS20003610, SMINT20026890, SMINT20033400, SPLEN20020070, SPLEN20079510, TESTI20001000, TESTI20094020, THYMU20027560, THYMU20180280, THYMU20271250, TRACH20003590, UMVEN10001560, UTERU20022940, UTERU20046640, UTERU20119060, UTERU20144640, UTERU20176130, ASTRO20008010, 20 BRACE20276430, BRAMY20103570, BRAMY20120910, BRAMY20162510, BRAMY20196000, BRAWH20164460, BRCAN20273640, BRCOC20105100, BRHIP20198190, BRHIP20222280, BRHIP20254480, BRHIP30004570, CTONG20028410, CTONG20091080, CTONG20103480, CTONG20126070, CTONG20139340, DFNES20001530, HCHON20008150, HHDP20001040, HLUNG20016330, HLUNG20017120, IMR3220002430, KIDNE20007210, KIDNE20021910, KIDNE20124400, MESAN10001260, MESAN20029400, MESAN20121130, MESAN20153910, 25 NT2NE20159740, NT2NE20177520, NT2RI20086220, NT2RI20250750, NT2RP60000850, NT2RP70044280, NT2RP70056750, NT2RP70081610, NTONG20009770, OCBBF10000540, OCBBF10001750, OCBBF20006770, OCBBF20013890, OCBBF20019830, OCBBF20020150, OCBBF20020830, OCBBF20023570, OCBBF20028050, OCBBF20028650, OCBBF20029800, OCBBF20030280, OCBBF20030910, OCBBF20035930, OCBBF20037440, OCBBF20041680, OCBBF20045330, OCBBF20046120, OCBBF20046470, OCBBF20046690, OCBBF20048660, 30 OCBBF20050770, OCBBF20051610, OCBBF20053430, OCBBF20053490, OCBBF20053730, OCBBF20054200, OCBBF20054760, OCBBF20060300, OCBBF20062140, OCBBF20062410, OCBBF20066390, OCBBF20071210, OCBBF20071840, OCBBF20072240, OCBBF20073540, OCBBF20074140, OCBBF20076220, OCBBF20079310, OCBBF20079460, OCBBF20081380, OCBBF20082830, OCBBF20085200, OCBBF20086400, OCBBF20086910, OCBBF20088140, OCBBF20088220, OCBBF20091150, OCBBF20100400, OCBBF20103130, OCBBF20104040, 35 OCBBF20105570, OCBBF20107090, OCBBF20107920, OCBBF20108580, OCBBF20108630, OCBBF20109310, OCBBF20111770, OCBBF20116850, OCBBF20118970, OCBBF20120390, OCBBF20121390, OCBBF20122620, OCBBF20124360, OCBBF20127040, OCBBF20127140, OCBBF20127550, OCBBF20128120, OCBBF20129360, OCBBF20130910, OCBBF20132850, OCBBF20140890, OCBBF20145760, OCBBF20148280, OCBBF20151150, OCBBF20153340, OCBBF20153350, OCBBF20155060, OCBBF20164670, OCBBF20170690, OCBBF20173060, 40 OCBBF20173250, OCBBF20178150, OCBBF20180840, OCBBF20186870, OCBBF20189560, PEBLM20044520, PEBLM20071880, PLACE60060420, PROST20047390, PUAEN20003740, SMINT20029760, SPLEN20008820, SPLEN20084600, SPLEN20095550, SPLEN20099700, SPLEN20140800, SPLEN20173510, SPLEN20211220, SPLEN20250170, STOMA20067800, TESTI20031270, TESTI20116830, TESTI20121550, TESTI20234140, TESTI20442760, THYMU20039810, THYMU20070360, TRACH20033230, TRACH20084720, BRACE20067430, 45 BRAWH10000930, BRHIP20003120, BRSSN20152380, FEBRA20024100, FEBRA20027810, FEBRA20037500, FEBRA20082100, FEBRA20098460, FEBRA20144170, FEBRA20145780, FEBRA20233770, HHDP20000830, MESAN20025190, MESAN20089360, NT2RI20048840, NT2RP70043480, OCBBF20032460, OCBBF20039250, OCBBF20049300, OCBBF20061720, OCBBF20078920, OCBBF20084660, OCBBF20087010, PROST20087700, PROST20153320, TRACH20135520, ADIPS20004250, ASTRO10001650, BRACE20056810, BRACE20059370, 50 BRACE20106690, BRACE20210140, BRAWH20103290, BRAWH20121640, BRHIP20005530, BRHIP20217620, BRHIP20218580, BRHIP20238880, CTONG20075860, CTONG20129960, FCBBF10000240, FCBBF10000630, FCBBF10001150, FCBBF10004120, FCBBF10005740, FCBBF20075560, FCBBF30018550, FCBBF30025560, FCBBF30086440, FCBBF30090690, FCBBF30189490, FCBBF30233680, FCBBF30240020, HCHON20007510, HCHON20016650, HHDP20095280, KIDNE20002520, KIDNE20009470, NT2RI20003480, NT2RI20055790, 55 NT2RP70027380, NT2RP70032610, NT2RP70062230, OCBBF10001850, OCBBF20022900, OCBBF20026630, OCBBF20049840, OCBBF20059560, OCBBF20068490, OCBBF20071960, OCBBF20080410, OCBBF20094240, OCBBF20097720, OCBBF20108190, OCBBF20108430, OCBBF20126780, OCBBF20130110, OCBBF20139260, OCBBF20148730, OCBBF20149280, OCBBF20164050, OCBBF20173980, OCBBF20178880, OCBBF20180120,

OCBBF20188730, PROST20057930, SPLEN20162680, SPLEN20211940, TESTI20184620, TESTI20211240, TESTI20369690, THYMU20141670, TRACH20028030, UTERU20099720, UTERU20135860, BRACE20057190, BRHIP20191860, BRHIP20214950, FCBBF10003670, FCBBF10004370, FCBBF30013770, FCBBF30095260, FCBBF30246230, FEBRA20002100, FEBRA20034360, FEBRA20095140, FEBRA20130190, FEBRA20204060, HCHON20008320, LIVER20028420, TRACH20111130, ASTRO20108190, BRACE20003070, BRACE20060550, BRAWH20004600, BRAWH20011710, BRAWH20016620, BRHIP10001740, BRSTN10000830, CTONG10000940, CTONG20150910, D3OST10002670, FCBBF10000380, FCBBF10000770, FCBBF10003770, FCBBF20059090, FCBBF30016320, FCBBF30016570, FCBBF30049550, FCBBF30083820, FCBBF30238870, FCBBF40001420, FEBRA10001880, FEBRA20004620, FEBRA20080810, FEBRA20086620, FEBRA20095880, HHDP20034390, HLUNG10000550, NT2RI20023160, NT2RI20023910, NT2RI20025400, NT2RI20028470, NT2RI20054050, NT2RI20076290, NT2RI20091730, NT2RI20091940, NT2RP70036880, NT2RP70078420, OCBBF20047570, OCBBF20080050, OCBBF20125530, OCBBF20140640, TRACH20032720, TRACH20141240, UTERU20004240

[0298] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were the following clones (Table 49). FEHRT20003250, OCBBF20189560, BRAWH20029630, CTONG20150910, HCHON20007510, HEART20003060, HEART20005410, HEART20021840, HEART20025980, HEART20034320, HEART20037810, HEART20049400, HEART20049410, HEART20049800, HEART20061950, HEART20063340, HEART20067870, HEART20067890, HEART20072310, HEART20074430, HEART20077670, HEART20089940, HEART20090000, HEART20095990, HLUNG10000550, HLUNG20017120, KIDNE20028390, KIDNE20028830, NTONG20029480, OCBBF10001750, PROST20127800, SKMUS20001980, SKMUS20003610, SMINT20026890, SMINT20121220, SMINT20122910, SMINT20183530, SPLEN20008740, SPLEN20027440, SPLEN20162680, STOMA20062290, TESTI20254220, THYMU20271250, TRACH20141240, UTERU20004240

[0299] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 50).

ASTRO10001650, ASTRO20108190, BGGI120006160, BRACE20039040, BRACE20060550, BRAMY20102080, BRAWH20004600, BRAWH20125380, BRAWH20162690, BRHIP20115760, BRHIP20205090, BRHIP20238880, CTONG20052650, CTONG20108210, CTONG20128470, CTONG20133480, CTONG20139070, D9OST20000310, DFNES20001530, FCBBF10001820, FEBRA20002100, HCHON20008980, HCHON20016650, HLUNG20033780, KIDNE20002520, KIDNE20003940, KIDNE20006780, KIDNE20007210, KIDNE20007770, KIDNE20008010, KIDNE20009470, KIDNE20011170, KIDNE20011400, KIDNE20013730, KIDNE20017130, KIDNE20018730, KIDNE20018970, KIDNE20020150, KIDNE20021680, KIDNE20021910, KIDNE20021980, KIDNE20022620, KIDNE20024830, KIDNE20027250, KIDNE20027950, KIDNE20028390, KIDNE20028830, KIDNE20029800, KIDNE20067330, KIDNE20079440, KIDNE20096280, KIDNE20096470, KIDNE20100070, KIDNE20100840, KIDNE20101370, KIDNE20101510, KIDNE20102650, KIDNE20102710, KIDNE20104300, KIDNE20106740, KIDNE20107390, KIDNE20107500, KIDNE20107620, KIDNE20109730, KIDNE20109890, KIDNE20112000, KIDNE20115080, KIDNE20118580, KIDNE20120090, KIDNE20121880, KIDNE20122910, KIDNE20124400, KIDNE20125630, KIDNE20126010, KIDNE20126130, KIDNE20127100, KIDNE20127450, KIDNE20127750, KIDNE20130450, KIDNE20131580, KIDNE20132180, KIDNE20137340, KIDNE20138010, KIDNE20141190, KIDNE20144890, KIDNE20148900, KIDNE20163880, KIDNE20180710, KIDNE20181660, KIDNE20182690, KIDNE20186780, KIDNE20190740, LIVER20035110, MESAN20025190, NOVAR20000380, NT2RI20054050, NT2RP70043480, PROST20107820, PROST20123530, PROST20161950, PUAEN20030180, SKMUS20003610, SMINT20033400, TBAES20000590, TESTI20044310, TESTI20082330, TRACH20032720, UTERU20099720, BRACE20003070, BRCOC20031870, CTONG20125640, FCBBF30016320, HCHON20002260, HLUNG10000550, PROST20130530, SPLEN20169720, SPLEN20194050, KIDNE20028720

[0300] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 51). BRACE20096200, BRAWH20004600, BRAWH20030250, BRCAN20006390, BRCAN20280360, BRHIP20238880, CTONG10000940, CTONG20103480, CTONG20129960, CTONG20155180, FCBBF10001210, FEBRA20144170, FEBRA20197110, HHDP20034390, HLUNG20016330, HLUNG20016770, HLUNG20017120, HLUNG20023340, HLUNG20033780, HLUNG20084390, IMR3220002430, LIVER20028420, NOVAR20000380, NT2RI20054050, NT2RI20091730, NT2RP70044280, OCBBF20020830, OCBBF20125530, PLACE60004630, PROST20057930, PROST20107820, PROST20185830, PUAEN20030180, SMINT20121220, SPLEN20002220, SPLEN20054290, SPLEN20128000, SPLEN20157300, SPLEN20176200, SPLEN20179180, SPLEN20211940, STOMA20013890, TBAES20000590, TESTI20094230, TESTI20184620, TESTI20334410, THYMU20000570, THYMU20039810, TRACH20007020, TRACH20141240, TRACH20183170, D9OST20033970, FELNG20002410, HCHON20016650, KIDNE20029800, OCBBF20145760, SPLEN20162680, TESTI20214250, TRACH20005400, HCHON20002260, HLUNG10000550, NT2RI20023910, SPLEN20008740

[0301] These genes are involved in regeneration of tissues and/or cells.

EXAMP_E 8

Expression frequency analysis by PCR

[0302] Specific PCR primers were prepared based on the full-length nucleotide sequences, and the expression frequency was analyzed by the ATAC-PCR method (Adaptor-tagged competitive PCR method: Nucleic Acids Research 1997 25(22) 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Inflammation-related genes can be identified by revealing the genes whose expression levels are altered depending on the presence of an inflammation-inducing factor. Then, by using THP-1 cell line, which is a cell line of monocyte line, and TNF- α , which is inflammation-inducing factor, suitable for this system, the genes whose expression levels are altered depending on the presence of the factors were searched for by the system.

[0303] THP-1 cell line (purchased from DAINIPPON PHARMACEUTICAL) was cultured to be confluent in RPMI1640 medium (sigma) containing 5% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 10 ng/ml TNF- α (human recombinant TNF- α : Pharmacia Biotech), and the culture was continued at 37°C under 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without stimulation of TNF- α .

[0304] The genes involved in the onset of gastritis and gastroduodenal ulcer induced by the infection of *Helicobacter pylori* to the epithelia of stomach can be identified by revealing the genes whose expression levels are altered depending on co culturing the cells with *Helicobacter pylori*. A recent study has suggested that various substances derived from *Helicobacter pylori* trigger the inflammation reaction. In particular, the members belonging to the family of genes called "cag pathogenicity island (cag PAI)" contribute to the activation of the NF- κ B pathway (Gastroenterology 2000, 119: 97-108). Further, it has been found that cag PAI is involved in the onset of gastritis and the like by the study using an animal model (Journal of Experimental Medicine 2000 192:1601-1610). Then, by using co-culture of a gastric cancer cell line with cag PAI-positive *Helicobacter pylori* (TN2), suitable for this system, the genes whose expression levels are altered depending on the presence of *Helicobacter pylori* were searched for by the system. Further, in order to study the involvement of cag PAI in the alterations of gene expression levels depending on the co-culture with *Helicobacter pylori*, the altered expression levels were compared between the cells co-cultured with a strain of *Helicobacter pylori* (TN2, Δ cagE strain) having a mutation in cagE which is one of the cag PAI genes, and the cag PAI-positive strain (TN2).

[0305] A gastric cancer cell line MKN45 (provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research) was cultured to be confluent in RPMI1640 medium (sigma) containing 10% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 100-fold excess (in terms of the number of cells or the number of colonies) of *Helicobacter pylori* (cag PAI positive strain (TN2) and cagE mutant (TN2 Δ cagE): both were provided by Prof. Omata, Faculty of Medicine, The University of Tokyo), as compared with the number of the cancer cells. The culture was continued at 37°C under 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without *Helicobacter pylori*.

[0306] The analysis by the ATAC-PCR method was carried out basically according to "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement (Genome Science Series 1, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Adapter ligation to the internal standard sample (sample to make the calibration curve for the clone of interest) and test sample was carried out in the two separate reaction systems indicated below. The combination of 6 types of adapters (AD-1, AD-2, AD-3, AD-4, AD-5 and AD-6: see the sequences indicated below) and the samples are as follows.

Reaction system A

[0307]

- AD1 internal standard, 10-fold
- AD2 THP-1 cells, unstimulated
- AD3 internal standard, 3-fold
- AD4 THP-1 cells, TNF- α stimulation for one hour
- AD5 THP-1 cells, TNF- α stimulation for three hours

AD6; internal standard, 1-fold

Reaction system B

5 [0308]

AD1; internal standard, 1-fold
 AD2; MKN45 cells, unstimulated
 AD3; internal standard, 3-fold
 10 AD4; MKN45 cells, co-cultured with TN2 (*Helicobacter pylori*)
 AD5; internal standard, 10-fold
 AD6; MKN45 cells, co-cultured with TN2ΔcagE(cagE gene mutant)

Adapter sequences:

15 [0309]

SEQ ID NO : 4887//5'-GTACATATTGTCGTTAGAACGCG-3'
 20 SEQ ID NO : 4888//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'
 AD2;
 SEQ ID NO : 4889//5'-GTACATATTGTCGTTAGAACGCGACT-3'
 25 SEQ ID NO : 4890//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'

 AD3;
 30 SEQ ID NO : 4891//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'
 SEQ ID NO : 4892//3'-CATGTATAACAGCAATCTTGCGCGTATGACTAG-5'
 AD4;
 35 SEQ ID NO : 4893//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'
 SEQ ID NO : 4894//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'
 AD5;
 40 SEQ ID NO : 4895//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'
 SEQ ID NO : 4896//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'
 AD6;
 45 SEQ ID NO : 4897//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'
 SEQ ID NO : 4898//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0310] The internal standard sample used for this assay was a mixture of total RNAs from tissues (or culture cells; all from UNITECH) of Fetal Brain, Testis, Trachea, and Spleen. RNA was prepared according to the standard method.

50 [0311] The sequences of primers specific to the genes and the names of clones of interest in the analysis are as follows. The gene specific primers were designed to produce the PCR products of 70 to 200 bp, which are derived from the adapter-containing cDNA. The sequence of adapter-specific primer (labeled with fluorescence (FAM)) used in the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides; SEQ ID NO: 4899). PCR was basically carried out with a cycling profile of preheating at 94°C for 3 minutes, and 35 or 40 cycles of denaturation at 94°C for 30 seconds/annealing at 50°C for 60 seconds/extension at 72°C for 90 seconds.

55 [0312] The nucleotide sequences of clone specific primers used in the experiments

[0313] Clone name, primer sequence and SEQ ID NO are indicated below in this order. Each is demarcated by a double slash mark (/). For a clone for which a primer used in Reaction system A (THP-1 cells) was different from a primer used in Reaction system B (MKN45 cells), the sequence of each of the primers was shown.

EP 1 347 046 A1

3NB6920014080//GTCCTGAAGGTAGATGCT//SEQ ID NO : 4900

5

ADRGL20013010//GGAGGATAGAGCTTGGAG//SEQ ID NO : 4901

ADRGL20067670//ATAAACAGGACCAAGGA//SEQ ID NO : 4902

10

ADRGL20083310//AAATAAGGCTAAATGGAACT//SEQ ID NO : 4903

ASTRO20032120//AGTGCTCCCAATTATCCG//SEQ ID NO : 4904

ASTRO20084250//TAGAAAATATGCTGGGTG//SEQ ID NO : 4905

ASTRO20152140//TCATTCTTCTCCACAGC//SEQ ID NO : 4906

15

ASTRO20166810//AGTTTTATTTCAGGCTATC//SEQ ID NO : 4907

ASTRO20181690//ATGGAGAACAGGACAGCT//SEQ ID NO : 4908

BLADE20004630//CAAACATCAACCAGAGAA//SEQ ID NO : 4909

20

BRACE20006400//TCCCAATCAGCTAAGGTC//SEQ ID NO : 4910

BRACE20019540//CAGGTTATCGAGAGTTACAT//SEQ ID NO : 4911

BRACE20038480//TCTGGTTGGATTTTGTGC//SEQ ID NO : 4912

BRACE20039040//TGAACCTTGTGGTCTGGT//SEQ ID NO : 4913

25

BRACE20039440//TGAACAGTGACATTTTAGG//SEQ ID NO : 4914

BRACE20052160//AAGAATAAAAGGGACGAG//SEQ ID NO : 4915

BRACE20053630//GTTTGATACAGATGATTAGGTTA//SEQ ID NO : 4916

BRACE20057620//GGACAGGTAAGAACTAGGC//SEQ ID NO : 4917

30

BRACE20058810//ATCATCTTTCCAATCCAG//SEQ ID NO : 4918

BRACE20060720//GTACCACCTGACCTTCTG//SEQ ID NO : 4919

BRACE20060840//AGAAGTTTTATCCACATTT//SEQ ID NO : 4920

35

BRACE20061740//(Reaction system A)//TAACATAACCCTCCCGTC//SEQ ID NO : 4921

//(Reaction system B)//ATAGTGGTGACGTTCCCC//SEQ ID NO : 4922

BRACE20062640//TCTGTTGCTGAAGGAAAA//SEQ ID NO : 4923

40

BRACE20063780//TCCTGTGTGCTATTTGAA//SEQ ID NO : 4924

BRACE20067430//AATAACAGCAACTCCAGA//SEQ ID NO : 4925

BRACE20090440//CCCAACATTACCAAAAGT//SEQ ID NO : 4926

45

BRACE20101700//CAACATTTTCAAGCACTG//SEQ ID NO : 4927

BRACE20114780//GATGTTGGGTTTGAAG//SEQ ID NO : 4928

BRACE20151320//ACCAGCTGCCCATAGAAG//SEQ ID NO : 4929

BRACE20152870//GAAGGCAAGATGGTAAGT//SEQ ID NO : 4930

50

BRACE20163150//CATAGAGAAAGCGGGGAA//SEQ ID NO : 4931

BRACE20165830//(Reaction system A)//TCTCCCTGTTCTCTCTTT//SEQ ID NO : 4932

55

//(Reaction system B)//TATGACCCAAACGCCTAG//SEQ ID NO : 4933

BRACE20201570//CCTTCTCATCTAGCTTGC//SEQ ID NO : 4934

EP 1 347 046 A1

BRACE20210140//TACTGATTGGGAAGCACT//SEQ ID NO : 4935
5 BRACE20223330//GTTGAAATGCTTGAGCAC//SEQ ID NO : 4936
BRACE20224500//ATTTAGAGCGCCATCCTT//SEQ ID NO : 4937
BRACE20229280//CTGAGGGTAAAGGAAGGG//SEQ ID NO : 4938
BRACE20235400//TTTTACGATTGCCTTTGC//SEQ ID NO : 4939
10 BRACE20266750//TTAGGAGTGAAGACAGGA//SEQ ID NO : 4940
BRACE20267250//GTGCAGTGATAAGTGGCT//SEQ ID NO : 4941
BRACE20269710//AGGCAGGGAAAGTAGGGT//SEQ ID NO : 4942
15 BRALZ20018340//AGGAGAGGCTTGAGGACT//SEQ ID NO : 4943
BRALZ20058880//AAGGGACCAAAATGAGAG//SEQ ID NO : 4944
BRALZ20059500//AACAGCCCTCTAATGAAA//SEQ ID NO : 4945
BRALZ20064740//ACTCATGTTGCTCCACCT//SEQ ID NO : 4946
20 BRALZ20069760//TATGTATGGCTTTGAGCA//SEQ ID NO : 4947
BRALZ20075450//GCTGAAGAAATGTGCTGC//SEQ ID NO : 4948
BRALZ20088690//ATCATAGTTGTACATACTTTGGG//SEQ ID NO : 4949
25 BRAMY20002770//TTCTTTCTGTAAATAGTTGG//SEQ ID NO : 4950
BRAMY20004110//AGCTATCTGTGAAAGTCCT//SEQ ID NO : 4951
BRAMY20060920// (Reaction system A) //TGCTGTCTCGTGATAAAG//SEQ ID
NO : 4952
30 //(Reaction system B) //TTTCTAATGGTTTGGCAC//SEQ ID NO : 4953
BRAMY20103570// (Reaction system A) //TCAACAGTGCTTTTCCTT//SEQ ID
NO : 4954
35 //(Reaction system B) //GACTCTTCTCCAGGGTGC//SEQ ID NO : 4955
BRAMY20144620//CACGCCATTCTGTTAAAA//SEQ ID NO : 4956
BRAMY20152110//AATGGGCTAAATATTGCT//SEQ ID NO : 4957
BRAMY20152510//GCAAATACAGGTAAATGACAG//SEQ ID NO : 4958
40 BRAMY20153250//CAAGAGAAATTAAAGAAGACC//SEQ ID NO : 4959
BRAMY20163270// (Reaction system A) //TGCTTTCAACTGTCATTT//SEQ ID
NO : 4960
45 //(Reaction system B) //GAATGATGCCCCGATGTAG//SEQ ID NO : 4961
BRAMY20168920//GAATATCCCTGTGGAGTC//SEQ ID NO : 4962
BRAMY20178640//AGTCTCACTCTATTGCCA//SEQ ID NO : 4963
BRAMY20184670//AACGAATAGCAGGGTAGC//SEQ ID NO : 4964
50 BRAMY20204450//GGTGACTTACTGGCTGCA//SEQ ID NO : 4965
BRAMY20210400//AAGATTAACCATAACAACAGAAA//SEQ ID NO : 4966
BRAMY20215230//TGAACAAGAAACACCAGT//SEQ ID NO : 4967

55

EP 1 347 046 A1

BRAMY20218670//AGGAGGCACGGTAACAAT//SEQ ID NO : 4968
 BRAMY20229800//GTCTTCTGTCTCATGGGG//SEQ ID NO : 4969
 5 BRAMY20229840//AAAGTTCATGAGGGGCTG//SEQ ID NO : 4970
 BRAMY20231720//CAGCACAAAATCAGTTAAA//SEQ ID NO : 4971
 BRAMY20247280//GGTTTAGATTATGAGACAAGA//SEQ ID NO : 4972
 10 BRAMY20261680//GTTACTGCAGGGCTTCAG//SEQ ID NO : 4973
 BRAMY20266850//TGCATGGAATTAAAGGAGT//SEQ ID NO : 4974
 BRAMY20267130//AATCTGTAAAATGGGAATAAG//SEQ ID NO : 4975
 BRAMY20277140//(Reaction system A)//ATGAGATTGTGTTGTCCA//SEQ ID
 15 NO : 4976
 //(Reaction system B)//TTCCAGCATTTTCGTTTT//SEQ ID NO : 4977
 BRAMY20280720//(Reaction system A)//TTCCAAGTCCAGATTTT//SEQ ID
 20 NO : 4978
 //(Reaction system B)//CTGAGGAGCAGTGACAAG//SEQ ID NO : 4979
 BRAWH10000930//GGGAGAGAAGAGTCCTGC//SEQ ID NO : 4980
 BRAWH20015350//GCTATGAAGACAACCAAAC//SEQ ID NO : 4981
 25 BRAWH20017010//AGGAAGAGATGGGTCAGC//SEQ ID NO : 4982
 BRAWH20029630//GGAGTATCACCATGTAAAGA//SEQ ID NO : 4983
 BRAWH20100690//(Reaction system A)//AAATGAGCACTCCATTCC//SEQ ID
 30 NO : 4984
 //(Reaction system B)//AATGAGCACTCCATTCCC//SEQ ID NO : 4985
 BRAWH20106180//(Reaction system A)//CATTTTATTGTACCCAC//SEQ ID
 NO : 4986
 35 //(Reaction system B)//CCTTTAACAGCATCTCTAGTG//SEQ ID NO : 4987
 BRAWH20107540//GTTGAGCTATTTGCAGAG//SEQ ID NO : 4988
 BRAWH20110660//CTTAGCAACTTTCCACAC//SEQ ID NO : 4989
 40 BRAWH20113230//GTCAGAAACTCACACCA//SEQ ID NO : 4990
 BRAWH20122770//AAGTTGATAGGGAAGGTTT//SEQ ID NO : 4991
 BRAWH20126190//ACCATGTGCTCAGAATCA//SEQ ID NO : 4992
 BRAWH20132190//TAAGATTACAGGGTGGA//SEQ ID NO : 4993
 45 BRAWH20138650//GATGGAAAATGTAAGGCT//SEQ ID NO : 4994
 BRAWH20139410//CCATCCTCTACACAGCAG//SEQ ID NO : 4995
 BRAWH20155950//(Reaction system A)//CTCTCATTTTGGCTCTGC//SEQ ID
 50 NO : 4996
 //(Reaction system B)//CTACTCCACCTCTGCTGC//SEQ ID NO : 4997
 BRAWH20158530//AGTTTTCTGATGGCCTTG//SEQ ID NO : 4998

BRCAN20060190//AGGTAGCCCCAGAGTCAC//SEQ ID NO : 4999
 BRCAN20147880//ACTCAGCAATCAGGTCCA//SEQ ID NO : 5000
 5 BRCAN20273340//AATTATGAGATAGGATGTTAGCT//SEQ ID NO : 5001
 BRCAN20273640//CTGCACCGATTTTATAGC//SEQ ID NO : 5002
 BRCAN20275130//CACTATCCAGACACACCT//SEQ ID NO : 5003
 10 BRCAN20280210//CACTGGATTTTCTTCACTT//SEQ ID NO : 5004
 BRCAN20280400//GGAAGGATAGCAGTTGAT//SEQ ID NO : 5005
 BRCOC20021550//TCCAAGCAGAGTTTTCAC//SEQ ID NO : 5006
 BRCOC20037400//CAAGTCTGTTTCATCTGGT//SEQ ID NO : 5007
 15 BRCOC20105100// (Reaction system A) //ACTTGAGGTTTCTTGGCA//SEQ ID
 NO : 5008
 //(Reaction system B) //GATTCTTCCCCGACTCAG//SEQ ID NO : 5009
 20 BRHIP10001740//GTACACACCTGCTCCAC//SEQ ID NO : 5010
 BRHIP20001630//GGTCAGTAAGTGGTTGTG//SEQ ID NO : 5011
 BRHIP20096170//TTATTTTGGATGCCCTG//SEQ ID NO : 5012
 BRHIP20103090//ACTCCAACAACCTTCATT//SEQ ID NO : 5013
 25 BRHIP20105710//TTTCAAGTATCCTCCCCA//SEQ ID NO : 5014
 BRHIP20110800//TAGAACTGCCTCCAACCC//SEQ ID NO : 5015
 BRHIP20111200//TACTGAACGGTGACTGGC//SEQ ID NO : 5016
 BRHIP20118910//ACAGGAAGGGGAAAGAGT//SEQ ID NO : 5017
 30 BRHIP20129720//GAGGAGAGTGAGAAGGGG//SEQ ID NO : 5018
 BRHIP20143860//AGGTCAGGAGAACAAGCC//SEQ ID NO : 5019
 BRHIP20173150//CTTTTGCAGAGTTTTCCT//SEQ ID NO : 5020
 35 BRHIP20175420//TCTCTAGGGCAAAACATT//SEQ ID NO : 5021
 BRHIP20186120// (Reaction system A) //AATTGATACGCAGGGGAG//SEQ ID
 NO : 5022
 40 //(Reaction system B) //AAGGTCAGTTGAAGTGCT//SEQ ID NO : 5023
 BRHIP20194940//TAGAGAAGGTGAGGCCAG//SEQ ID NO : 5024
 BRHIP20196410//GGCATAGAAGTAATCAGAGA//SEQ ID NO : 5025
 BRHIP20207430//AAGCTGAACCCCAATAAA//SEQ ID NO : 5026
 45 BRHIP20218560//GATTACCAGAACACAGCC//SEQ ID NO : 5027
 BRHIP20233090//GTCCATTTACCAACGGCT//SEQ ID NO : 5028
 BRHIP20284800//CACATCTTTACATTTATTGCTATT//SEQ ID NO : 5029
 50 BRHIP30004880//TCTTCTCGTAGGGCTTGA//SEQ ID NO : 5030
 BRSSN20046570//AAACACGAAATGGATGAA//SEQ ID NO : 5031
 BRSSN20142940//AGAATCAGAGAAGCCGGT//SEQ ID NO : 5032

EP 1 347 046 A1

BRSSN20152380//ATACCCATTTTCAGTTCCT//SEQ ID NO : 5033
 5 BRSSN20176820//CAGTCCCAATACAGCTCA//SEQ ID NO : 5034
 BRSSN20187310//(Reaction system A)//CAATGACTAGTTTGTGCA//SEQ ID
 NO : 5035
 //(Reaction system B)//AAAGAAGCCAGGAAGATT//SEQ ID NO : 5036
 10 BRTHA20046390//ACATGGAGCCTGGTTTAG//SEQ ID NO : 5037
 CD34C30004240//TGGAAGATACGGATAACTC//SEQ ID NO : 5038
 CD34C30004940//(Reaction system A)//ACCACTGTTCTCTGGTGC//SEQ ID
 NO : 5039
 15 //(Reaction system B)//CCACCACTGTTCTCTGGT//SEQ ID NO : 5040
 COLON20043180//TCGGATTGGGTTAAGGTC//SEQ ID NO : 5041
 CTONG10000620//CTCCATTCATCAGACCAC//SEQ ID NO : 5042
 20 CTONG20014280//TCCAAAGACAGAACAGC//SEQ ID NO : 5043
 CTONG20095270//GTTTTGTTCCCTGCTCAC//SEQ ID NO : 5044
 CTONG20095290//AACACAGCTCAACAACCTC//SEQ ID NO : 5045
 CTONG20096750//TGACTAAGCATGGAGACT//SEQ ID NO : 5046
 25 CTONG20100240//AGTCATAATCATCTTCCTCA//SEQ ID NO : 5047
 CTONG20103480//GGTGGAGTAATGTATATAACGTAA//SEQ ID NO : 5048
 CTONG20105660//CCATTAACACAAACCAA//SEQ ID NO : 5049
 30 CTONG20121010//GGAAGATGGGACCTCAGT//SEQ ID NO : 5050
 CTONG20128470//TTGGGGTATCTTGGAGCT//SEQ ID NO : 5051
 CTONG20138030//GGCATAGAAGTAATCAGAGA//SEQ ID NO : 5052
 CTONG20139070//TCAAACCTCCTATCTTCTG//SEQ ID NO : 5053
 35 CTONG20146970//TTTTAATCCTCAGTACATTTTC//SEQ ID NO : 5054
 CTONG20158150//AAATAGGTTGATGTTGGC//SEQ ID NO : 5055
 CTONG20186320//TGACTTTGGCCCTTTACC//SEQ ID NO : 5056
 40 CTONG20265130//GGGTAGGTGCTAGAAATC//SEQ ID NO : 5057
 D3OST20006540//GGAGACCACACATAACAT//SEQ ID NO : 5058
 D3OST20037970//CACTGACGAAAGGGAAGA//SEQ ID NO : 5059
 D9OST20031370//CGACTTGCCAGACTCACT//SEQ ID NO : 5060
 45 DFNES10001850//GTGGCTCAAAGTAGGATT//SEQ ID NO : 5061
 DFNES20031920//CTTACTCCAACCCAGGCT//SEQ ID NO : 5062
 FCBBF10005060//TGCATGTTTTCTTCCTCA//SEQ ID NO : 5063
 50 FCBBF20032970//CCAGACACAACAATACCA//SEQ ID NO : 5064
 FCBBF20035280//(Reaction system A)//ATACAATTTGTGCCTGTTA//SEQ ID
 NO : 5065

EP 1 347 046 A1

// (Reaction system B) //CGGTAAGTAGTCTTCATGTG//SEQ ID NO : 5066
 FCBBF20054280//GGTGCATCTGTACTTGAA//SEQ ID NO : 5067
 5 FCBBF20071860//TGGAGGAGTAGTTATCAGTTG//SEQ ID NO : 5068
 FCBBF30001840//AGTGCTCCCAATTATCCG//SEQ ID NO : 5069
 FCBBF30016320//GGCTACTCAAGGACACAG//SEQ ID NO : 5070
 10 FCBBF30016570//AGGGATAAGATGGCAGGT//SEQ ID NO : 5071
 FCBBF30033050//TCCTGTACTCCTTTCCAT//SEQ ID NO : 5072
 FCBBF30071520//CAGGCATAAGAGGTGGCT//SEQ ID NO : 5073
 FCBBF30083820//CCTGTGTGATACCAAATACT//SEQ ID NO : 5074
 15 FCBBF30215060//CAGCCCCAATTACTAGAA//SEQ ID NO : 5075
 FCBBF30251420//AGCATGTACTGGGAAAGC//SEQ ID NO : 5076
 FCBBF30252520//AGGGATAAAGAATGCAAA//SEQ ID NO : 5077
 20 FCBBF30262360//GAGCTTCAGGGGCATTTA//SEQ ID NO : 5078
 FCBBF30266920//ATACGCAATTTTCAGACC//SEQ ID NO : 5079
 FCBBF30273630//AAAAGACAACGATGCCTG//SEQ ID NO : 5080
 FCBBF30285280//AAAGCAAAGTGATATAGGAGT//SEQ ID NO : 5081
 25 FCBBF40001420//ACATTTTCAGTCCATTTCAC//SEQ ID NO : 5082
 FEBRA10001830//TTGTTCATGGTGGTAATCC//SEQ ID NO : 5083
 FEBRA20010120//GGACCAGACTCACAAATT//SEQ ID NO : 5084
 30 FEBRA20017050//TATACTAAAACCCAGCCA//SEQ ID NO : 5085
 FEBRA20034360//CGGCAGCTAGAAAACCTC//SEQ ID NO : 5086
 FEBRA20037260//CGTTGGTTTTCTGGACAC//SEQ ID NO : 5087
 FEBRA20037500//CTCGGGCAGGATTAATCTC//SEQ ID NO : 5088
 35 FEBRA20082100//AGAAGATGCTAGGTTTGC//SEQ ID NO : 5089
 FEBRA20095880//AGCATGTACTGGGAAAGC//SEQ ID NO : 5090
 FEBRA20167390//GCTTATGTTGCAGTTTCA//SEQ ID NO : 5091
 40 FEBRA20176800//TCAGTTTCAGGGGTCAAG//SEQ ID NO : 5092
 FEBRA20226010//TCAGGGTATCAGCTTTCC//SEQ ID NO : 5093
 HCASM10000500//TGTGGTGACTTACTGCCT//SEQ ID NO : 5094
 HCHON20002260//CTCTCCAACAACTGCAC//SEQ ID NO : 5095
 45 HCHON20008980//CTGCTGCCTTACACAACC//SEQ ID NO : 5096
 HCHON20009350//AGGTAATGAGGAATGCAC//SEQ ID NO : 5097
 HCHON20010990//GATTCCACCCTCAAGATT//SEQ ID NO : 5098
 50 HCHON20011160//CTCCTCCACGCTTGTTTT//SEQ ID NO : 5099
 HCHON20015230//CTTGGTCACAGTTTTTCAT//SEQ ID NO : 5100
 HCHON20022470//CACACTTTCAATCCGAGG//SEQ ID NO : 5101

55

EP 1 347 046 A1

HCHON20035130//GTGGAAGATGCTCGACTG//SEQ ID NO : 5102
HCHON20043590//AGGATTAGGTATTGCTTCTC//SEQ ID NO : 5103
5 HCHON20067220//TAAGGAAAACCCAACCAC//SEQ ID NO : 5104
HCHON20076500//GAAAGACACCTGGCACAC//SEQ ID NO : 5105
HEART20021840//GTACCCCAAAAGAAACAT//SEQ ID NO : 5106
10 HEART20067870//GAACTATCTAATCACATGGG//SEQ ID NO : 5107
HEART20083640// (Reaction system A) //TCTTGATGTCTCCTGCCT//SEQ ID
NO : 5108
// (Reaction system B) //CTCGGCTGGAAGGTAAAA//SEQ ID NO : 5109
15 HHDPC10000650//ACTGGTAAGATATGGGCA//SEQ ID NO : 5110
HHDPC20034390//CTCTCCCAAACTCAGGTC//SEQ ID NO : 5111
HHDPC20095280//TGACCCAAAGACATACTG//SEQ ID NO : 5112
20 HLUNG10000550//GATTTACTTCCGGTTTCG//SEQ ID NO : 5113
KIDNE20018970//AAGAGAATAAGGCTGGGC//SEQ ID NO : 5114
KIDNE20028720//AACAAAATAAGGGGCCAG//SEQ ID NO : 5115
KIDNE20079440//AAGTTCATCTGGGTGTGG//SEQ ID NO : 5116
25 KIDNE20096470//ATCACCTGGAGAGCTTTG//SEQ ID NO : 5117
KIDNE20106740//AGGGACACTGAGAACTGG//SEQ ID NO : 5118
KIDNE20120090//GAAGCAGGGAAGTGTGAG//SEQ ID NO : 5119
30 KIDNE20127750//GCTATTACACATTCTGCATT//SEQ ID NO : 5120
KIDNE20130450//CAGCTACTTGGGACAGGA//SEQ ID NO : 5121
KIDNE20132180// (Reaction system A) //ACCAGCTCAGCAAGAACT//SEQ ID
NO : 5122
35 // (Reaction system B) //CTCTGACATGAACTGGTG//SEQ ID NO : 5123
KIDNE20141190//CACATTGCCTAGAGAAAG//SEQ ID NO : 5124
KIDNE20148900//ACAACAGCAGATGACTCG//SEQ ID NO : 5125
40 KIDNE20163880//CAGTCACATCTCCCTTTA//SEQ ID NO : 5126
KIDNE20182690//TCACTGTATCACCATCTG//SEQ ID NO : 5127
LIVER10004790//TCCCTGCTAAGATGTTGA//SEQ ID NO : 5128
LIVER20011130//GAGGTCAAGGACACACAG//SEQ ID NO : 5129
45 LIVER20038540// (Reaction system A) //AAGCAATGTGGCAGACTC//SEQ ID
NO : 5130
// (Reaction system B) //AGTGGGTTCTTTATCATTTT//SEQ ID NO : 5131
50 LIVER20055440//GTTTGCCAGGGAATGTTT//SEQ ID NO : 5132
LIVER20062510//GTAACGTGCTCTGAATGA//SEQ ID NO : 5133
LIVER20085800//GCTCTGCTGTTTCTAATTT//SEQ ID NO : 5134

EP 1 347 046 A1

MAMGL10000830//TCGATACGTGGAAGAATT//SEQ ID NO : 5135
 MESAN20031900//TCCCAAGGCTGTAGTTCA//SEQ ID NO : 5136
 5 MESAN20121130//AGCTTGATCTAAATTCGTG//SEQ ID NO : 5137
 MESAN20127350//CAGAAGACAGGTTGCCAG//SEQ ID NO : 5138
 MESAN20130220//CCTAAGATTGGTCGTCCT//SEQ ID NO : 5139
 10 MESAN20154010//ATCCTGTCTCTTTTCGC//SEQ ID NO : 5140
 MESAN20174170//TGGCTAAGGTTCTCAGGA//SEQ ID NO : 5141
 NOVAR10001020//GGGTCAGTAAATCTAATGC//SEQ ID NO : 5142
 NT2NE20053580//CAAAACACAGAGTTATCAGAA//SEQ ID NO : 5143
 15 NT2NE20089610//TGCTGTCCTAGAAGAATAAA//SEQ ID NO : 5144
 NT2NE20089970//ACAATTATACTGGAAAAGCA//SEQ ID NO : 5145
 NT2NE20146810//GCTGAGACCTTTTGCTAG//SEQ ID NO : 5146
 20 NT2NE20155110//AGCCGAGGTTTTGAGTTA//SEQ ID NO : 5147
 NT2NE20156260//ACATTTGCACTGGAAGT//SEQ ID NO : 5148
 NT2NE20158600//CTCAGAAGCCCAGCAATT//SEQ ID NO : 5149
 NT2NE20172590//ACATCATAATCAAGCAGTAAA//SEQ ID NO : 5150
 25 NT2NE20174920//AGGACAGCAACAAGAGAG//SEQ ID NO : 5151
 NT2NE20181650//AGAGCTGATTTATACGCA//SEQ ID NO : 5152
 NT2RI20005750//AAGGAGTCTACGAAGCAC//SEQ ID NO : 5153
 30 NT2RI20009870//AAGATGACCCCGAGTTTG//SEQ ID NO : 5154
 NT2RI20023160//CATGCAAATAGAGGACTG//SEQ ID NO : 5155
 NT2RI20040930//CCATACTGTTCTCTGCTG//SEQ ID NO : 5156
 NT2RI20046080//CCGTAACCTTTTATATGCCTG//SEQ ID NO : 5157
 35 NT2RI20055790//GCAAGAGCTACAGACAAA//SEQ ID NO : 5158
 NT2RI20069730//AGTGTGCAGAAATCCGTG//SEQ ID NO : 5159
 NT2RI20203900//AGCAGTAGCACAGCCTTA//SEQ ID NO : 5160
 40 NT2RP70062230//(Reaction system A)//ACTCTAACACATTTGGCA//SEQ ID
 NO : 5161
 //(Reaction system B)//TATTAGTGTGAGCTGGCA//SEQ ID NO : 5162
 NT2RP70102350//(Reaction system A)//ATAGGAGGTGTCATGCCC//SEQ ID
 45 NO : 5163
 //(Reaction system B)//TCTTTTGACCTACACTGC//SEQ ID NO : 5164
 NT2RP70110860//GGGGAAGGGAGTAAGGTC//SEQ ID NO : 5165
 50 NT2RP70111320//ACTTAGCATCCAGACCTC//SEQ ID NO : 5166
 NT2RP70130020//ATACTCTCTGCTCATGGA//SEQ ID NO : 5167
 NT2RP70143480//TTCTTGGCATCCTTCATT//SEQ ID NO : 5168

55

EP 1 347 046 A1

NT2RP70150800// (Reaction system A) //GAGGCTGTCTAGGGGAA//SEQ ID
NO : 5169

5 // (Reaction system B) //GAACAAGGGATGCAGGAT//SEQ ID NO : 5170
NT2RP70157890// (Reaction system A) //TATGTGATGTTTTCCCA//SEQ ID
NO : 5171

10 // (Reaction system B) //CTGCCTAAATAACACTGAAG//SEQ ID NO : 5172
NT2RP70169110//CTGTCCTCATCTGTGCAT//SEQ ID NO : 5173
NT2RP70175670//GGTAGAACGGGAAATCAT//SEQ ID NO : 5174
NT2RP70188020//AGGTTTGAGTAGAGGGAA//SEQ ID NO : 5175
15 NT2RP70188710//ATACAGCAGGGAAGAGGC//SEQ ID NO : 5176
NT2RP70190640//CAATGTGTCTTCAGTTTCC//SEQ ID NO : 5177
NTONG20029480//TCTTGATGTCTCCTGCCT//SEQ ID NO : 5178
20 NTONG20064840//AAAGCCATCGTACACCAT//SEQ ID NO : 5179
NTONG20067090//AATTCTTTAGCTCTGTTGC//SEQ ID NO : 5180
NTONG20070340//ATCCACTGCCCCCTATCA//SEQ ID NO : 5181
NTONG20077560//CTGCTAGAATACGCCTTA//SEQ ID NO : 5182
25 NTONG20083650//CTCATAGTTCAAGGCAGC//SEQ ID NO : 5183
NTONG20090680//GAGTAAGGTCGTAGTCAGTG//SEQ ID NO : 5184
OCBBF20005230//GCAAGAGCTACAGACAAA//SEQ ID NO : 5185
30 OCBBF20019380//GTGGTCAGTGGAATGG//SEQ ID NO : 5186
OCBBF20020150//GGGACAGTATGGCAGAGA//SEQ ID NO : 5187
OCBBF20020830//GCTTGCCATAGGTGTACT//SEQ ID NO : 5188
OCBBF20039250//TTTCAGCAGTTAAGTGTTTT//SEQ ID NO : 5189
35 OCBBF20041680//TCAGAAGGTATGCCCCACT//SEQ ID NO : 5190
OCBBF20047570//ACCCTTATGTCAAACCTGC//SEQ ID NO : 5191
OCBBF20051610//TTTTCTACCTGCAATGG//SEQ ID NO : 5192
40 OCBBF20054200//GTCAGAAGCCATACGTGC//SEQ ID NO : 5193
OCBBF20061720//CAAAGTGGCCTAAACCCT//SEQ ID NO : 5194
OCBBF20062140//CTGGGGAGATAAGAGCCT//SEQ ID NO : 5195
OCBBF20071960// (Reaction system A) //CTCAGTCACGCAATAGAT//SEQ ID
45 NO : 5196
// (Reaction system B) //TCTCTGGAAGGGAAAATT//SEQ ID NO : 5197
OCBBF20072320//AAGAAGGAATGGGCACAC//SEQ ID NO : 5198
50 OCBBF20079310//CAGTAGCAAAACCAGAGC//SEQ ID NO : 5199
OCBBF20081380//GTGGAAGTGCCTGATGAG//SEQ ID NO : 5200
OCBBF20085200//TACAGGGTCAGTTGGCAG//SEQ ID NO : 5201

EP 1 347 046 A1

5 OCBBF20094240//ACACAATTCATCACTGCT//SEQ ID NO : 5202
 OCBBF20107920//GGTTGCTGTGAGTGCATT//SEQ ID NO : 5203
 OCBBF20127040//TAGAGGAGGCAGTAAGGG//SEQ ID NO : 5204
 OCBBF20130110//AGTGTCTATGGCTCTTCC//SEQ ID NO : 5205
 OCBBF20139260//GGGTGGTTCTGTTAGGAG//SEQ ID NO : 5206
 10 OCBBF20164050//TGCTGGAAATAATCGCTT//SEQ ID NO : 5207
 OCBBF20178990//TGAGTGTGGTGAAGATAGT//SEQ ID NO : 5208
 OCBBF20180840//AGAAACCTGAACGATGTC//SEQ ID NO : 5209
 15 PEBLM10000240//ATTACGATGCTTTGTTCA//SEQ ID NO : 5210
 PEBLM20013120//TAAAATTCTTGTGGTTGG//SEQ ID NO : 5211
 PEBLM20024550//TTGTGCCCTTAGAAAATC//SEQ ID NO : 5212
 PEBLM20052820//CCTGATAACCATGAATTG//SEQ ID NO : 5213
 20 PEBLM20074370//AGCATTTGGTTTTTATACTGTTA//SEQ ID NO : 5214
 PERIC20002140//CGTTACCATCACAATTTCA//SEQ ID NO : 5215
 PERIC20004780//ACTTGAGCAGAGGAGAGC//SEQ ID NO : 5216
 25 PLACE60003480//ACTGGTATTTGCTGTGAA//SEQ ID NO : 5217
 PLACE60136720//AGGAACAGAGGCTACATC//SEQ ID NO : 5218
 PLACE60155130//GTCTAGCTGGGATGATGG//SEQ ID NO : 5219
 PLACE60169420//AAGACCCCGATAGAGAGC//SEQ ID NO : 5220
 30 PLACE60181070//CCTTCTTCAGTCTTGACAC//SEQ ID NO : 5221
 PROST10004800//AGTTTTGTTCACCCCTCC//SEQ ID NO : 5222
 PROST20120160//TAGAATGGTGGGAAGTGG//SEQ ID NO : 5223
 PROST20144220//TTAGTGGTCTGTTGATAGTTTT//SEQ ID NO : 5224
 35 PROST20149160//TTGGGCTTAGGTGAGTCC//SEQ ID NO : 5225
 PROST20149250//GGTACATAAGGAATCGCT//SEQ ID NO : 5226
 PROST20151240// (Reaction system A) //ACTCTCGCTTCCTGTCAC//SEQ ID
 40 NO : 5227
 //(Reaction system B) //GACGGACCCTTGACATTA//SEQ ID NO : 5228
 PROST20153320//ACTGTGGAGAAGGAGGGA//SEQ ID NO : 5229
 PROST20161950//ATTTGACGTATCCATGCC//SEQ ID NO : 5230
 45 PROST20189770//TGGTAAAGTGGTGAAGCT//SEQ ID NO : 5231
 PUAEN20003740//CCAAAACAATAATCCAACAT//SEQ ID NO : 5232
 PUAEN20011880//AGCCGTTGTCATCATAGA//SEQ ID NO : 5233
 50 PUAEN20015260//ATTGGAAGTCCCTATGAT//SEQ ID NO : 5234
 PUAEN20025680//CTCCTCTGAAGTAGCTGC//SEQ ID NO : 5235
 PUAEN20040670//AATGGTTCTCTGGCTTGG//SEQ ID NO : 5236

55

EP 1 347 046 A1

PUAEN20045250//CAAAATGGTTAAACACAAA//SEQ ID NO : 5237
 PUAEN20078980//AGAAAGGCACACAATAAA//SEQ ID NO : 5238
 5 PUAEN20085150//AATTTAGGGGAACTGAGTAC//SEQ ID NO : 5239
 SKMUS20013230//TTCGCTCTTATCACCCAG//SEQ ID NO : 5240
 SKMUS20023210//ACTTGCCTTGGAATTGCT//SEQ ID NO : 5241
 10 SKMUS20031680//CAGAAGAACAGGAGGCAC//SEQ ID NO : 5242
 SKMUS20046670//GCAACGTCTTACTGTGAA//SEQ ID NO : 5243
 SKNSH20062340//GACATTGACGTATTCTAACTG//SEQ ID NO : 5244
 SKNSH20080430//TACCCTCCGCTGTGTTAG//SEQ ID NO : 5245
 15 SMINT20001750//CTCCTCCAGCTCTTGTCC//SEQ ID NO : 5246
 SMINT20013430//GGCACGTTTTTAATATACCAC//SEQ ID NO : 5247
 SMINT20014530//CCCTCCAGACAGTTCAAA//SEQ ID NO : 5248
 20 SMINT20033400//CGATGGGTAGGACTTAAA//SEQ ID NO : 5249
 SMINT20047810//(Reaction system A)//CTCCTGACATTTCCTTTT//SEQ ID
 NO : 5250
 //(Reaction system B)//TAGGAAAAGAGCAGGGC//SEQ ID NO : 5251
 25 SMINT20051610//AGTGAGGTTAGGGAAATATC//SEQ ID NO : 5252
 SMINT20052210//TATTCCTGTTTGATGGGG//SEQ ID NO : 5253
 SMINT20050780//TCTGTAATAGGGAGGTGTC//SEQ ID NO : 5254
 30 SMINT20080540//GAGGTACTTTTCAGACAGG//SEQ ID NO : 5255
 SMINT20105000//(Reaction system A)//AAAATGAGGTTTCAGTCCC//SEQ ID
 NO : 5256
 //(Reaction system B)//TCACCTCCCCATTAAGT//SEQ ID NO : 5257
 35 SMINT20108530//CACCTCGTTTTCTTTAG//SEQ ID NO : 5258
 SMINT20122850//AGCTAAATCCACTGAGGT//SEQ ID NO : 5259
 SMINT20122910//GGACAGACTTGCAGAGAA//SEQ ID NO : 5260
 40 SMINT20153530//GGGCCTAGAGTGGAAGTG//SEQ ID NO : 5261
 SMINT20161220//AGAACCAGTCCAAGCCAT//SEQ ID NO : 5262
 SMINT20163960//TTGATAAAATAGAGCCCA//SEQ ID NO : 5263
 SMINT20164770//AGTGTGCAGAAATCCGTG//SEQ ID NO : 5264
 45 SMINT20168570//(Reaction system A)//TGGTCCTCATGGTACAGC//SEQ ID
 NO : 5265
 //(Reaction system B)//ATGGCTGCTAGCTTGTCA//SEQ ID NO : 5266
 50 SPLEN20008320//CTGTCTGCCCTGAATCTT//SEQ ID NO : 5267
 SPLEN20011410//TTTTGGGACTGGAAGGAG//SEQ ID NO : 5268
 SPLEN20013540//TCACTCACACCAATCCTG//SEQ ID NO : 5269

EP 1 347 046 A1

5 SPLEN20019450//TTCGTAAACATCTGGGCA//SEQ ID NO : 5270
 SPLEN20022230//AAGTTGCACCCAGACATC//SEQ ID NO : 5271
 SPLEN20040600//TCTTATTTACAGTTTCCA//SEQ ID NO : 5272
 SPLEN20076530//CCCCACAGAACTTACT//SEQ ID NO : 5273
 SPLEN20101190//AGACGTAGCAGCAACTCC//SEQ ID NO : 5274
 10 SPLEN20126190//TAGACCCAACCTCACAC//SEQ ID NO : 5275
 SPLEN20152760//TGAGACGAATTGGTAAAA//SEQ ID NO : 5276
 SPLEN20157300//CTTGACATTTGCTCTCCA//SEQ ID NO : 5277
 SPLEN20158990//AAACTGGGTCAAATAAAA//SEQ ID NO : 5278
 15 SPLEN20163560//TGCCCAGATAGAAAAGTG//SEQ ID NO : 5279
 SPLEN20174260//GGCCTTGTTGAATCTGAA//SEQ ID NO : 5280
 SPLEN20211570//CTCAACACAACCTCCAAGC//SEQ ID NO : 5281
 20 SPLEN20214580//CCAAACGAATGTCAAGCT//SEQ ID NO : 5282
 SPLEN20245300//ATCTGCTCTTCATCCCTT//SEQ ID NO : 5283
 SPLEN20279950//CCTGTTCTAGACCGCAT//SEQ ID NO : 5284
 SPLEN20280660//GGCCAGACAGGAAGAGTT//SEQ ID NO : 5285
 25 SPLEN20283650//AAGTTGATGCTCCTGTTG//SEQ ID NO : 5286
 SPLEN20329240//(Reaction system A)//TAACACATGGACTGCTGG//SEQ ID
 NO : 5287
 30 //(Reaction system B)//AAGGTAGGAAATGCCAGC//SEQ ID NO : 5288
 STOMA20010250//TTTTGACCATAAGCTCCT//SEQ ID NO : 5289
 STOMA20032890//CGAGAAATAACTAATACACCTG//SEQ ID NO : 5290
 STOMA20048520//GAGGGTGAAGCAGGTAGG//SEQ ID NO : 5291
 35 STOMA20057820//GGCATTTCCTTGATATTT//SEQ ID NO : 5292
 STOMA20062290//CCGTGTATTCAGCTCCCT//SEQ ID NO : 5293
 STOMA20076800//TAAACGGGAATCAGGAAG//SEQ ID NO : 5294
 40 TESTI20001170//TTTCAGACATATCAAGTTCA//SEQ ID NO : 5295
 TESTI20002780//ATTCCAGCCATACGGTTA//SEQ ID NO : 5296
 TESTI20004890//AAAACCACAGGAAGAAAG//SEQ ID NO : 5297
 TESTI20011200//TACAAGTTCACCTGCATT//SEQ ID NO : 5298
 45 TESTI20018230//AACCACTCAGCAGAAAGA//SEQ ID NO : 5299
 TESTI20035960//TGTCATAGAGCCAGTTA//SEQ ID NO : 5300
 TESTI20038270//GTTCTGTTGGAGGTGCTG//SEQ ID NO : 5301
 50 TESTI20044230//AGGTCTTTTGTGTGCTGA//SEQ ID NO : 5302
 TESTI20046750//GTAGTTGTCCTGCATGGC//SEQ ID NO : 5303
 TESTI20060400//GGCCAGGATACTACACTT//SEQ ID NO : 5304

EP 1 347 046 A1

TESTI20066770//AACTGGCATTGGAGACCT//SEQ ID NO : 5305
 TESTI20076850//TTGGTTTGTGATGTTAAGT//SEQ ID NO : 5306
 5 TESTI20083940//TTTGTCTTCCGGTAGTTA//SEQ ID NO : 5307
 TESTI20087620//TGCCACTCTTGAAAACCTC//SEQ ID NO : 5308
 TESTI20098530//TCCATTACACAACAGCCT//SEQ ID NO : 5309
 10 TESTI20105720//GGCAGACTTGTTTGAGCT//SEQ ID NO : 5310
 TESTI20108720//TAGTTCTGTTGAGGCCCC//SEQ ID NO : 5311
 TESTI20123080//(Reaction system A)//CCTGTTTCTCTTCCTGAA//SEQ ID
 NO : 5312
 15 //(Reaction system B)//CTAAGTCCAGAAGCCTCG//SEQ ID NO : 5313
 TESTI20128350//ATACCATGCTCCAACACC//SEQ ID NO : 5314
 TESTI20136100//TTCACCTTTTGTCTCCAG//SEQ ID NO : 5315
 20 TESTI20137670//CCTCCACTCTTCCTGTTG//SEQ ID NO : 5316
 TESTI20143240//CTAAGAAGTCCTGGTTGG//SEQ ID NO : 5317
 TESTI20143620//(Reaction system A)//TTTTGTCTGAATTTGGAA//SEQ ID
 NO : 5318
 25 //(Reaction system B)//TGTAGAAAGCCTAACCCC//SEQ ID NO : 5319
 TESTI20156100//ACTGGGCACATTCATAAA//SEQ ID NO : 5320
 TESTI20161970//GTTCTATGCCTTGAGCCT//SEQ ID NO : 5321
 30 TESTI20168480//AACTCTGGGTACCAACTT//SEQ ID NO : 5322
 TESTI20168960//CTCCCTCTCCTTTCCTCA//SEQ ID NO : 5323
 TESTI20178160//CGTTTTCTCGATGTCCAG//SEQ ID NO : 5324
 TESTI20185810//AACATTCTTGCAGCTCA//SEQ ID NO : 5325
 35 TESTI20199170//AGAGTGAGCTGTGCCTTG//SEQ ID NO : 5326
 TESTI20200260//CCAAGACATACCCAGGCT//SEQ ID NO : 5327
 TESTI20200710//AATTGTGACAAGCAGCAG//SEQ ID NO : 5328
 40 TESTI20202650//TGTTTCATGTCACTGGCTG//SEQ ID NO : 5329
 TESTI20220100//(Reaction system A)//CTTCATAGGGCAGACTCC//SEQ ID
 NO : 5330
 //(Reaction system B)//GCTGTGAACCTAGAGGGGC//SEQ ID NO : 5331
 45 TESTI20224620//GGAGAAACCGATGAAGAA//SEQ ID NO : 5332
 TESTI20229600//(Reaction system A)//TTTAATAGTGCCCTGTGG//SEQ ID
 NO : 5333
 50 //(Reaction system B)//CTCTGGAATTTGCATTGA//SEQ ID NO : 5334
 TESTI20230850//CAAGACTATGGAGGGGAG//SEQ ID NO : 5335
 TESTI20231920//CTCCTCTTGCAATTCTCCC//SEQ ID NO : 5336

55

EP 1 347 046 A1

TEST120234140//CCAGTTATATCCCCAAAA//SEQ ID NO : 5337
 TEST120234270//CATAAAACCGAATAACTGAG//SEQ ID NO : 5338
 5 TEST120238000//AGTGTTTGTGGGCATAGA//SEQ ID NO : 5339
 TEST120238610//ACTTCAGACCTCCCTAGA//SEQ ID NO : 5340
 TEST120239510//TTATTGAAGGAAAGCCGC//SEQ ID NO : 5341
 10 TEST120242990//CCCTGCCTTCCCTATAGA//SEQ ID NO : 5342
 TEST120265250//GGGAAATAGAGGAGTGAT//SEQ ID NO : 5343
 TEST120265370//TGGTTTCAGATGTGCCTT//SEQ ID NO : 5344
 TEST120266740//TGGAAGAACGAAAGAGCC//SEQ ID NO : 5345
 15 TEST120272390//TCCAGGGTGTCTGATAGAAG//SEQ ID NO : 5346
 TEST120275630//GCACGTTAAGGACTGTTT//SEQ ID NO : 5347
 TEST120275620// (Reaction system A) //TGTGCCTGACTAGGTGAG//SEQ ID
 20 NO : 5348
 //(Reaction system B) //AAGGACAGGTGAGTGTGG//SEQ ID NO : 5349
 TEST120277360//TGGAGTACAACCTGCATC//SEQ ID NO : 5350
 TEST120282540//TGTCTGGTAGAGTTGCGG//SEQ ID NO : 5351
 25 TEST120284880//TGATTTAATGAGTGAACC//SEQ ID NO : 5352
 TEST120285830// (Reaction system A) //CATGTGACCTTCTCTGGC//SEQ ID
 NO : 5353
 30 //(Reaction system B) //CAGTTCTTTAGCCAGGGA//SEQ ID NO : 5354
 TEST120288110//CCTTTTGTCTGATTCGTC//SEQ ID NO : 5355
 TEST120289850//CCTTACCAAACCTCATCCA//SEQ ID NO : 5356
 TEST120307540//CGTGCATGAAAGTGAGTC//SEQ ID NO : 5357
 35 TEST120308600//CTTCTCAATCATCAGGGA//SEQ ID NO : 5358
 TEST120311290//TTCTCTGCACTCCTTGAT//SEQ ID NO : 5359
 TEST120317600//GAGTGTCTGGCATGGTTA//SEQ ID NO : 5360
 40 TEST120319190//AAGCTGGGATGATAAGGG//SEQ ID NO : 5361
 TEST120332420// (Reaction system A) //CTTCTTGGTGCTGCTTTT//SEQ ID
 NO : 5362
 //(Reaction system B) //GCAGATATGTTTGTGAGAG//SEQ ID NO : 5363
 45 TEST120335200//AATAAACTACACCAGGGC//SEQ ID NO : 5364
 TEST120342430//TCCTACGTTGAGTTGCCT//SEQ ID NO : 5365
 TEST120345050//GTCCACTAGAAGAGGGTC//SEQ ID NO : 5366
 50 TEST120347300//GAAAGCTGTCGTTAAGGT//SEQ ID NO : 5367
 TEST120357960//AATGACAGGTGAGTGGGT//SEQ ID NO : 5368
 TEST120361140//AATTCACCAGGCTGTGTG//SEQ ID NO : 5369

EP 1 347 046 A1

TESTI20369220// (Reaction system A) // TGGATTTGGAAGAGACCT// SEQ ID
 NO : 5370
 5 // (Reaction system B) // TTTGGGTGGAAGTAGAGA// SEQ ID NO : 5371
 TESTI20369690// GCTGGTTATTACGTGGT// SEQ ID NO : 5372
 TESTI20370020// (Reaction system A) // TGGTCATACTCACTGCCC// SEQ ID
 10 NO : 5373
 // (Reaction system B) // GACCTGGTCATACTCACTG// SEQ ID NO : 5374
 TESTI20371030// CTAAAGTCCAAAATGTGTAAGT// SEQ ID NO : 5375
 15 TESTI20386230// (Reaction system A) // GCTAAGGTGCTATGAAGG// SEQ ID
 NO : 5376
 // (Reaction system B) // ACAGTAAAAGGGCAAGTG// SEQ ID NO : 5377
 TESTI20391210// AATACTCACATGCCAAGC// SEQ ID NO : 5378
 20 TESTI20392090// CTTGGTTACAGAGGACAG// SEQ ID NO : 5379
 TESTI20392250// ATTCCACTCTGCTCAAAG// SEQ ID NO : 5380
 TESTI20392270// CCTTGTTGTCCATGAGTC// SEQ ID NO : 5381
 25 TESTI20401020// CGTACACCACATAGCTGA// SEQ ID NO : 5382
 TESTI20401430// TGGTAGAAAGAGAGTCACAT// SEQ ID NO : 5383
 TESTI20409440// TAGAGCACGTTTCCCTGA// SEQ ID NO : 5384
 TESTI20415640// TCTGGAAAATGAGGGTTA// SEQ ID NO : 5385
 30 TESTI20424000// CCAGCTTCTTCATCATC// SEQ ID NO : 5386
 TESTI20424730// AGGAGTGTGGCATAGTCA// SEQ ID NO : 5387
 TESTI20425070// AAAGCCATCAGACCTCAT// SEQ ID NO : 5388
 35 TESTI20433130// GTCCCATGATTTAGAACTC// SEQ ID NO : 5389
 TESTI20438570// CTGCACTAGCCTTTTCCA// SEQ ID NO : 5390
 TESTI20443090// GGAAGACAGGACCCAAGT// SEQ ID NO : 5391
 TESTI20463520// TGTTGGACTAGAGGGGAA// SEQ ID NO : 5392
 40 TESTI20465520// TCCAGGTCTCATTCTCTC// SEQ ID NO : 5393
 TESTI20478010// TCCCTATCAGACGACCAG// SEQ ID NO : 5394
 TESTI20478180// AAATCACCCTGCTTGTCAT// SEQ ID NO : 5395
 45 THYMU20029100// AGAAGCCAGGGAAGAGGT// SEQ ID NO : 5396
 THYMU20061700// CTAGCTCTGAAGTGGCAT// SEQ ID NO : 5397
 THYMU20095960// (Reaction system A) // TGAAGAGATTACCCAGGT// SEQ ID
 NO : 5398
 50 // (Reaction system B) // GGACTCTGTAGATGTAAGTGA// SEQ ID NO : 5399
 THYMU20111180// (Reaction system A) // TTCTGGGTAAGCCTGATT// SEQ ID
 NO : 5400
 55

EP 1 347 046 A1

//(Reaction system B)//CAAAGAATACCACAAATAGC//SEQ ID NO : 5401
 THYMU20118060//CCAAGGCTAAAGAGAGAG//SEQ ID NO : 5402
 5 THYMU20130890//(Reaction system A)//AATCTCAAGGACCAGTTT//SEQ ID
 NO : 5403
 //(Reaction system B)//GACACAATGGACTCAAAA//SEQ ID NO : 5404
 10 THYMU20142040//ACAGAAGGCCACAGTCAG//SEQ ID NO : 5405
 THYMU20142970//CAAGGATACTGTGATGAAA//SEQ ID NO : 5406
 THYMU20153160//GGTGGTTAGGACATTTCTC//SEQ ID NO : 5407
 THYMU20158250//AAGGAGTGGATAGATGAATAG//SEQ ID NO : 5408
 15 THYMU20187720//TGGTTACAAAGTCACAGG//SEQ ID NO : 5409
 THYMU20194360//TTCACCTTTTGTTCCTCCAG//SEQ ID NO : 5410
 THYMU20208300//ATACCACTAAGGCCCAGG//SEQ ID NO : 5411
 20 THYMU20226600//GACTCTTTCAGCTGCTGC//SEQ ID NO : 5412
 THYMU20239000//CAAATGGACAGGAACTTA//SEQ ID NO : 5413
 THYMU20253250//(Reaction system A)//AGAAAACCAGATAGGGCC//SEQ ID
 NO : 5414
 25 //(Reaction system B)//TAATGCAGGGAATGGAGT//SEQ ID NO : 5415
 THYMU20272490//CATTATACACACGACGAA//SEQ ID NO : 5416
 THYMU20284120//AAACCCACAGTGCTTCAT//SEQ ID NO : 5417
 30 THYMU20285290//AGTCCCTCTCATTTCAG//SEQ ID NO : 5418
 TKIDN10000010//TGCCATAATTCTCCTTTT//SEQ ID NO : 5419
 TRACH20005020//GCTTTTCTCCTTCATGA//SEQ ID NO : 5420
 TRACH20032720//CTACGCCCCACTATATTCA//SEQ ID NO : 5421
 35 TRACH20041830//(Reaction system A)//AGATACTGAGAATGAGCCT//SEQ ID
 NO : 5422
 //(Reaction system B)//TTCCATGCCTACCCTTT//SEQ ID NO : 5423
 40 TRACH20060150//(Reaction system A)//AGTCTCCTGCTGGCTAAG//SEQ ID
 NO : 5424
 //(Reaction system B)//GTCCCTTCTGTCTCCTGA//SEQ ID NO : 5425
 TRACH20076760//GTGGAAGTGCCTGATGAG//SEQ ID NO : 5426
 45 TRACH20082780//CTTTCACCTGGGATGGAT//SEQ ID NO : 5427
 TRACH20091230//AACATAGTCATTTCTGTTCA//SEQ ID NO : 5428
 TRACH20099340//GAGCACTGTAAGAGCCAT//SEQ ID NO : 5429
 50 TRACH20109650//AACATACCACGGAGAGA//SEQ ID NO : 5430
 TRACH20115740//TATGAGCACACGAGGTCC//SEQ ID NO : 5431
 TRACH20134950//AAGAGGGAACATCAGGCT//SEQ ID NO : 5432

55

EP 1 347 046 A1

TRACH20135520//TTCTTGGGCTTTATGTGG//SEQ ID NO : 5433
 5 TRACH20153810//(Reaction system A)//GCAGTGAGTCGTAGATGA//SEQ ID
 NO : 5434
 //(Reaction system B)//CTGCCTAGCCCTCTCACT//SEQ ID NO : 5435
 TRACH20184490//ACTGTGAAGAGCCTGTTG//SEQ ID NO : 5436
 10 TSTOM20001390//GGAATAGTAAGGACATAATGACA//SEQ ID NO : 5437
 TSTOM20005690//GGAACCTTTTGTAACCCT//SEQ ID NO : 5438
 UMVEN10001560//GCCACAACATCATTTTACTT//SEQ ID NO : 5439
 UMVEN20003540//AAGTAAAAGACATCGGCA//SEQ ID NO : 5440
 15 UTERU20004240//TACCTCCAGACTTTTGTG//SEQ ID NO : 5441
 UTERU20046980//AGGATGGGAAGAAGGTTT//SEQ ID NO : 5442
 UTERU20055930//GGATGAGTTGTGTGAAAA//SEQ ID NO : 5443
 20 UTERU20068990//CCAAGGCTAAAGAGAGAG//SEQ ID NO : 5444
 UTERU20070810//AAGTAGAGAATCCCAGCT//SEQ ID NO : 5445
 UTERU20115740//TTTATGATTGAGGGGACC//SEQ ID NO : 5446
 UTERU20119060//ACAGCATCCAATCAAAGA//SEQ ID NO : 5447
 25 UTERU20124070//ACATCTGGTGGGAAGCATC//SEQ ID NO : 5448
 UTERU20126880//ACCTTAACCCCTCTTCCC//SEQ ID NO : 5449
 UTERU20134910//AAGGAAGCCAACTCATGC//SEQ ID NO : 5450
 30 UTERU20146680//ACCTTAACCCCTCTTCCC//SEQ ID NO : 5451
 UTERU20176130//TAGAAAGGGGTGGTGAGA//SEQ ID NO : 5452
 UTERU20185230//CGTTGAGAGCTTTTACAG//SEQ ID NO : 5453
 35 UTERU20186740//CCACTTTGAGAGAACCCT//SEQ ID NO : 5454

[0314] The result of expression frequency analysis is shown in Table 52. The clones not shown in the table contain clones whose expression levels could not be measured because the levels were too low or the sizes of the PCR products were different from the expected. It was confirmed that the expression levels of IL-8 genes used as positive control genes were elevated.

[0315] The result obtained by the search for the genes whose expression levels were altered depending on the presence of TNF- α in culturing THP-1 cell, which is a human monocyte cell line, showed that the clones whose expression levels were elevated by twofold or more one or three hours after the stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were ASTRO20152140, BRACE20057620, BRACE20060720, BRACE20090440, BRACE20152870, BRACE20229280, BRAMY20002770, BRAMY20266850, BRAMY20280720, BRAWH20106180, BRAWH20122770, BRHIP20096170, BRHIP20111200, BRHIP20186120, BRHIP20194940, BRHIP20207430, BRSSN20152380, CTONG20095270, CTONG20100240, CTONG20158150, CTONG20265130, D3OST20006540, D9OST20031370, FCBBF20071860, FCBBF30251420, FCBBF30252520, 50 FCBBF40001420, FEBRA20017050, FEBRA20082100, HCHON20011160, KIDNE20141190, KIDNE20163880, KIDNE20182690, LIVER10004790, LIVER20038540, LIVER20085800, MESAN20130220, MESAN20174170, NT2NE20158600, NT2RI20005750, NT2RP70110860, NT2RP70169110, NT2RP70175670, NT2RP70188710, PERIC20002140, PLACE60155130, PROST20120160, PROST20149250, PROST20161950, PUAEN20015260, SKNSH20080430, SMINT20051610, SMINT20060780, SMINT20161220, SMINT20163960, SPLEN20101190, 55 SPLEN20157300, SPLEN20163560, SPLEN20214580, SPLEN20279950, STOMA20048520, TESTI20076850, TESTI20087620, TESTI20108720, TESTI20220100, TESTI20239510, TESTI20266740, TESTI20342430, TESTI20370020, TESTI20391210, TESTI20401020, TESTI20415640, THYMU20130890, THYMU20286290, TRACH20060150, TRACH20099340, UTERU20004240, UTERU20068990, UTERU20119060.

[0316] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more by the TNF- α stimulation (the clones whose expression levels were increased 1 or 3 hours after the stimulation were excluded) were

ASTRO20032120, ASTRO20084250, ASTRO20181690, BRACE20062640, BRACE20067430, BRACE20235400, BRALZ20018340, BRALZ20069760, BRALZ20075450, BRAMY20163270, BRAMY20204450, BRAMY20218670, BRAMY20229800, BRAWH10000930, BRAWH20107540, BRAWH20132190, BRAWH20158530, BRCAN20273340, BRHIP20105710, BRHIP20186120, BRSSN20176820, CTONG20095290, DFNES20031920, FCBBF30033050, FCBBF30071520, FCBBF30083820, HCHON20008980, HCHON20022470, HHDPC20034390, KIDNE20028720, KIDNE20079440, KIDNE20127750, KIDNE20148900, LIVER20011130, MAMGL10000830, MESAN20127350, NT2NE20181650, NT2RI20023160, NT2RP70102350, NT2RP70157890, NTONG20029480, OCBBF20020830, OCBBF20041680, OCBBF20061720, OCBBF20127040, OCBBF20139260, OCBBF20178990, PEBLM20013120, PLACE60003480, PLACE60181070, PROST20151240, PUAEN20003740, PUAEN20011880, PUAEN20078980, PUAEN20085150, SKNSH20080430, SMINT20001760, SMINT20047810, SMINT20108530, SPLEN20158990, SPLEN20283650, STOMA20010250, STOMA20057820, TESTI20060400, TESTI20161970, TESTI20275620, TESTI20369690, TESTI20386230, TESTI20392250, TESTI20409440, TESTI20424730, THYMU20095960, THYMU20111180, THYMU20226600, THYMU20253250, THYMU20272490, TRACH20153810, UTERU20176130, UTERU20186740.

[0317] These clones were thus revealed to be involved in the inflammation reaction induced by TNF- α .

[0318] The result obtained by the search for the genes whose expression levels were altered depending on co-culturing gastric cancer cell line MKN45 with cag PAI positive *Helicobacter pylori* (TN2), showed that the clones whose expression levels were elevated by twofold or more (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were ADRGL20067670, BLADE20004630, BRACE20039040, BRACE20151320, BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20060920, BRAMY20184670, BRAMY20218670, BRAMY20229800, BRCAN20147880, BRHIP20196410, BRHIP20004880, BRSSN20187310, CD34C30004940, CTONG20265130, DFNES20031920, FCBBF30278630, FCBBF40001420, HHDPC20095280, KIDNE20130450, LIVER20011130, LIVER20038540, NT2NE20172590, NT2RP70169110, OCBBF20085200, OCBBF20180840, PEBLM10000240, PLACE60003480, PROST20120160, PROST20151240, PUAEN20011880, SKMUS20031680, SKNSH20080430, SMINT20056210, SMINT20105000, SPLEN20019450, SPLEN20211570, STOMA20048520, TESTI20004890, TESTI20083940, TESTI20168480, TESTI20239510, TESTI203C8600, TESTI20478010, UTERU20126880.

[0319] Of these clones, the expression levels of ADRGL20067670, BLADE20004630, BRACE20151320, BRACE20229280, BRACE20235400, BRALZ20058880, BRAMY20218670, BRAMY20229800, BRHIP20196410, BRHIP20004880, CD34C30004940, DFNES20031920, FCBBF30278630, FCBBF40001420, HHDPC20095280, KIDNE20130450, LIVER20011130, LIVER20038540, NT2NE20172590, NT2RP70169110, PEBLM10000240, PROST20151240, PUAEN20011880, SKMUS20031680, SKNSH20080430, SMINT20056210, SMINT20105000, SPLEN20019450, SPLEN20211570, STOMA20048520, TESTI20168480, TESTI20308600, TESTI20478010, UTERU20126880 were not increased by the co-culture with the cagE mutant (TN2 Δ cagE). There may be the possibility that the expression levels of the 34 clones are altered via the NF- κ B pathway. Among them, the expression levels of BRACE20229280, FCBBF40001420, LIVER20038540, NT2RP70169110, SKNSH20080430, STOMA20048520 were also increased when human monocyte cell line THP-1 was stimulated with TNF- α .

[0320] On the other hand, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value was 1 or higher), the clones whose expression levels were decreased by twofold or more in the presence of *Helicobacter pylori* were ASTRO20032120, BRACE20090440, BRACE20114780, BRALZ20064740, BRAMY20002770, BRAMY20210400, BRAMY20215230, BRAMY20247280, BRAMY20267130, BRAWH20029630, BRAWH20100690, BRAWH20118230, BRCOC20105100, BRHIP20218580, BRSSN20046570, CTONG20138030, CTONG20146970, CTONG20158150, D3OST20037970, FCBBF30001840, FCBBF30033050, FEBRA20082100, HCHON20035130, HCHON20043590, HCHON20067220, NT2NE20174920, NT2RI20009870, NT2RI20023160, NT2RP70062230, NT2RP70130020, NTONG20070340, OCBBF20020150, OCBBF20094240, OCBBF20107920, PROST201044220, PROST20149160, PROST20153320, PUAEN20003740, PUAEN20025680, PUAEN20040670, SMINT20014580, SPLEN20101190, STOMA20076800, TESTI20087620, TESTI20098530, TESTI20123080, TESTI20161970, TESTI20234140, TESTI20288110, TESTI20357960, TESTI20391210, TESTI20424730, THYMU20158250, THYMU20226600, TRACH20005020, TRACH20134950, TRACH20184490, TSTOM20001390, UTERU20119060, UTERU20134910, UTERU20176130.

[0321] These clones are involved in gastritis or gastroduodenal ulcer.

EP 1 347 046 A1

Table 3

CloneID	CD34C	D3OST	D6OST	D9OST
ASTRO20001410	0	17.731	0	20.479
D3OST10001090	0	62.515	0	24.068
D3OST20036070	0	46.404	0	53.596
THYMU20039810	0	18.291	0	21.126
KIDNE20028720	0	0	38.385	46.259
BRAWH10000930	0	0	0	6.219
BRHIP20005340	0	0	0	4.615
CTONG20141650	0	0	0	64.925
D9OST20000310	0	0	0	63.705
D9OST20002780	0	0	0	100
D9OST20023970	0	0	0	37.837
D9OST20026730	0	0	0	19.695
D9OST20031370	0	0	0	100
D9OST20033970	0	0	0	38.536
D9OST20035800	0	0	0	93.047
D9OST20035940	0	0	0	100
D9OST20040180	0	0	0	100
FCBBF30018550	0	0	0	37.763
FCBBF30233680	0	0	0	33.084
KIDNE20102650	0	0	0	63.715
NT2RI20023160	0	0	0	10.811
PROST20107820	0	0	0	3.279
SKNSH20089400	0	0	0	25.857
SMINT20033400	0	0	0	39.619
CTONG20108210	0	0	47.973	0
D6OST20003580	0	0	95.4	0
D6OST20005070	0	0	100	0
ASTRO20155290	0	21.631	0	0
D3OST10002670	0	50.415	0	0
D3OST10002700	0	30.165	0	0
D3OST20006180	0	100	0	0
D3OST20006540	0	100	0	0
D3OST20007340	0	93.334	0	0
D3OST20013280	0	100	0	0
D3OST20024170	0	100	0	0
D3OST20024360	0	100	0	0
D3OST20037970	0	100	0	0
D3OST30002580	0	72.574	0	0
D3OST30002910	0	93.334	0	0
FCBBF10004120	0	22.594	0	0
NT2RI20001330	0	29.915	0	0
NTONG20009770	0	11.477	0	0
SPLEN20084600	0	30.589	0	0
SPLEN20140800	0	55.315	0	0
THYMU20169680	0	86.295	0	0
TRACH20141240	0	12.051	0	0
CD34C30001250	97.628	0	0	0
CD34C30003140	100	0	0	0
CD34C30004240	96.167	0	0	0

EP 1 347 046 A1

Table 3 (continued)

CloneID	CD34C	D3OST	D6OST	D9OST
CD34C30004940	100	0	0	0
DFNES10001850	55.393	0	0	0
HHDPC20034390	21.364	0	0	0
NT2RI20091730	46.845	0	0	0
SKMUS20003610	44.913	0	0	0
SPLEN20225220	59.537	0	0	0
BRCOC20101230	46.01	0	0	14.772

Table 4

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
CTONG20027090	62.349	0	0	0
CTONG20160560	57.22	0	0	0
NT2RP70032610	39.095	3.274	0	0
OCBBF20188730	39.876	0	0	0
SPLEN20162680	12.432	0	2.355	6.263
BRCOC20101230	0	2.64	3.981	3.97
BRHIP20005340	0	0.825	1.244	1.24
BRHIP20238880	0	2.66	7.355	2.667
FCBBF30016320	0	7.441	2.805	5.595
FEBRA20080810	0	6.827	5.147	2.566
FEBRA20225040	0	3.958	2.985	5.952
HCHON20008320	0	17.053	19.287	12.822
HHDPC20034390	0	0.613	1.387	0.922
HLUNG10000550	0	2.609	0.984	1.962
NT2RI20028470	0	9.076	6.843	4.549
NT2RI20054050	0	2.03	1.02	4.069
NT2RI20091730	0	2.688	2.027	4.042
NT2RP70078420	0	4.623	3.485	13.902
PUAEN20003740	0	2.314	0.582	1.16
THYMU20271250	0	0.431	0.651	1.297
BRACE20003070	0	8.516	4.281	0
BRACE20039040	0	6.248	4.711	0
BRAWH20004600	0	1.471	5.545	0
BRAWH20011710	0	8.931	2.245	0
BRCOC20121720	0	13.559	5.112	0
BRHIP20005530	0	12.387	9.34	0
D3OST10002700	0	6.227	4.695	0
HCHON20007380	0	7.176	5.411	0
HEART20072310	0	11.675	17.605	0
KIDNE20121880	0	21.519	16.225	0
MESAN20121130	0	14.219	10.721	0
NT2RI20022600	0	57.012	42.988	0
NT2RI20023160	0	1.932	1.457	0
NT2RI20086220	0	7.606	5.735	0
NT2RI20216250	0	45.928	34.63	0
NT2RP60000850	0	11.147	16.809	0
NT2RP70036880	0	1.78	5.367	0
NT2RP70043480	0	10.893	4.107	0

EP 1 347 046 A1

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RP70062230	0	10.183	7.678	0
NT2RP70081610	0	15.131	22.818	0
NT2RP70102350	0	84.14	15.86	0
NT2RP70130020	0	57.012	42.988	0
NT2RP70190640	0	30.952	23.338	0
OCBBF10001850	0	20.293	7.65	0
OCBBF20097720	0	5.676	4.28	0
OCBBF20173980	0	3.1	2.338	0
PEBLM20044520	0	3.253	2.453	0
SPLEN20173510	0	7.249	10.932	0
TRACH20007020	0	9.462	7.134	0
UTERU20065930	0	10.676	8.05	0
HCHON20022470	0	6.766	0	10.174
NT2NE20010490	0	21.179	0	31.847
NT2NE20174800	0	39.941	0	60.059
NT2NE20177520	0	28.292	0	42.542
PROST20087700	0	1.88	0	14.135
PROST20107820	0	0.586	0	2.644
SMINT20028820	0	6.998	0	10.523
TESTI2O063830	0	9.768	0	14.689
ASTRO20125520	0	0	2.686	5.357
BRHIP30001110	0	0	1.86	3.71
HCHON20002260	0	0	0.733	1.461
HCHON20008150	0	0	5.075	20.242
KIDNE20002520	0	0	1.553	6.195
NT2NE20130190	0	0	33.397	66.603
NT2NE20158600	0	0	33.397	66.603
NT2RI20001330	0	0	4.656	9.286
NT2RI20025400	0	0	3.141	6.265
NT2RI20036670	0	0	33.397	66.603
NT2RI20048840	0	0	1.404	5.6
SKMUS20020840	0	0	11.346	22.628
BRACE20057190	0	0	0	10.763
BRACE20060550	0	0	0	14.499
BRACE20267250	0	0	0	66.449
BRAWH20107540	0	0	0	40.54
BRAWH20118230	0	0	0	78.374
CTONG20075860	0	0	0	21.782
CTONG20095290	0	0	0	22.915
FEBRA20086620	0	0	0	11.505
FEBRA20144170	0	0	0	1.957
FEBRA20196370	0	0	0	59.247
HLUNG20023340	0	0	0	33.313
NT2NE20003740	0	0	0	100
NT2NE20010050	0	0	0	84.719
NT2NE20010210	0	0	0	100
NT2NE20010400	0	0	0	56.184
NT2NE20015240	0	0	0	100
NT2NE20021620	0	0	0	44.305
NT2NE20043780	0	0	0	100

EP 1 347 046 A1

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2NE20053580	0	0	0	75.239
NT2NE20068130	0	0	0	100
NT2NE20072200	0	0	0	100
NT2NE20074250	0	0	0	100
NT2NE20080170	0	0	0	100
NT2NE20089610	0	0	0	100
NT2NE20089970	0	0	0	100
NT2NE20108540	0	0	0	84.719
NT2NE20110360	0	0	0	100
NT2NE20118960	0	0	0	100
NT2NE20122430	0	0	0	76.57
NT2NE20124480	0	0	0	100
NT2NE20125050	0	0	0	66.449
NT2NE20131890	0	0	0	100
NT2NE20132170	0	0	0	100
NT2NE20142210	0	0	0	100
NT2NE20146810	0	0	0	100
NT2NE20152750	0	0	0	100
NT2NE20155110	0	0	0	100
NT2NE20156260	0	0	0	100
NT2NE20157470	0	0	0	100
NT2NE20159740	0	0	0	27.684
NT2NE20172590	0	0	0	100
NT2NE20174920	0	0	0	61.159
NT2NE20181650	0	0	0	100
NT2NE20183760	0	0	0	100
NT2NE20184900	0	0	0	84.719
NT2NE20187390	0	0	0	100
OCBBF20108430	0	0	0	53.98
RECTM20005100	0	0	0	10.923
SMINT20001760	0	0	0	50.667
SPLEN20169720	0	0	0	7.349
TESTI20265250	0	0	0	15.768
ASTRO10001650	0	0	8.055	0
ASTRO20033160	0	0	10.721	0
BRACE20011070	0	0	26.748	0
BRACE20039440	0	0	0.941	0
BRACE20151320	0	0	29.94	0
BRAMY20104640	0	0	40.041	0
BRAMY20137560	0	0	68.63	0
BRAMY20167060	0	0	9.007	0
BRAWH20028110	0	0	15.672	0
BRCAN20280360	0	0	4.387	0
BRCOC20004870	0	0	0.526	0
BRHIP20207990	0	0	9.197	0
BRHIP20217620	0	0	5.063	0
BRHIP20249110	0	0	67.372	0
BRSTN10000830	0	0	3.481	0
CTONG10000940	0	0	1.415	0
CTONG20004690	0	0	5.307	0

EP 1 347 046 A1

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
CTONG20050280	0	0	12.439	0
CTONG20105660	0	0	24.642	0
CTONG20125640	0	0	7.18	0
CTONG20133520	0	0	49.384	0
CTONG20186320	0	0	29.069	0
FCBBF10000770	0	0	1.472	0
FCBBF10002800	0	0	10.265	0
FCBBF10003770	0	0	19.652	0
FCBBF30018550	0	0	5.089	0
FCBBF30123470	0	0	3.989	0
FCBBF30246230	0	0	5.091	0
FEBRA20018280	0	0	9.887	0
FEBRA20095140	0	0	6.019	0
FEBRA20192420	0	0	58.974	0
HCHON20064590	0	0	19.614	0
HHDPC10000830	0	0	1.779	0
HLUNG20016770	0	0	6.385	0
HLUNG20033780	0	0	16.824	0
IMR3220002430	0	0	3.118	0
KIDNE20104300	0	0	17.33	0
MESAN20004570	0	0	7.197	0
MESAN20089360	0	0	14.459	0
NOVAR10000910	0	0	3.519	0
NT2RI20003480	0	0	32.207	0
NT2RI20005750	0	0	100	0
NT2RI20009870	0	0	100	0
NT2RI20023590	0	0	29.911	0
NT2RI20023910	0	0	11.79	0
NT2RI20025640	0	0	100	0
NT2RI20040930	0	0	100	0
NT2RI20041880	0	0	10.436	0
NT2RI20046080	0	0	6.723	0
NT2RI20050960	0	0	73.545	0
NT2RI20055790	0	0	17.054	0
NT2RI20056700	0	0	100	0
NT2RI20069730	0	0	100	0
NT2RI20076290	0	0	14.653	0
NT2RI20091940	0	0	5.358	0
NT2RI20198260	0	0	100	0
NT2RI20203900	0	0	100	0
NT2RI20207030	0	0	100	0
NT2RI20240080	0	0	61.866	0
NT2RI20244600	0	0	100	0
NT2RI20244960	0	0	100	0
NT2RI20250750	0	0	30.809	0
NT2RI20252550	0	0	62.102	0
NT2RI20273230	0	0	60.375	0
NTONG20067090	0	0	16.469	0
OCBBF10001750	0	0	13.09	0
OCBBF20047570	0	0	4.504	0

EP 1 347 046 A1

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
OCBBF20054760	0	0	8.495	0
OCBBF20059560	0	0	10.318	0
OCBBF20073540	0	0	3.651	0
OCBBF20125530	0	0	2.131	0
OCBBF20126780	0	0	12.535	0
OCBBF20127040	0	0	37.942	0
OCBBF20140890	0	0	35.863	0
SKMUS20003610	0	0	1.943	0
SKNSH20008190	0	0	4.523	0
SKNSH20080430	0	0	18.4	0
SMINT20144800	0	0	2.887	0
SPLEN20027440	0	0	4.053	0
SPLEN20095550	0	0	15.436	0
SPLEN20140800	0	0	8.61	0
TESTI20094020	0	0	16.66	0
TESTI20369690	0	0	6.529	0
TESTI20391770	0	0	7.531	0
TESTI20442760	0	0	17.235	0
TRACH20084720	0	0	5.703	0
TRACH20107710	0	0	61.866	0
TRACH20118940	0	0	16.16	0
UTERU20022940	0	0	9.896	0
ASTRO20108190	0	1.622	0	0
BGGI120006160	0	2.155	0	0
BRAMY20136210	0	70.518	0	0
BRAWH20016620	0	22.162	0	0
BRAWH20164460	0	20.968	0	0
BRCOC20144000	0	40.488	0	0
BRHIP20132860	0	82.532	0	0
BRSSN20146100	0	17.209	0	0
CTONG10000100	0	15.625	0	0
CTONG20103480	0	4.268	0	0
CTONG20108210	0	1.722	0	0
CTONG20139070	0	10.392	0	0
FCBBF10000240	0	10.583	0	0
FCBBF10000630	0	14.415	0	0
FCBBF20067810	0	30.502	0	0
FCBBF30010810	0	6.328	0	0
FCBBF30012810	0	49.073	0	0
FCBBF30013770	0	24.817	0	0
FCBBF30039020	0	56.608	0	0
FCBBF40001420	0	8.811	0	0
FEBRA10001880	0	5.044	0	0
FEBRA20082010	0	17.339	0	0
HHDPC20001040	0	4.459	0	0
KIDNE20021910	0	34.358	0	0
NT2RP6000077	0	15.492	0	0
NT2RP70010740	0	100	0	0
NT2RP70027380	0	27.748	0	0
NT2RP70037240	0	22.256	0	0

EP 1 347 046 A1

Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RP70044280	0	16.256	0	0
NT2RP70045590	0	20.543	0	0
NT2RP70056750	0	7.009	0	0
NT2RP70063950	0	82.532	0	0
NT2RP70072690	0	56.608	0	0
NT2RP70077660	0	74.295	0	0
NT2RP70085440	0	100	0	0
NT2RP70105210	0	100	0	0
NT2RP70110860	0	100	0	0
NT2RP70111320	0	100	0	0
NT2RP70122910	0	100	0	0
NT2RP70125160	0	100	0	0
NT2RP70133740	0	100	0	0
NT2RP70134990	0	100	0	0
NT2RP70137290	0	100	0	0
NT2RP70137640	0	54.725	0	0
NT2RP70143480	0	100	0	0
NT2RP70147210	0	100	0	0
NT2RP70150800	0	100	0	0
NT2RP70157890	0	100	0	0
NT2RP70159960	0	100	0	0
NT2RP70169110	0	100	0	0
NT2RP70175670	0	100	0	0
NT2RP70179710	0	100	0	0
NT2RP70181970	0	100	0	0
NT2RP70188020	0	100	0	0
NT2RP70188710	0	100	0	0
NT2RP70192730	0	100	0	0
NT2RP70194450	0	100	0	0
NT2RP70195430	0	50.987	0	0
NT2RP70198350	0	2.512	0	0
NT2RP70203790	0	100	0	0
OCBBF20039250	0	4.016	0	0
OCBBF20080410	0	5.038	0	0
OCBBF20108190	0	30.231	0	0
OCBBF20108580	0	16.054	0	0
OCBBF20122620	0	34.956	0	0
OCBBF20130110	0	18.197	0	0
OCBBF20151150	0	43.004	0	0
OCBBF20189560	0	4.079	0	0
PROST10003220	0	57.613	0	0
TESTI20001720	0	20.618	0	0
TESTI20121550	0	15.444	0	0
TESTI20152460	0	28.533	0	0
TESTI20211240	0	13.774	0	0
TESTI20234140	0	39.241	0	0
UMVEN20003540	0	1.985	0	0
UTERU20006960	0	6.858	0	0
UTERU20094350	0	12.888	0	0
UTERU20164260	0	30.63	0	0

EP 1 347 046 A1

Table 5

CloneID	BEAST	TBAES
BRACE20039040	0	18.237
BRAMY20163250	0	26.506
BRCOG20031250	0	39.975
BRHIP20005340	0	2.408
BRHIP20217620	0	19.598
BRHIP30001110	0	7.202
FCBBF10000770	0	5.697
FCBBF30010810	0	18.471
FEBRA20080810	0	9.963
FEBRA20144170	0	3.798
FEBRA20196630	0	61.269
FEBRA20197110	0	14.875
HCHON20002260	0	11.347
HCHON20040020	0	5.523
HHDPC20034390	0	1.789
HLUNG10000550	0	3.808
NOVAR10000910	0	27.245
NT2RI20023160	0	11.28
NT2RI20054050	0	1.975
NT2RI20091730	0	7.846
OCBBF20188730	0	9.748
SMINT20144800	0	22.352
SPLEN20128000	0	2.403
SPLEN20171210	0	54.539
SPLEN20264110	0	80.173
TBAES20000590	0	84.801
TBAES20002550	0	100
TBAES20003150	0	100
TESTI20334410	0	15.439
TESTI20432750	0	62.244
TRACH20003590	0	20.978
TRACH20084720	0	11.037
UTERU20046640	0	11.937
BEAST20004540	100	0
SPLEN20008740	10.632	0

Table 6

CloneID	CERVX	TCERX
BGGI120006160	0	18.869
BRAMY20063970	0	59.264
BRHIP20218580	0	70.621
FEBRA20002100	0	14.918
SPLEN20162680	0	9.118
TESTI20214250	0	36.333
CTONG20105080	84.727	0
HCHON20015980	50.212	0
PROST20175290	52.453	0

EP 1 347 046 A1

Table 6 (continued)

CloneID	CERVX	TCERVX
TESTI20254220	51.293	0
THYMU20279750	82.6	0

Table 7

CloneID	COLON	TCOLN
ASTRO20001410	0	32.199
BRAWH20162690	0	27.951
CTONG20132220	0	79.674
HCHON20002260	0	17.098
NT2RI20001330	0	54.324
TCOLN20001390	0	100
3NB6910001910	42.978	0
BRAMY20120910	41.689	0
BRAWH20004600	4.285	0
BRCOC20031250	39.895	0
BRCOC20031870	11.042	0
COLON10001350	100	0
COLON20043180	100	0
COLON20093370	100	0
FEBRA20002100	4.963	0
FEBRA20082010	16.836	0
FEBRA20197110	29.691	0
KIDNE20007770	53.588	0
KIDNE20013730	50.02	0
NT2RP70045590	59.84	0
OCBBF20078920	29.908	0
PROST20083600	12.636	0
SPLEN20011410	6.63	0
TRACH20084720	11.015	0
THYMU20271250	1.257	15.18

Table 8

CloneID	NESOP	TESOP
ASTRO20033160	0	20.183
ASTRO20125520	0	10.113
BRAMY20266850	0	16.957
BRAWH20164460	0	59.524
BRHIP20005340	0	9.367
BRHIP20191490	0	75.561
CTONG20095290	0	43.261
CTONG20143690	0	28.473
CTONG20161850	0	17.787
DFNES20001530	0	21.906
DFNES20071130	0	45.721
FCBBF30123470	0	15.017
FCBBF30175310	0	10.97
FEBRA20095140	0	45.326

EP 1 347 046 A1

Table 8 (continued)

CloneID	NESOP	TESOP
HCHON20016650	0	10.558
MESAN20025190	0	31.731
NT2RI20028470	0	8.588
NT2RI20054050	0	1.921
NT2RP70036880	0	5.052
NTONG20009770	0	6.726
NTONG20064840	0	29.574
NTONG20076930	0	48.142
SMINT20042990	0	61.748
SPLEN20008820	0	12.019
SPLEN20128000	0	2.337
SPLEN20149110	0	7.218
STOMA20013890	0	39.515
TESOP20000900	0	100
TESOP20003120	0	66.097
TESOP20004000	0	100
TESOP20005270	0	70.604
TESOP20005690	0	100
TESTI20334410	0	7.508
THYMU20271250	0	2.449
TRACH20141240	0	7.062
UTERU20022940	0	12.42
NESOP10001080	100	0
NT2RI20023160	17.058	0
NTONG20013620	74.273	0
TRACH20077540	31.967	0
NTONG20015870	69.673	12.221

Table 9

CloneID	KIDNE	TKIDN
ASTRO20008010	0	3.776
ASTRO20181690	0	3.496
BRACE20111830	0	23.795
BRACE20152870	0	8.501
BRACE20237270	0	73.082
BRAMY20147540	0	5.185
BRAMY20286820	0	78.604
BRAWH20015350	0	12.794
BRAWH20096780	0	78.731
BRAWH20132190	0	35.86
BRAWH20182060	0	40.908
BRCAN20060190	0	13.906
BRCOC20004870	0	1.072
BRCOC20176520	0	51.098
BRHIP20000870	0	24.363
BRHIP20198190	0	32.096
BRHIP20233090	0	43.183
BRHIP30001110	0	3.79

EP 1 347 046 A1

Table 9 (continued)

CloneID	KIDNE	TKIDN
BRSSN20015790	0	49.863
BRSTN20000580	0	8.929
CTONG10000940	0	1.442
CTONG20098440	0	66.526
CTONG20150910	0	6.012
CTONG20165050	0	66.526
DFNES20014040	0	38.579
DFNES20037420	0	38.579
FCBBF10000770	0	2.998
FCBBF30083820	0	39.87
FCBBF30247930	0	59.143
FEBRA20037500	0	6.758
FEBRA20072120	0	14.531
FEBRA20080810	0	2.621
FEBRA20086620	0	17.626
FEBRA20140100	0	59.757
FEBRA20144170	0	1.999
FEBRA20176800	0	35.198
HCHON20008320	0	13.096
HCHON20059870	0	36.909
HLUNG10000550	0	2.004
MESAN20106640	0	32.125
NT2RI20025400	0	6.399
NT2RI20076290	0	7.462
NT2RI20091940	0	3.638
OCBBF20019830	0	26.741
OCBBF20022900	0	37.332
OCBBF20039250	0	3.084
OCBBF20080050	0	11.755
OCBBF20097720	0	8.718
OCBBF20125530	0	4.341
OCBBF20130110	0	27.949
OCBBF20140640	0	5.056
OCBBF20173980	0	9.523
PANCR10000910	0	1.114
PROST20087700	0	2.887
PUAEN20044000	0	26.668
SPLEN20144520	0	68.029
SPLEN20160980	0	68.029
TKIDN10000010	0	41.198
TKIDN20004640	0	68.029
TKIDN20005210	0	55.069
TKIDN20030590	0	78.393
TKIDN20030620	0	100
TKIDN20047480	0	35.796
TRACH20003590	0	11.039
TRACH20028030	0	7.714
TRACH20183170	0	10.844
TRACH20184490	0	56.123
UMVEN20003540	0	3.049

EP 1 347 046 A1

Table 9 (continued)

CloneID	KIDNE	TKIDN
UTERU20004240	0	3.144
UTERU20055930	0	12.464
ASTRO10001650	7.727	0
ASTRO20108190	2.346	0
BGGI120006160	3.117	0
BRACE20039040	9.038	0
BRAMY20102080	63.37	0
BRAWH20004600	2.128	0
BRAWH20125380	35.37	0
BRAWH20162690	4.596	0
BRHIP20115760	66.835	0
BRHIP20205090	65.282	0
CTONG20052650	65.178	0
CTONG20108210	2.491	0
CTONG20128470	6.004	0
CTONG20133480	19.179	0
CTONG20139070	7.516	0
D9OST20000310	16.47	0
DFNES20001530	11.162	0
FCBBF10001820	59.128	0
FEBRA20002100	4.929	0
HCHON20008980	35.524	0
HCHON20016650	5.38	0
HLUNG20033780	32.277	0
KIDNE20002520	2.979	0
KIDNE20003940	100	0
KIDNE20006780	100	0
KIDNE20007210	73.728	0
KIDNE20007770	19.958	0
KIDNE20008010	100	0
KIDNE20009470	8.811	0
KIDNE20011170	77.71	0
KIDNE20011400	100	0
KIDNE20013730	24.839	0
KIDNE20017130	54.019	0
KIDNE20018730	100	0
KIDNE20018970	100	0
KIDNE20020150	100	0
KIDNE20021680	100	0
KIDNE20021910	24.85	0
KIDNE20021980	100	0
KIDNE20022620	100	0
KIDNE20024830	100	0
KIDNE20027250	35.87	0
KIDNE20027950	100	0
KIDNE20028390	25.593	0
KIDNE20028720	1.993	0
KIDNE20028830	7.907	0
KIDNE20029800	10.988	0
KIDNE20067330	100	0

EP 1 347 046 A1

Table 9 (continued)

CloneID	KIDNE	TKIDN
KIDNE20079440	35.045	0
KIDNE20096280	100	0
KIDNE20096470	100	0
KIDNE20100070	100	0
KIDNE20100840	100	0
KIDNE20101370	100	0
KIDNE20101510	100	0
KIDNE20102650	8.237	0
KIDNE20102710	100	0
KIDNE20104300	33.246	0
KIDNE20106740	100	0
KIDNE20107390	100	0
KIDNE20107500	74.264	0
KIDNE20107620	100	0
KIDNE20109730	100	0
KIDNE20109890	100	0
KIDNE20112000	100	0
KIDNE20115080	65.178	0
KIDNE20118580	100	0
KIDNE20120090	33.186	0
KIDNE20121880	62.256	0
KIDNE20122910	83.085	0
KIDNE20124400	6.171	0
KIDNE20125630	100	0
KIDNE20126010	100	0
KIDNE20126130	100	0
KIDNE20127100	33.012	0
KIDNE20127450	100	0
KIDNE20127750	100	0
KIDNE20130450	100	0
KIDNE20131580	63.24	0
KIDNE20132180	100	0
KIDNE20137340	100	0
KIDNE20138010	100	0
KIDNE20141190	49.697	0
KIDNE20144890	100	0
KIDNE20148900	100	0
KIDNE20163880	100	0
KIDNE20180710	49.105	0
KIDNE20181660	100	0
KIDNE20182690	100	0
KIDNE20186780	100	0
KIDNE20190740	100	0
LIVER20035110	28.683	0
MESAN20025190	16.169	0
NT2RP70043480	7.879	0
PROST20107820	1.696	0
PROST20123530	32.771	0
PROST20161950	20.387	0
PUAEN20030180	46.744	0

EP 1 347 046 A1

Table 9 (continued)

CloneID	KIDNE	TKIDN
SKMUS20003610	3.728	0
SMINT20033400	10.243	0
TBAES20000590	5.253	0
TESTI20044310	29.162	0
TESTI20082330	45.847	0
TRACH20032720	12.917	0
UTERU20099720	12.351	0

Table 10

CloneID	LIVER	TLIVE
BRAWH20166790	83.525	0
CTONG20103480	15.35	0
HEART20005410	11.598	0
LIVER10001260	66.455	0
LIVER10004790	100	0
LIVER20002160	100	0
LIVER20011130	92.988	0
LIVER20011910	100	0
LIVER20028420	16.548	0
LIVER20035110	71.317	0
LIVER20035680	100	0
LIVER20038540	100	0
LIVER20045650	100	0
LIVER20055200	100	0
LIVER20055440	100	0
LIVER20059810	24.82	0
LIVER20062510	100	0
LIVER20064100	88.658	0
LIVER20064690	100	0
LIVER20075680	100	0
LIVER20080530	100	0
LIVER20084730	100	0
LIVER20085800	100	0
LIVER20087510	75.266	0
LIVER20091180	100	0
NTONG20063010	47.641	0
PROST20087700	6.762	0
PROST20107820	2.108	0
TRACH20005400	12.349	0
ASTRO20001410	0	10.441
ASTRO20125520	0	10.162
BRACE20152870	0	15.788
BRAMY20167060	0	34.076
BRAMY20181220	0	87.217
BRAMY20285160	0	81.346
BRCOC20001860	0	20.45
FEBRA20144170	0	3.712
HLUNG10000550	0	3.721

EP 1 347 046 A1

Table 10 (continued)

CloneID	LIVER	TLIVE
OCBBF20073540	0	6.907
OCBBF20088220	0	16.388
PLACE60169420	0	26.895
SMINT20152940	0	54.735
SPLEN20242320	0	45.601
THYMU20000570	0	18.649
TRACH20077540	0	30.987
UTERU20055930	0	15.433
UTERU20065930	0	10.151

Table 11

CloneID	HLUNG	TLUNG
BRACE20096200	70.38	0
BRAWH20004600	2.238	0
BRAWH20030250	11.121	0
BRCAN20006390	61.519	0
BRCAN20280360	8.855	0
BRHIP20238880	1.35	0
CTONG10000940	1.428	0
CTONG20103480	6.495	0
CTONG20129960	10.709	0
CTONG20155180	48.707	0
FCBBF10001210	36.439	0
FEBRA20144170	1.98	0
FEBRA20197110	7.756	0
HCHON20002260	2.958	0
HDPC20034390	0.933	0
HLUNG10000550	3.971	0
HLUNG20016330	29.367	0
HLUNG20016770	12.888	0
HLUNG20017120	12.093	0
HLUNG20023340	33.714	0
HLUNG20033780	33.957	0
HLUNG20084390	100	0
IMR3220002430	3.147	0
LIVER20028420	14.004	0
NOVAR20000380	2.278	0
NT2RI20023910	8.923	0
NT2RI20054050	2.059	0
NT2RI20091730	4.091	0
NT2RP70044280	12.369	0
OCBBF20020830	40.304	0
OCBBF20125530	4.302	0
PLACE60004630	28.618	0
PROST20057930	14.383	0
PROST2010782	0.892	0
PROST20185830	33.898	0
PUAEN20030180	12.294	0

EP 1 347 046 A1

Table 11 (continued)

CloneID	HLUNG	TLUNG
SMINT20121220	12.822	0
SPLEN20002220	44.799	0
SPLEN20008740	1.788	0
SPLEN20054290	26.875	0
SPLEN20128000	1.253	0
SPLEN20157300	51.319	0
SPLEN20176200	18.8	0
SPLEN20179180	3.344	0
SPLEN20211940	12.373	0
STOMA20013890	21.183	0
TBAES20000590	5.527	0
TESTI20094230	59.311	0
TESTI20184620	10.365	0
TESTI20334410	8.049	0
THYMU20000570	4.974	0
THYMU20039810	1.915	0
TRACH20007020	14.4	0
TRACH20141240	3.786	0
TRACH20183170	10.745	0
ASTRO20108190	0	13.924
ASTRO20155290	0	38.341
BRHIP20096850	0	73.716
FEBRA20080810	0	14.654
MESAN20014500	0	59.68
SMINT20028820	0	60.089
SPLEN20162680	0	8.941

Table 12

CloneID	NOVAR	TOVAR
BGGI120006160	21.31	0
BRHIP20005340	8.158	0
BRHIP20191860	47.038	0
HHDPC20001040	44.094	0
NOVAR10000150	72.374	0
NOVAR10000910	46.155	0
NOVAR10001020	99.094	0
NOVAR20000380	14.805	0
NOVAR20003520	100	0
THYMU20271250	4.266	0
ASTRO20141350	0	75.66
BRAMY20157820	0	85.296
BRCOC20001860	0	64.79
HLUNG20016770	0	76.536
NT2Ri20054050	0	12.229
NTONG20090600	0	60.694
PROST20087700	0	16.991
PUAEN20015860	0	62.197
SPLEN20029310	0	88.828

EP 1 347 046 A1

Table 12 (continued)

CloneID	NOVAR	TOVAR
TOVAR20004760	0	49.428
TOVAR20005750	0	96.313
TRACH20079690	0	55.276
UTERU20004240	0	18.499

Table 13

CloneID	STOMA	TSTOM
BRACE20060840	0	65.917
FEBRA20052910	0	77.883
HCHON20002260	0	8.66
HLUNG10000550	0	11.625
NTONG20009770	0	21.112
PROST20107820	0	5.223
THYMU20039810	0	11.216
TSTOM10001860	0	100
TSTOM20001390	0	89.823
TSTOM20003150	0	48.943
TSTOM20005690	0	100
ASTRO20125520	10.059	0
BRACE20039040	17.642	0
BRAMY20124260	42.064	0
BRCOC20031870	10.704	0
BRHIP20191860	13.43	0
CTONG20128470	11.719	0
FEBRA20037500	12.423	0
HCHON20040020	5.343	0
HHDFC10000830	6.661	0
IMR3220002430	5.838	0
KIDNE20007770	12.986	0
NOVAR20000380	4.227	0
NT2RI20054050	1.91	0
NT2RI20091730	7.59	0
PROST20130530	20.156	0
SPLEN20149110	7.179	0
SPLEN20157880	32.942	0
STOMA20001830	100	0
STOMA20005390	100	0
STOMA20005670	100	0
STOMA20006400	100	0
STOMA20006780	100	0
STOMA20006860	100	0
STOMA20008880	100	0
STOMA20010250	100	0
STOMA20013890	39.303	0
STOMA20026880	100	0
STOMA20032890	100	0
STOMA20034770	100	0
STOMA20036460	100	0

EP 1 347 046 A1

Table 13 (continued)

CloneID	STOMA	TSTOM
STOMA20046680	100	0
STOMA20048520	100	0
STOMA20048840	100	0
STOMA20051200	85.988	0
STOMA20056640	100	0
STOMA20056670	100	0
STOMA20057820	91.236	0
STOMA20062130	100	0
STOMA20062290	40.913	0
STOMA20063250	100	0
STOMA20063980	100	0
STOMA20064470	100	0
STOMA20067800	59.113	0
STOMA20069040	100	0
STOMA20072690	100	0
STOMA20076800	100	0
STOMA20077450	100	0
STOMA20080500	100	0
STOMA20083610	100	0
STOMA20086	100	0
STOMA20088380	100	0
STOMA20092530	100	0
STOMA20092560	100	0
STOMA20092890	39.042	0
TEST120184620	19.231	0
TRACH20003590	40.588	0
TRACH20183170	19.936	0
PROST20083600	12.248	38.653
TRACH20068660	6.753	21.311

Table 14

CloneID	UTERU	TUTER
DFNES10001850	0	29.393
NT2RI20023910	0	18.073
SMINT20144800	0	35.406
SPLEN20162680	0	9.628
TOVAR20004760	0	50.572
TUTER20002830	0	100
ASTRO20008010	1.217	0
ASTRO20033160	10.555	0
ASTRO20058630	4.534	0
ASTRO20105820	20.644	0
ASTRO20108190	3.21	0
BRACE20039040	3.092	0
BRACE20057190	3.542	0
BRACE20060840	3.661	0
BRACE20111830	7.667	0
BRACE20223330	10.589	0

EP 1 347 046 A1

Table 14 (continued)

CloneID	UTERU	TUTER
BRAMY20266850	2.956	0
BRAWH20113430	8.367	0
BRAWH20126980	22.868	0
BRCOC20031870	0.938	0
BRCOC20107300	12.892	0
BRCOC20121720	6.71	0
BRCOC20155970	25.187	0
BRHIP20105710	18.366	0
BRHIP20191490	13.172	0
BRHIP20207990	12.072	0
BRHIP20217620	6.646	0
BRHIP20222280	10.898	0
BRHIP20238880	0.439	0
BRHIP20249110	11.054	0
BRSSN20018690	3.6	0
BRTHA20000570	51.819	0
CTONG10000940	0.464	0
CTONG10002770	24.668	0
CTONG20095290	7.541	0
CTONG20099380	23.863	0
CTONG20103480	6.336	0
CTONG20108210	2.557	0
CTONG20118250	10.239	0
CTONG20129960	3.482	0
CTONG20131560	24.668	0
CTONG20139070	2.571	0
CTONG20139340	8.273	0
CTONG20143690	4.963	0
CTONG20160560	2.372	0
D3OST30002580	22.242	0
FCBBF10000240	5.237	0
FCBBF10001820	10.114	0
FCBBF10003670	1.812	0
FCBBF10004120	2.308	0
FCBBF10005740	4.952	0
FCBBF30175310	1.912	0
FCBBF30240020	6.769	0
FCBBF30246230	6.682	0
FCBBF40001420	4.36	0
FEBRA20002100	0.843	0
FEBRA20004620	6.733	0
FEBRA20018280	6.489	0
FEBRA20025270	3.416	0
FEBRA20034360	6.63	0
FEBRA20037500	19.596	0
FEBRA20080810	0.845	0
FEBRA20082100	15.999	0
FEBRA20144170	1.288	0
FEBRA20225040	1.959	0
HCHON20002260	0.962	0

EP 1 347 046 A1

Table 14 (continued)

CloneID	UTERU	TUTER
HCHON20007380	3.551	0
HCHON20015980	5.796	0
HCHON20016650	1.84	0
HCHON20022470	3.348	0
HCHON20040020	0.936	0
HCHON20076500	7.263	0
HEART20072310	11.555	0
HHDFC20034390	1.517	0
HLUNG10000550	1.937	0
HLUNG20016770	4.191	0
KIDNE20131580	21.635	0
LIVER20028420	9.107	0
MAMGL10000830	0.346	0
MESAN20171520	24.337	0
NOVAR10000150	3.622	0
NOVAR10000910	2.31	0
NT2NE20053580	24.761	0
NT2NE20159740	9.111	0
NT2NE20174920	20.127	0
NT2RI20023160	0.956	0
NT2RI20041880	3.425	0
NT2RI20054050	1.004	0
NT2RI20076290	2.404	0
NT2RI20273230	39.625	0
NT2RP60000770	30.666	0
NT2RP60000850	11.032	0
NT2RP70036880	0.881	0
NT2RP70043480	2.695	0
NT2RP70045590	10.166	0
NT2RP70056750	10.406	0
NT2RP70062230	5.039	0
NT2RP70081610	7.488	0
OCBBF10001750	8.591	0
OCBBF20006770	19.428	0
OCBBF20032460	11.672	0
OCBBF20039250	0.994	0
OCBBP20047570	2.956	0
OCBBF20054760	16.727	0
OCBBF20059560	3.386	0
OCBBF20068490	2.41	0
OCBBF20080050	3.787	0
OCBBF20094240	8.655	0
OCBBF20097720	1.404	0
OCBBF20103130	16.359	0
OCBBF20105570	43.708	0
OCBBF20140640	3.258	0
OCBBF20173980	3.068	0
OCBBF20180120	10.043	0
OCBBF20188730	6.611	0
OCBBF20189560	2.019	0

EP 1 347 046 A1

Table 14 (continued)

CloneID	UTERU	TUTER
PEBLM20044520	6.439	0
PLACE60060420	6.493	0
PROST20087700	0.93	0
PROST20107820	0.29	0
PROST20149160	4.345	0
PROST20159240	8.082	0
PROST20176170	25.167	0
PROST20189770	15.499	0
PUAEN20003740	1.145	0
PUAEN20015860	3.406	0
SKMUS20003610	1.275	0
SKNSH20008190	5.937	0
SKNSH20080430	12.076	0
SMINT20026890	51.875	0
SMINT20029760	6.221	0
SMINT20068010	19.209	0
SMINT20110330	25.261	0
SMINT20121220	4.169	0
SPLEN20008390	10.886	0
SPLEN20011410	2.253	0
SPLEN20054290	17.478	0
SPLEN20128000	0.407	0
SPLEN20140800	5.651	0
SPLEN20145720	7.423	0
SPLEN20169720	4.837	0
SPLEN20179180	3.262	0
SPLEN20193110	57.827	0
SPLEN20194050	3.416	0
SPLEN20211940	8.047	0
SPLEN20212730	17.589	0
SPLEN20225220	1.691	0
TBAES20000590	1.797	0
TESTI20061110	24.59	0
TESTI20116830	38.615	0
TESTI20184620	3.37	0
TESTI20208710	64.596	0
TESTI20211240	6.816	0
TESTI20213580	40.357	0
TESTI20214250	4.107	0
TESTI20334410	2.618	0
TESTI20369130	24.204	0
TESTI20369690	4.285	0
TESTI20391770	4.943	0
THYMU20039810	2.491	0
THYMU20216840	58.853	0
THYMU20240710	39.309	0
TRACH20003590	3.557	0
TRACH20032720	4.419	0
TRACH20033230	2.123	0
TRACH20141240	3.693	0

EP 1 347 046 A1

Table 14 (continued)

CloneID	UTERU	TUTER
TRACH20149970	25.316	0
UMVEN10001860	0.63	0
UTERU20000740	62.692	0
UTERU20004240	1.013	0
UTERU20006290	100	0
UTERU20020010	40.126	0
UTERU20022940	2.165	0
UTERU20030570	3.085	0
UTERU20040610	100	0
UTERU20046640	4.048	0
UTERU20046980	100	0
UTERU20050690	64.596	0
UTERU20054460	24.816	0
UTERU20055330	100	0
UTERU20055930	4.016	0
UTERU20056010	3.04	0
UTERU20059050	100	0
UTERU20061030	100	0
UTERU20064000	15.228	0
UTERU20064860	51.819	0
UTERU20065930	3.522	0
UTERU20067050	100	0
UTERU20068990	100	0
UTERU20070040	24.856	0
UTERU20070810	17.449	0
UTERU20076390	100	0
UTERU20081300	53.896	0
UTERU20084260	26.26	0
UTERU20094350	12.756	0
UTERU20095380	40.674	0
UTERU20095400	100	0
UTERU20097760	10	0
UTERU20099720	16.901	0
UTERU20101240	100	0
UTERU20114100	100	0
UTERU20115740	100	0
UTERU20116570	100	0
UTERU20118110	100	0
UTERU20118970	100	0
UTERU20119060	16.267	0
UTERU20119680	100	0
UTERU20120310	53.896	0
UTERU20124070	29.356	0
UTERU20126880	51.568	0
UTERU20134910	13.929	0
UTERU20135860	7.858	0
UTERU20143980	100	0
UTERU20144640	16.101	0
UTERU20145480	39.231	0
UTERU20146310	100	0

EP 1 347 046 A1

Table 14 (continued)

CloneID	UTERU	TUTER
UTERU20146680	39.231	0
UTERU20150870	100	0
UTERU20151980	100	0
UTERU20158300	58.853	0
UTERU20158800	100	0
UTERU20161570	100	0
UTERU20164260	15.158	0
UTERU20168220	19.178	0
UTERU20176130	12.264	0
UTERU20176320	64.596	0
UTERU20178100	100	0
UTERU20179880	100	0
UTERU20183640	53.896	0
UTERU20185230	40.126	0
UTERU20186740	100	0
UTERU20188110	100	0
UTERU20188810	100	0
BRAWH10000930	2.2	10.279
CTONG20128470	2.054	38.378
UTERU20006960	3.394	63.416

Table 15

CloneID	NTONG	CTONG
ADRGL20018300	0	22.262
ASTRO20058630	0	14.161
ASTRO20072210	0	34.963
ASTRO20108190	0	5.013
BRACE20003070	0	2.194
BRACE20039040	0	4.829
BRACE20060720	0	36.712
BRACE20061050	0	39.515
BRACE20210140	0	11.034
BRACE20276430	0	26.828
BRAMY20152110	0	24.194
BRAMY20266850	0	4.616
BRAMY20271400	0	48.032
BRAWH10000930	0	3.436
BRAWH20004600	0	1.137
BRCAN20280360	0	4.497
BRCOC20004870	0	0.54
BRHIP20005340	0	5.1
BRHIP20005530	0	4.786
BRHIP20238880	0	2.741
BRSSN20146100	0	6.65
CTONG10000100	0	12.075
CTONG10000220	0	100
CTONG10000620	0	100
CTONG10000930	0	74.021

EP 1 347 046 A1

Table 15 (continued)

CloneID	NTONG	CTONG
CTONG10000940	0	0.725
CTONG10001650	0	100
CTONG10002770	0	38.523
CTONG20002180	0	100
CTONG20004690	0	5.439
CTONG20009770	0	100
CTONG20014280	0	62.446
CTONG20027090	0	4.036
CTONG20028410	0	19.729
CTONG20038890	0	100
CTONG20049410	0	100
CTONG20050280	0	25.499
CTONG20052650	0	34.822
CTONG20052900	0	42.764
CTONG20075860	0	11.194
CTONG20076130	0	16.303
CTONG20077790	0	62.68
CTONG20082690	0	12.672
CTONG20085950	0	100
CTONG20091080	0	44.201
CTONG20091320	0	100
CTONG20092570	0	100
CTONG20092580	0	100
CTONG20092680	0	100
CTONG20092700	0	100
CTONG20093950	0	100
CTONG20095270	0	100
CTONG20095290	0	11.777
CTONG20095340	0	14.323
CTONG20096430	0	100
CTONG20096750	0	100
CTONG20097660	0	100
CTONG20098440	0	33.474
CTONG20099380	0	37.266
CTONG20099550	0	100
CTONG20099630	0	38.502
CTONG20100240	0	100
CTONG20101480	0	100
CTONG20103480	0	13.193
CTONG20105080	0	15.273
CTONG20105660	0	25.256
CTONG20106230	0	100
CTONG20106520	0	29.937
CTONG20108210	0	2.662
CTONG20114290	0	100
CTONG20114740	0	100
CTONG20118150	0	100
CTONG20118250	0	15.991
CTONG20119200	0	100
CTONG20120770	0	100

EP 1 347 046 A1

Table 15 (continued)

CloneID	NTONG	CTONG
CTONG20121010	0	29.404
CTONG20121580	0	33.983
CTONG20124010	0	7.835
CTONG20124220	0	69.076
CTONG20124470	0	100
CTONG20124730	0	100
CTONG20125540	0	100
CTONG20125640	0	7.359
CTONG20126070	0	3.221
CTONG20127450	0	10.331
CTONG20128470	0	9.622
CTONG20129960	0	32.63
CTONG20131490	0	24.817
CTONG20131560	0	38.523
CTONG20132220	0	6.999
CTONG20133390	0	100
CTONG20133480	0	10.246
CTONG20133520	0	50.616
CTONG20136300	0	100
CTONG20138030	0	100
CTONG20139070	0	8.031
CTONG20139340	0	12.919
CTONG20139860	0	100
CTONG20140320	0	100
CTONG20140580	0	100
CTONG20141650	0	8.968
CTONG20146300	0	100
CTONG20147050	0	34.963
CTONG20149460	0	100
CTONG20149950	0	100
CTONG20153300	0	52.97
CTONG20153580	0	74.021
CTONG20155180	0	24.734
CTONG20155400	0	100
CTONG20156780	0	62.446
CTONG20158040	0	100
CTONG20158150	0	16.385
CTONG20158660	0	100
CTONG20159530	0	100
CTONG20160560	0	3.704
CTONG20161850	0	19.368
CTONG20162170	0	100
CTONG20163550	0	100
CTONG20164990	0	65.066
CTONG20165050	0	33.474
CTONG20186320	0	14.897
CTONG20200310	0	100
CTONG20265130	0	100
CTONG20267700	0	100
CTONG20273610	0	100

EP 1 347 046 A1

Table 15 (continued)

CloneID	NTONG	CTONG
FCBBF10000240	0	12.268
FCBBF10005740	0	3.866
FCBBF30123470	0	4.088
FCBBF30233680	0	9.14
FEBRA20025270	0	5.334
FEBRA20037500	0	6.8
HCHON20002260	0	1.502
HCHON20007380	0	5.546
HCHON20007510	0	6.65
HCHON20015350	0	17.176
HCHON20040020	0	1.462
HHDPC20034390	0	0.474
HLUNG10000550	0	2.016
KIDNE20002520	0	3.184
KIDNE20009470	0	9.415
KIDNE20115080	0	34.822
KIDNE20127100	0	35.274
LIVER20028420	0	3.556
MESAN20029400	0	5.924
NT2RI20023160	0	1.493
NT2RI20023910	0	1.51
NT2RI20091730	0	4.155
NT2RP70043480	0	4.209
NT2RP70078420	0	3.572
NT2RP70081610	0	11.694
OCBBF20006770	0	30.34
OCBBF20059560	0	5.287
OCBBF20073540	0	1.871
OCBBF20094240	0	13.516
OCBBF20108580	0	12.407
PEBLM20044520	0	15.083
PEBLM20071880	0	16.259
PROST20107820	0	0.453
PUAEN20030180	0	6.243
SKNSH20008190	0	4.636
SMINT20023280	0	34.547
SMINT20089170	0	20.839
SPLEN20179180	0	5.094
TESTI20094020	0	17.075
TESTI20094230	0	30.119
TESTI20152460	0	22.051
TESTI20184620	0	5.263
TESTI20211240	0	10.645
TESTI20442760	0	8.832
THYMU20039810	0	0.973
TRACH20028030	0	11.644
TRACH20141240	0	1.923
TSTOM20003150	0	4.245
UTERU20004240	0	1.582
UTERU20055930	0	2.091

EP 1 347 046 A1

Table 15 (continued)

CloneID	NTONG	CTONG
UTERU20065930	0	2.75
UTERU20119060	0	12.702
UTERU20124070	0	45.844
BRACE20039440	34.336	0
BRACE20068590	74.88	0
FCBBF30018550	20.639	0
IMR3220002430	6.323	0
KIDNE20028830	16.715	0
NT2RI20028470	9.251	0
NT2RI20054050	2.069	0
NT2RI20086220	23.258	0
NTONG20009770	7.245	0
NTONG20013620	25.727	0
NTONG20028070	86.921	0
NTONG20029480	32.729	0
NTONG20029700	100	0
NTONG20046140	43.643	0
NTONG20048060	51.123	0
NTONG20049910	100	0
NTONG20050620	100	0
NTONG20050860	100	0
NTONG20051530	58.314	0
NTONG20052650	100	0
NTONG20056570	100	0
NTONG20061870	100	0
NTONG20063010	40.505	0
NTONG20064400	100	0
NTONG20064840	31.857	0
NTONG20065010	100	0
NTONG20066460	100	0
NTONG20067090	66.789	0
NTONG20067830	20.865	0
NTONG20070200	100	0
NTONG20070340	52.247	0
NTONG20075220	100	0
NTONG20076930	51.858	0
NTONG20077560	49.744	0
NTONG20083650	100	0
NTONG20088620	100	0
NTONG20090600	20.536	0
NTONG20090680	100	0
NTONG20092290	100	0
NTONG20092330	100	0
OCBBF20068490	14.895	0
SKMUS20001980	23.281	0
SMINT20138900	67.622	0
SPLEN20008390	67.269	0
SPLEN20162680	3.184	0
UTERU20134910	86.071	0
ASTRO20155290	13.655	3.451

EP 1 347 046 A1

Table 15 (continued)

CloneID	NTONG	CTONG
FEBRA20080810	10.438	1.319
NT2RP70032610	10.013	27.835
NT2RP70036880	5.442	16.504
NTONG20015870	17.552	0.554
OCBBF20188730	10.213	2.581
SMINT20122910	33.985	8.589
SPLEN20099700	37.585	9.499

Table 16

Clone ID	F2BBF	FEBRA	DCBBF	BRACE	BRALZ	BRAMY	BRAMH	BRCAN	BRCCO	BRHIP	BRSSN	BRSTN	BRTHA
JNB691000191C	0	0	0	0	0	0	6.122	0	0	6.246	0	0	0
ADRL20018300	0	0	0	8.483	0	0	0	0	0	0	0	0	0
ASTR0200141C	0	0	0	0	0	3.06	0	0	0	0	0	0	0
ASTR02003318C	0	0	0	2.094	0	0	2.95	0	0	0	0	0	0
ASTR02005863C	0	0	0	0	0	0	7.603	0	0	0	0	0	0
ASTR020064750	0	0	0	0	0	7.505	0	0	0	0	0	0	16.519
ASTR020100720	0	0	0	0	0	0	0	39.838	0	0	0	0	0
ASTR020141350	0	0	0	0	0	0	0	0	12.305	0	0	0	0
ASTR020145760	0	0	0	0	0	11.388	0	0	0	0	42.066	0	0
ASTR020181690	0	0	0	0	0	0.952	0	2.167	0	1.927	0	0	0
BGG120006160	0	0	0	1.269	0	0.901	0	2.051	0	0	0	3.224	0.991
BRACE20006400	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20011070	0	0	0	10.447	53.184	0	0	0	0	0	0	0	0
BRACE20019540	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20027620	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20037660	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20038000	0	0	0	38.906	0	0	0	0	0	0	0	0	30.394
BRACE20038470	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20038480	0	0	0	38.787	0	0	0	0	0	0	0	0	0
BRACE20038850	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20039440	0	0	0	0.367	0	2.086	0.518	1.188	1.834	0	1.927	1.867	0
BRACE20039540	0	0	0	16.746	0	0	0	0	0	0	0	0	0
BRACE20050900	0	0	0	52.057	0	0	0	0	0	0	0	0	0
BRACE20051380	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20051690	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20052160	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20053280	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20053480	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20053630	0	0	0	10.086	0	0	0	0	0	0	0	0	0
BRACE20054500	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20055180	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20057420	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20057620	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20057730	0	0	0	100	0	0	0	0	0	0	0	0	0
BRACE20058580	0	0	0	14.668	0	0	41.331	0	0	21.084	0	0	22.917
BRACE20058810	0	0	0	100	0	0	0	0	0	0	0	0	0

5

10

15

20

2.

3

2

•

5

10

19

21

2

(3)

1

-

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

[illegible]

Table 22

BRAW20285160	0	0	0	0	0	0	3.974	0	0	0	0	0	0	0	0	14.68	0	0	0
BRAW20285930	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0
BRAW20286820	0	0	0	0	0	0	21.396	0	0	0	0	0	0	0	0	0	0	0	0
BRAW20002320	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20012390	0	0	0	0	0	0	0	7.296	0	0	0	0	0	0	0	27.166	0	8.091	0
BRAW20014920	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20015350	0	0	0	0	0	5.352	6.965	1.975	15.859	5.247	10.075	16.539	14.243	10.951	0	0	0	0	0
BRAW20015890	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20016660	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20016860	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20017010	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20018730	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20028110	0	0	0	0	8.469	31.162	17.379	8.624	0	0	17.598	0	0	0	9.564	0	0	0	0
BRAW20029630	0	0	0	0	0	0	0	11.932	0	0	0	0	0	0	0	0	0	0	0
BRAW20064050	0	0	0	0	0	0	0	12.977	0	0	13.24	0	0	0	0	0	0	0	0
BRAW20075700	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20096780	0	0	0	0	0	0	0	21.269	0	0	0	0	0	0	0	0	0	0	0
BRAW20100690	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20101360	0	0	0	0	0	0	26.605	26.404	0	0	0	0	0	0	0	0	0	0	0
BRAW20103180	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20105840	0	0	0	0	0	0	0	30.356	69.644	0	0	0	0	0	0	0	0	0	0
BRAW20106180	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20107540	0	0	0	0	7.94	0	0	11.186	0	0	0	0	0	0	40.334	0	0	0	0
BRAW20110660	0	0	0	0	0	0	0	21.178	0	0	0	78.822	0	0	0	0	0	0	0
BRAW20110790	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20110960	0	0	0	0	0	0	0	54.53	0	0	0	0	0	0	0	0	0	0	0
BRAW20111550	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20112940	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20114000	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20117950	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20118230	0	0	0	0	0	0	0	21.626	0	0	0	0	0	0	0	0	0	0	0
BRAW20122580	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20125380	0	0	0	0	0	0	0	10.145	0	0	0	0	18.88	0	0	0	0	0	0
BRAW20126190	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0
BRAW20126980	0	0	0	0	0	0	57.958	19.174	0	0	0	0	0	0	0	0	0	0	0
BRAW20132190	0	0	0	0	0	35.004	9.761	19.375	0	0	0	0	0	0	0	0	0	0	0
BRAW20137480	0	0	0	0	0	0	8.068	2.669	6.123	9.455	2.723	9.934	0	0	2.96	0	0	0	0

Table 23

10

15

20

24

30

35

4

4

5

202

5
10
15
20
25
30
35
40
45
50
55

[illegible]

Table 27

[illegible]

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

Table 30

NOVAR20000380	0	0	0	0	3.968	15.711	0.626	1.242	4.275	6.602	0	9.248	17.918	0
NT2NE20010400	0	0	0	0	11.003	0	15.621	0	0	0	0	0	17.192	0
NT2NE20010490	0	0	0	0	0	0	0	0	0	0	0	0	31.686	0
NT2NE20021620	0	0	0	0	0	0	0	0	0	0	0	45.501	0	0
NT2NE20122430	0	0	0	0	0	0	0	0	0	0	0	0	23.43	0
NT2NE20125050	0	0	0	0	13.014	0	0	0	0	0	0	0	18.714	0
NT2NE20174920	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RI20001330	0	0	0	0	1.819	0	0	0	0	0	0	0	0	0
NT2RI20023590	0	0	0	0	0	0	0	8.23	0	0	0	0	0	0
NT2RI20041880	0	0	0	0	0	0	0	0	0	0	0	0	10.353	0
NT2RI20046080	0	0	0	0	0	0	0	0	8.488	0	0	0	0	0
NT2RI20216250	0	0	0	0	0	0	0	0	0	0	19.442	0	0	0
NT2RI20252550	0	0	0	0	0	0	0	0	0	0	0	0	37.898	0
NT2RP60000770	0	0	0	0	0	0	0	0	0	0	0	0	7.128	0
NT2RP70045590	0	0	0	0	0	0	0	0	0	0	0	0	9.452	0
NT2RP70063950	0	0	0	0	0	0	0	0	0	0	17.468	0	0	0
NT2RP70195430	0	0	0	0	0	38.221	0	0	0	0	10.792	0	0	0
NT2RP70198350	0	0	0	0	0	0	0	1.042	0	0	0	0	3.758	0
NTONG20028070	0	0	0	0	0	0	0	0	0	0	0	0	13.079	0
NTONG20046140	0	0	0	0	0	0	0	0	0	0	0	0	6.567	0
NTONG20064840	0	0	0	0	3.088	0	0	0	0	0	0	0	0	0
NTONG20067830	0	0	0	0	0	0	2.853	0	0	0	0	0	0	0
NTONG20071560	0	0	0	0	4.791	0	0	0	0	0	0	0	0	0
PANCR10000910	0	0	0	0	0.214	0	0	0	0	0	0	0	0	0
PEBLW20024550	0	0	0	0	0	0	0	0	0	0	0	33.118	0	0
PEBLW20052820	0	0	0	0	0	0	11.82	0	0	0	0	0	0	0
PEBLW20074370	0	0	0	0	0	21.543	0	0	0	0	0	0	0	0
PERIC20004780	0	0	0	0	7.727	0	0	0	0	0	0	0	0	0
PLACE50000660	0	0	0	0	0	0	18.438	0	0	0	0	0	32.991	0
PLACE60079250	0	0	0	0	0	0	0	0	23.248	0	0	0	0	0
PLACE60136720	0	0	0	0	0	0	27.825	0	0	0	0	0	0	0
PLACE60138830	0	0	0	0	0	0	0	0	0	0	0	0	38.39	0
PROST20005670	0	0	0	0	0	0	14.432	0	0	0	0	0	0	0
PROST20050670	0	0	0	0	11.45	0	0	0	0	0	0	0	17.889	0
PROST20107820	0	0	0	0	0	0	0	0.243	0	0	0	0	0	0
PROST2011050	0	0	0	0	25.26	0	0	0	0	0	0	0	0	0
PROST20116600	0	0	0	0	16.676	0	0	0	0	0	0	0	0	0

Table 31

[illegible]

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

10

15

5
10
15
20
25
30
35
40
45
50
55

211

Table 35

[illegible]

Table 36

[illegible]

5
10
15
20
25
30
35
40
45
50
55

5
10
15
20
25
30
35
40
45
50
55

Table 38

[illegible]

Table 39

[illegible]

ASTRO20008010	0	0	1.267	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRACE20276430	0	0	17.893	10.223	0	0	0	0	33.045	0	0	0	0	0	0	0	0
BRAWY20103570	0	0	18.549	21.196	0	0	30.09	14.931	0	0	15.234	0	0	0	0	0	0
BRAWY20120910	0	0	7.377	0	0	5.983	0	0	0	0	0	0	0	0	0	0	0
BRAWY20162510	0	0	8.934	5.104	25.986	43.477	0	16.499	0	0	0	0	0	0	0	0	0
BRAWY20196000	0	0	30.091	0	0	8.136	16.148	0	0	0	0	0	0	0	0	0	8.954
BRANI20164460	0	0	10.808	0	0	0	0	8.7	0	0	0	0	0	0	0	0	0
BRCANZ20273640	0	0	7.379	0	10.731	5.985	2.97	20.44	21.042	0	11.054	0	0	0	0	0	13.174
BRCOC20105100	0	0	14.918	0	0	0	0	0	85.082	0	0	0	0	0	0	0	0
BRHIP20198190	0	0	10.771	30.77	0	0	0	8.671	0	0	17.692	0	0	0	0	0	0
BRHIP20222280	0	0	11.352	0	0	0	0	9.138	20.964	0	9.323	0	0	0	0	0	0
BRHIP20254480	0	0	37.989	0	0	30.812	0	0	0	0	31.199	0	0	0	0	0	0
BRHIP30004570	0	0	33.739	38.553	0	0	0	0	0	0	27.708	0	0	0	0	0	0
CTONG20028410	0	0	26.318	15.036	0	0	0	21.185	0	0	10.807	0	0	0	0	0	0
CTONG20091080	0	0	29.481	0	0	0	0	0	0	0	0	0	0	0	0	0	26.317
CTONG20103480	0	0	2.2	7.541	0	0	1.784	3.542	4.063	0	1.807	6.691	0	0	0	0	3.927
CTONG20126070	0	0	2.148	0	0	0	0	0	0	0	0	0	0	0	0	0	5.764
CTONG20139340	0	0	8.617	24.615	0	0	0	6.936	0	0	7.077	0	0	0	0	0	7.692
DFNES20001530	0	0	3.977	0	0	0	0	0	0	0	0	0	0	0	0	0	3.551
HCHON20008150	0	0	3.469	0	0	0	2.814	2.793	0	0	10.394	0	0	0	0	0	0
IHHDPG20001040	0	0	4.596	1.313	0	0	0	0	0	0	0	0	0	0	0	0	2.052
HLUNG20016330	0	0	9.947	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HLUNG20017120	0	0	4.096	0	0	35.74	0	0	0	0	0	0	0	0	0	0	0
IMR3220002430	0	0	2.132	1.218	0	0	1.729	0	0	0	2.626	0	0	0	0	0	0.951
KIDNE20007210	0	0	26.272	0	0	0	0	0	0	0	0	0	0	0	0	0	0
KIDNE20021910	0	0	17.71	15.177	0	0	0	0	0	0	0	0	0	0	0	0	7.905
KIDNE20124400	0	0	2.199	2.513	0	0	0	0	0	0	3.612	6.598	0	0	0	0	3.926
MESAN10001260	0	0	2.218	7.605	0	0	0	1.786	0	0	3.644	0	0	0	0	0	1.98
MESAN20029400	0	0	3.951	0	0	0	0	3.18	0	0	0	0	0	0	0	0	0
MESAN20121130	0	0	7.329	0	0	0	0	0	0	0	6.019	0	0	0	0	0	6.543
MESAN20153910	0	0	25.095	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2NE20159740	0	0	18.979	21.687	0	0	7.697	0	0	0	0	0	0	0	0	0	8.471
NT2NE20177520	0	0	29.166	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RI20086220	0	0	3.92	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT2RI20250750	0	0	21.061	12.033	0	0	0	0	0	0	0	0	0	0	0	0	6.999
NT2RP60000850	0	0	5.745	3.283	0	0	4.66	4.625	0	0	17.297	0	0	0	0	0	18.801
NT2RP70044280	0	0	12.569	7.181	0	0	6.796	16.862	0	0	6.881	0	0	0	0	0	5.129
																	0

Table 41

NT2RP70056750	0	0	7.226	8.256	0	5.861	11.633	0	0	8.901	0	0	3.225
NT2RP70081610	0	0	15.599	4.456	0	0	0	0	0	6.405	0	0	0
NTONG20009770	0	0	2.442	0	0	0	0	2.255	3.482	0	0	0	0
OCBBF10000540	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF10001750	0	0	17.896	5.112	0	7.258	0	0	0	0	0	0	0
OCBBF20006770	0	0	20.236	0	0	16.413	0	0	0	0	0	0	0
OCBBF20013890	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20019830	0	0	8.974	0	0	0	0	0	0	0	0	0	0
OCBBF20020150	0	0	17.182	9.817	0	0	0	0	0	0	0	15.338	0
OCBBF20020830	0	0	27.302	0	0	0	0	25.211	0	0	0	0	0
OCBBF20023570	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20028050	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20028650	0	0	65.522	0	0	0	0	0	0	0	0	0	0
OCBBF20029800	0	0	54.907	0	0	0	0	0	0	45.093	0	0	0
OCBBF20030280	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20030910	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20035930	0	0	55.403	0	0	44.597	0	0	0	0	0	0	0
OCBBF20037440	0	0	52.585	0	0	0	0	0	0	0	0	0	0
OCBBF20041680	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20045330	0	0	25.025	0	0	0	0	0	0	0	74.975	0	0
OCBBF20046120	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20046470	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20046690	0	0	54.907	0	0	0	0	0	0	45.093	0	0	0
OCBBF20048660	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20050770	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20051610	0	0	54.907	0	0	0	0	0	0	45.093	0	0	0
OCBBF20053430	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20053490	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20053730	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20054200	0	0	78.844	0	0	21.156	0	0	0	0	0	0	0
OCBBF20054760	0	0	5.808	0	0	4.71	0	0	0	0	0	0	0
OCBBF20060300	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20062140	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20062410	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20066390	0	0	100	0	0	0	0	0	0	0	0	0	0
OCBBF20071210	0	0	52.585	0	0	0	0	0	0	0	0	0	0
OCBBF20071840	0	0	100	0	0	0	0	0	0	0	0	0	0

Table 44

TRACH20033230	0	0	4.422	0	7.173	7.119	0	0	9.079	0	0	3.947
TRACH20084720	0	0	3.898	1.114	0	0	0	5.558	0	0	0	8.7
BRACE20067430	0	22.168	11.047	16.779	0	4.48	8.892	0	4.536	33.098	0	0
BRAMH10000930	0	1.16	2.292	0.655	0	0	0.461	0	0	1.717	0	0.511
BRHIP20003120	0	16.166	8.056	9.205	0	6.534	32.424	0	13.232	0	0	14.383
BRSSN20152380	0	8.534	8.505	4.859	0	0	10.27	0	6.985	12.742	0	0
FEBRA20024100	0	66.741	33.259	0	0	0	0	0	0	0	0	0
FEBRA20027810	0	17.057	25.5	43.707	0	6.894	6.842	0	0	0	0	0
FEBRA20037500	0	9.102	2.268	2.591	0	1.839	0	12.934	1.862	0	0	6.073
FEBRA20082100	0	16.72	8.332	4.761	0	6.768	0	23.761	0	0	0	0
FEBRA20098460	0	51.462	25.645	0	0	0	0	0	0	0	0	22.893
FEBRA20144170	0	4.038	2.012	0.766	0	3.264	7.559	6.194	3.826	4.019	5.841	1.198
FEBRA20145780	0	54.561	27.189	0	0	0	0	0	0	0	0	0
FEBRA20233770	0	19.338	9.637	0	28.03	0	15.515	0	27.481	0	0	0
HHDPC10000830	0	2.44	2.432	1.389	0	1.972	0	2.246	0	0	3.643	0
MESAN20025190	0	11.561	5.761	0	0	4.673	0	0	4.732	0	0	5.143
MESAN20089360	0	9.917	4.942	5.647	0	12.025	3.978	0	4.059	0	0	0
NT2R120048840	0	11.556	0.96	0	0	0	0	0	0.788	2.876	0	0
NT2RP70043480	0	5.634	16.844	0	0	0	0	0	8.006	0	0	0
OCBBF20032460	0	24.396	24.315	0	0	9.861	9.786	0	19.969	0	0	0
OCBBF20039250	0	2.077	1.035	0	3.011	1.679	0	0	0	0	3.004	0
OCBBF20049300	0	25.873	12.893	0	0	0	0	23.811	0	0	37.423	0
OCBBF20061720	0	13.071	13.027	0	0	5.283	0	12.029	18.574	0	19.515	0
OCBBF20078920	0	21.239	5.292	0	0	0	0	0	0	0	15.36	0
OCBBF20084660	0	42.651	10.627	0	0	0	0	0	0	0	31.84	0
OCBBF20087010	0	27.016	40.389	0	0	10.92	21.675	0	0	0	0	0
PROST20087700	0	1.945	2.907	7.197	0	3.93	4.68	0	6.387	2.903	2.813	3.46
PROST20153320	0	6.425	3.202	27.441	0	2.597	10.31	0	18.262	5.259	0	0
TRACH20135520	0	25.898	12.906	7.374	0	0	10.389	0	31.797	0	0	0
ADIPS20004250	1.434	0	0.964	0	0	0	1.553	0	1.584	0	0	0
ASTRO10001650	4.095	0	11.014	0	0	0	0	0	0	0	0	0
BRACE20056810	3.689	0	4.961	14.879	0	13.076	16.971	4.581	20.37	7.431	7.199	3.321
BRACE20059370	22.318	0	7.504	8.574	0	0	0	0	0	0	0	0
BRACE20106690	11.777	0	31.677	9.049	0	0	19.124	0	6.504	0	0	7.069
BRACE20210140	10.945	0	14.719	4.205	0	0	17.772	0	18.132	0	0	0
BRAWH20103290	13.868	0	6.217	21.311	0	10.085	20.017	0	15.317	0	0	11.099
BRAWH20121640	38.493	0	25.884	14.788	0	0	20.835	0	0	0	0	0

Table 45

BRHIP20005530	4.747	0	12.769	1.824	0	2.589	2.57	0	0	5.243	0	0	2.85
BRHIP20217620	5.147	0	3.461	7.91	0	0	8.358	0	0	11.369	0	0	3.09
BRHIP20218580	6.182	0	8.314	4.75	0	3.372	3.346	0	0	3.414	0	0	0
BRHIP20238880	0.68	0	3.2	2.089	0	1.854	2.208	1.688	1.303	0.751	1.369	2.653	4.488
CTONG20075860	11.104	0	14.933	0	0	0	0	0	21.292	0	0	0	0
CTONG20129960	5.394	0	7.255	0	0	0	2.92	0	0	0	0	0	6.476
FCBBF10000240	8.112	0	10.91	0	0	8.637	6.587	0	0	6.72	0	7.916	0
FCBBF10000630	11.049	0	7.43	0	0	8.026	11.982	0	0	6.102	0	0	0
FCBBF10001150	37.553	0	25.252	14.427	0	0	0	0	0	0	0	0	0
FCBBF10004120	3.576	0	7.212	0	0	0	5.806	0	0	0	0	0	0
FCBBF10005740	7.67	0	15.473	2.947	0	10.458	8.303	0	7.354	6.353	0	0	2.146
FCBBF20075560	16.883	0	11.353	0	0	0	0	0	0	0	0	0	4.604
FCBBF30018550	31.042	0	3.479	1.988	0	0	0	0	0	0	0	0	0
FCBBF30025560	59.793	0	40.207	0	0	0	0	0	0	0	0	0	0
FCBBF30086440	15.918	0	10.704	0	0	0	8.616	0	0	0	0	0	0
FCBBF30090690	8.273	0	5.563	6.357	0	22.561	17.913	0	0	4.569	0	0	34.763
FCBBF30189490	52.288	0	17.58	0	0	0	0	0	0	14.438	0	0	15.693
FCBBF30233680	4.533	0	6.096	0	0	0	7.361	0	0	2.503	0	0	2.721
FCBBF30240020	10.485	0	28.201	16.112	0	5.718	5.675	0	0	0	0	0	0
HCHON20007510	6.596	0	4.435	0	0	0	3.57	0	0	0	0	0	3.959
HCHON20016650	2.851	0	5.751	2.191	0	9.329	0	0	0	6.297	0	0	0
HHDFC20095280	12.007	0	8.074	4.613	0	0	0	0	0	6.631	0	0	0
KIDNE20002520	1.579	0	6.37	1.213	0	3.444	6.837	0	6.055	3.488	0	3.082	2.843
KIDNE20009470	9.338	0	9.419	0	9.132	0	2.527	0	0	0	0	0	2.803
NT2R120003480	16.371	0	44.033	0	0	0	0	0	0	0	0	0	0
NT2R120055790	17.338	0	11.659	0	0	0	0	0	0	19.149	0	0	0
NT2RP70027380	10.635	0	35.756	4.086	0	0	5.756	0	0	5.873	0	0	6.384
NT2RP70032610	2.51	0	3.376	0	0	0	0	0	0	0	0	0	0
NT2RP70062230	7.806	0	10.498	17.994	0	0	4.225	0	0	8.622	15.726	0	0
OCBBF10001850	15.555	0	31.379	0	0	0	4.21	0	0	0	0	0	0
OCBBF20022900	18.632	0	12.529	0	0	20.324	0	0	0	0	0	0	11.184
OCBBF20026630	59.793	0	40.207	0	0	0	0	0	0	0	0	0	0
OCBBF20049840	44.001	0	29.587	0	0	0	0	0	0	0	0	0	0
OCBBF20059560	5.245	0	3.527	6.045	10.258	5.721	0	6.513	0	0	0	26.412	0
OCBBF20068490	3.734	0	7.532	0	0	0	0	0	0	0	10.566	0	3.148
OCBBF20071960	33.142	0	66.858	0	0	0	0	0	0	0	0	0	0
OCBBF20080410	7.723	0	2.597	0	0	0	4.18	0	0	0	0	0	0

10

15

20

25

30

35

40

45

50

0	51	36	0
---	----	----	---

224

Table 48

NT2R120091730	2.061	5.561	1.386	0	0	1.124	0	0	0	1.138	0	0	1.237
NT2R120091940	1.816	9.799	9.767	0	0	0.99	1.965	0	0	1.003	0	0	0
NT2RP70036880	2.728	1.841	8.256	4.193	0	6.696	3.692	0	0	0	0	0	4.913
NT2RP70078420	3.543	4.781	2.383	4.084	6.93	0	0	0	0	1.957	7.139	0	2.127
OC8BF20047570	18.314	30.89	12.315	3.518	8.955	2.497	0	5.686	0	0	0	0	0
OC8BF20080050	11.733	7.916	21.697	6.762	0	6.399	0	0	0	1.62	0	0	0
OC8BF20125530	4.333	11.695	4.371	0	4.238	1.182	0	2.691	0	2.393	4.366	4.229	0
OC8BF20140640	2.523	10.215	3.394	0	0	1.376	0	0	0	4.18	10.167	4.925	0
TRACH20032720	6.845	9.236	9.205	2.63	0	11.2	3.705	8.5	13.125	3.78	0	0	4.109
TRACH20141240	3.814	5.146	2.565	1.465	0	4.16	2.064	0	3.657	0	0	0	3.434
UTERU20004240	3.138	4.234	1.055	3.014	3.069	0.856	1.699	3.897	3.009	0	0	3.062	0

EP 1 347 046 A1

Table 49

CloneID	FEHRT	HEART
FEHRT20003250	100	0
OCBBF20189560	35.243	0
BRAWH20029630	0	79.6
CTONG201509	0	5.418
HCHON20007510	0	23.818
HEART20003060	0	90.384
HEART20005410	0	53.555
HEART20021840	0	100
HEART20025980	0	100
HEART20034320	0	100
HEART20037810	0	100
HEART200494	0	100
HEART20049410	0	63.375
HEART20049800	0	100
HEART20061950	0	63.227
HEART20063340	0	100
HEART20067870	0	100
HEART20067890	0	100
HEART20072310	0	32.316
HEART20074430	0	100
HEART20077670	0	100
HEART20089940	0	100
HEART20090000	0	68.952
HEART20095990	0	100
HLUNG10000550	0	3.611
HLUNG20017120	0	21.996
KIDNE20028390	0	48.974
KIDNE20028830	0	15.131
NTONG20029480	0	44.44
OCBBF10001750	0	48.053
PROST20127800	0	48.531
SKMUS20001980	0	21.074
SKMUS20003610	0	7.134
SMINT20026890	0	7.842
SMINT20121220	0	23.322
SMINT20122910	0	30.763
SMINT20183530	0	65.405
SPLEN20008740	0	3.252
SPLEN20027440	0	14.879
SPLEN20162680	0	2.882
STOMA20062290	0	40.108
TESTI20254220	0	16.559
THYMU20271250	0	3.582
TRACH20141240	0	6.886
UTERU20004240	0	5.666

EP 1 347 046 A1

Table 50

CloneID	FEKID	KIDNE
ASTRO10001650	0	7.727
ASTRO20108190	0	2.346
BGGI120006160	0	3.117
BRACE20039040	0	9.038
BRACE20060550	0	6.974
BRAMY20102080	0	63.37
BRAWH20004600	0	2.128
BRAWH20125380	0	35.37
BRAWH20162690	0	4.596
BRHIP20115760	0	66.835
BRHIP20205090	0	65.282
BRHIP20238880	0	1.283
CTONG20052650	0	65.178
CTONG20108210	0	2.491
CTONG20128470	0	6.004
CTONG20133480	0	19.179
CTONG20139070	0	7.516
D9OST20000310	0	16.47
DFNES20001530	0	11.162
FCBBF10001820	0	59.128
FEBRA20002100	0	4.929
HCHON20008980	0	35.524
HCHON20016650	0	5.38
HLUNG20033780	0	32.277
KIDNE20002520	0	2.979
KIDNE20003940	0	100
KIDNE20006780	0	100
KIDNE20007210	0	73.728
KIDNE20007770	0	19.958
KIDNE20008010	0	100
KIDNE20009470	0	8.811
KIDNE20011170	0	77.71
KIDNE20011400	0	100
KIDNE20013730	0	24.839
KIDNE20017130	0	54.019
KIDNE20018730	0	100
KIDNE20018970	0	100
KIDNE20020150	0	100
KIDNE20021680	0	100
KIDNE20021910	0	24.85
KIDNE20021980	0	100
KIDNE20022620	0	100
KIDNE20024830	0	100
KIDNE20027250	0	35.87
KIDNE20027950	0	100
KIDNE20028390	0	25.593
KIDNE20028830	0	7.907
KIDNE20029800	0	10.988
KIDNE20067330	0	100

EP 1 347 046 A1

Table 50 (continued)

CloneID	FEKID	KIDNE
KIDNE20079440	0	35.045
KIDNE20096280	0	100
KIDNE20096470	0	100
KIDNE20100070	0	100
KIDNE20100840	0	100
KIDNE20101370	0	100
KIDNE20101510	0	100
KIDNE20102650	0	8.237
KIDNE20102710	0	100
KIDNE20104300	0	33.246
KIDNE20106740	0	100
KIDNE20107390	0	100
KIDNE20107500	0	74.264
KIDNE20107620	0	100
KIDNE20109730	0	100
KIDNE20109890	0	100
KIDNE20112000	0	100
KIDNE20115080	0	65.178
KIDNE20118580	0	100
KIDNE20120090	0	33.186
KIDNE20121880	0	62.256
KIDNE20122910	0	83.085
KIDNE20124400	0	6.171
KIDNE20125630	0	100
KIDNE20126010	0	100
KIDNE20126130	0	100
KIDNE20127100	0	33.012
KIDNE20127450	0	100
KIDNE20127750	0	100
KIDNE20130450	0	100
KIDNE20131580	0	63.24
KIDNE20132180	0	100
KIDNE20137340	0	100
KIDNE20138010	0	100
KIDNE20141190	0	49.697
KIDNE20144890	0	100
KIDNE20148900	0	100
KIDNE20163880	0	100
KIDNE20180710	0	49.105
KIDNE20181660	0	100
KIDNE20182690	0	100
KIDNE20186780	0	100
KIDNE20190740	0	100
LIVER20035110	0	28.683
MESAN20025190	0	16.169
NOVAR20000380	0	2.166
NT2RI20054050	0	2.936
NT2RP70043480	0	7.879
PROST20107820	0	1.696
PROST2012353	0	32.771

EP 1 347 046 A1

Table 50 (continued)

CloneID	FEKID	KIDNE
PROST20161950	0	20.387
PUAEN20030180	0	46.744
SKMUS20003610	0	3.728
SMINT20033400	0	10.243
TBAES20000590	0	5.253
TESTI20044310	0	29.162
TESTI20082330	0	45.847
TRACH20032720	0	12.917
UTERU20099720	0	12.351
BRACE20003070	25.479	0
BRCOC20031870	34.023	0
CTONG20125640	85.462	0
FCBBF30016320	33.393	0
HCHON20002	8.723	0
HLUNG10000550	11.709	0
PROST20130530	64.069	0
SPLEN20169720	43.864	0
SPLEN20194050	30.978	0
KIDNE20028720	12.368	1.993

Table 51

CloneID	FELNG	HLUNG
BRACE20096200	0	70.38
BRAWH20004600	0	2.238
BRAWH20030250	0	11.121
BRCAN20006390	0	61.519
BRCAN20280360	0	8.855
BRHIP20238880	0	1.35
CTONG10000940	0	1.428
CTONG20103480	0	6.495
CTONG20129960	0	10.709
CTONG20155180	0	48.707
FCBBF10001210	0	36.439
FEBRA20144170	0	1.98
FEBRA20197110	0	7.756
HHDPC20034390	0	0.933
HLUNG20016330	0	29.367
HLUNG20016770	0	12.888
HLUNG20017120	0	12.093
HLUNG20023340	0	33.714
HLUNG20033780	0	33.957
HLUNG20084390	0	100
IMR3220002430	0	3.147
LIVER20028420	0	14.004
NOVAR2000	0	2.278
NT2RI20054050	0	2.059
NT2RI20091730	0	4.091
NT2RP70044280	0	12.369

EP 1 347 046 A1

Table 51 (continued)

CloneID	FELNG	HLUNG
OCBBF20020830	0	40.304
OCBBF20125530	0	4.302
PLACE60004630	0	28.618
PROST2005793	0	14.383
PROST20107820	0	0.892
PROST2018583	0	33.898
PUAEN20030180	0	12.294
SMINT20121220	0	12.822
SPLEN20002220	0	44.799
SPLEN20054290	0	26.875
SPLEN20128000	0	1.253
SPLEN20157300	0	51.319
SPLEN20176200	0	18.8
SPLEN20179180	0	3.344
SPLEN20211940	0	12.373
STOMA20013890	0	21.183
TBAES20000590	0	5.527
TESTI20094230	0	59.311
TESTI20184620	0	10.365
TESTI20334410	0	8.049
THYMU20000570	0	4.974
THYMU20039810	0	1.915
TRACH20007020	0	14.4
TRACH20141240	0	3.786
TRACH20183170	0	10.745
D9OST20033970	61.464	0
FELNG20002410	100	0
HCHON20016650	33.188	0
KIDNE20029800	67.783	0
OCBBF20145760	78.585	0
SPLEN20162680	9.292	0
TESTI20214250	37.027	0
TRACH20005400	30.64	0
HCHON20002	8.672	2.958
HLUNG10000550	11.642	3.971
NT2RI20023910	34.882	8.923
SPLEN20008740	10.483	1.788

EP 1 347 046 A1

Table 52

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*. ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
3NR6920014080	4	4	4.1			
ADRG_20013010	0.1	0.1	0.1	0.04	0.04	0.04
ADRG_20067670				0	2.6	0
ADRG_20083310	0.3	0.3	0.3			
ASTRO20032120	1.4	1.7	0.6	1.2	0	1
ASTRO20084250	1.2	1.1	0.4	0.1	0.04	0.1
ASTRO20152140	0.1	0.9	0.4	1.6	1.8	1.6
ASTRO20166810	0.7	0.7	0.2	4.3	3.5	4.4
ASTRO20181690	1.5	1.9	0.2	1.8	2.2	0.2
BLADE20004630	3.3	2.9	2.2	0.3	0.8	0
BRACE20006400	3.6	3.5	3.6			
BRACE20019540	0.7	0	0			
BRACE20038480	0.5	0.6	0.3	0.2	0.2	0.2
BRACE20039040	2.5	2.2	2.3	0.1	0.7	1.1
BRACE20039440	0.3	0.3	0.2			
BRACE20052160	2.7	2.3	1.9	1.3	0.8	1
BRACE20053630	0.2	0.2	0	3.4	3	2.6
BRACE20057620	0	3.7	0.5	0	0	0.3
BRACE20058810	3.8	2	2.8	0.6	0	0.9
BRACE20060720	0	1.3	0	0	0	0.04
BRACE20060840	2.2	1.7	1.6	3.9	3.8	1.6
BRACE20061740	1.9	2.1	2.7			
BRACE20062640	1.9	0.2	2.4	2.3	1.2	1
BRACE20063780	0	0.1	0	0.4	0.2	0.2
BRACE20067430	2.4	0	1.7	0.04	0	0
BRACE20090440	1.1	1.8	2.2	1	0.5	1.3
BRACE20101700	3.1	1.8	1.7	0.5	0.4	1
BRACE20114780	1	1.5	0.6	1.2	0.4	0.2
BRACE20151320	0	0	0.1	0.1	0.2	0
BRACE20152870	0.6	1.3	1.5	0.4	0.3	0.3
BRACE20163150	1.5	1.7	0.9	1.4	1.4	1.7
BRACE20165830	2.6	4.9	3.3			
BRACE20201570	0	0	0	0	0	0
BRACE20210140	1.7	1.4	1	1	0.6	0.5
BRACE20223330	0.1	0	0	0	0.1	0
BRACE20224500	0.2	0	0.2	0	0	0.1
BRACE20229280	0.2	0.04	0.4	0	2.1	0
BRACE20235400	1.8	0.6	1	0.3	0.6	0.1
BRACE20266750	1.8	2.1	1	1.3	1.1	0.9
BRACE20267250				0.8	0.8	0

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
BRACE20269710	0.9	0.9	0.7	0.4	0.2	0.1
BRALZ20018340	1.1	1	0.5	0.3	0.4	0
BRALZ20058880				1	3.1	2.5
BRALZ20059500	1.7	1.5	2.3			
BRALZ20064740	1.9	2.8	1.2	8.9	0	0
BRALZ20069760	1.3	0.4	0	0.04	0.04	0.04
BRALZ20075450	1.3	0	0	0.04	0.04	0.04
BRALZ20088690	1.8	1.4	1.5	0	0	1.6
BRAMY20002770	0.8	2.4	0.3	1.2	0	0
BRAMY20004110				0.8	0	0
BRAMY20060920				0.3	11.8	12.2
BRAMY20103570	0	0.1	0.1	0.6	0	0
BRAMY20144620	0.7	0	0.9			
BRAMY20152110	1.8	1.7	1.2	2.5	2.3	0.8
BRAMY20162510	0.1	0	0	0.7	0.7	0
BRAMY20163250	3.4	4.2	2.4	2.2	1.5	0.9
BRAMY20163270	3.8	0.7	4.5			
BRAMY20168920	2.4	2.5	2.2	0.2	0.04	0.1
BRAMY20178640	1.7	1.6	1.9	0.9	1	0.5
BRAMY20184670	0.4	0.3	0.2	0.04	0.2	0.6
BRAMY20204450	3.6	3.6	1.6	0	0	0
BRAMY20210400	0.5	0.5	0.5	1	0.2	0.9
BRAMY20215230	1	0.7	1.1	1.9	0.8	1
BRAMY20218670	1.6	0	1.5	0.2	2.6	0.1
BRAMY20229800	5	3.9	0.5	1.4	4	1
BRAMY20229840	0.04	0	0.04	0.3	0	0.2
BRAMY20231720	1.1	1.3	1.6			
BRAMY20247280	3.5	2.2	1.9	2	0.7	0.5
BRAMY20261680	5.2	4	3	3.5	3.2	2.5
BRAMY20266850	0.4	4.4	6.9	2.2	2.9	2.7
BRAMY20267130				13.7	0	0
BRAMY20277140	3.3	2.5	3	0.7	0.8	0
BRAMY20280720	0	9.8	1.1			
BRAWH10000930	2.6	1.3	1.9	0	0	0
BRAWH20015350				0	0	0
BRAWH20017010	0.9	0	0	0.6	0.2	0.9
BRAWH20029630	1.9	2.4	1.8	1.4	0.2	0.04
BRAWH20100690				3.2	0.9	0.8
BRAWH20106180	0	2.7	0.5			
BRAWH20107540	2.1	1.3	0.8	1.1	1.1	0.6

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
BRAWH20110660	1.7	2.1	2.4	1.4	1.4	0.9
BRAWH20118230	0	0	0.04	2.3	0.9	1.9
BRAWH20122770	0	0	0.8			
BRAWH20126190	0.0		0	0	0	0
BRAWH20132190	2.2	2.2	1	1.8	1.5	0.4
BRAWH20138660	3.3	2.2	2.1			
BRAWH20139410	0.9	1.7	0.2	2.1	1.9	0.7
BRAWH20155950	1.5	1.8	1.5	0.9	0	0
BRAWH20158530	58.9	19.3	41.1			
BRCAN20060190				0.2	0	0.2
BRCAN20147880	0.3	0.3	0	0.5	1	1.3
BRCAN20273340	2.8	3.5	0	0.3	0.3	0.3
BRCAN20273640	0.3	0.4	0.2	0.7	0.8	0.3
BRCAN20275130	3.9	3.6	2.3	0.2	0	0
BRCAN20280210	0	0	0	0.8	0	0
BRCAN20280400	3	3.6	2.6	1.8	1.7	1
BRCOC20021550	0.7	0	0.2	0.3	0.3	0
BRCOC20037400	1.5	1	1.2	0.1	0	0.2
BRCOC2010510				3.8	1	1.5
BRHIP10001740	0.8	0.7	0.9	0.4	0	0
BRHIP20001630	0.5	0	0			
BRHIP20096170	0	0.4	0.3			
BRHIP20103090	1	1	1.3	0.9	0	0.7
BRHIP20105710	1.5	0	1.9	0.7	0.7	0.9
BRHIP20110800	1.9	2.7	2.2	0.8	0	0
BRHIP20111200	0.3	0.9	1.1			
BRHIP20118910				0	0	0
BRHIP20129720	0	0.1	0	0	0	0
BRHIP20143860	6.2	5.3	6.7	3.6	2.7	2.4
BRHIP20173150	0	0.04	0	0.9	1.6	2.8
BRHIP20175420	2.4	2.4	2.5	0.6	0	0
BRHIP20186120	1.2	2.9	0			
BRHIP20194940	0.04	0.7	0.3			
BRHIP20196410	1.7	2.6	1.8	0.9	2	1
BRHIP20207430	0	0	0.2	0	0	0.1
BRHIP20218580	1.1	1.8	0.9	1.2	0.6	0.3
BRHIP20233090	2.8	1.5	1.8	0.5	0	0.4
BRHIP20284800	2.3	1.5	1.7			
BRHIP30004880				0.04	0.2	0.04
BRSSN20046570	2.5	2	1.7	2.6	1	1.2

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ctl, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	Δ cagE
BRSSN20142940	0	0	0.04	1.2	1.3	1.2
BRSSN20152380	0.5	1	0.7	0.04	0.04	0.04
BRSSN20176820	1.2	0.5	0.04	1.5	1	1.4
BRSSN20187310				2.5	9.6	27.6
BRTHA20045390	2	2.1	2	3.2	3.2	2.4
CD34C30004240	1	1.3	1.8	2	1.7	1.3
CD34C30004940				0	2.9	0
CO_ON20043180				7.2	6.6	7.2
CTONG100C0620	0.04	0.04	0.04			
CTONG20014230	0.4	0.5	0			
CTONG20045270	0	1.9	1.6	0	0	0
CTONG20045240	1.5	0.5	0.8	0	0	0
CTONG20046750	0	0.1	0	0	0	0
CTONG201C0240	0.2	0.8	0.04	0.2	0.04	0.04
CTONG201C3480	2.7	2.9	3.7	0	0.1	0
CTONG201C5650	7.2	4.3	3.7	3.1	2.8	3.1
CTONG20121010	0	0	0	1.7	1.6	0
CTONG20128470	0.8	1	1	0.2	0.3	0.2
CTONG20138030	2.7	2.1	1.9	2.2	0.8	1.8
CTONG20139070	2.4	2.3	2.2	0.9	0.4	1.1
CTONG20146970	7	6.9	5.4	7.3	2.7	6.8
CTONG20158150	0.2	3	0.4	1.6	0	1
CTONG20186320	3.6	2.5	3.8	1.8	1.8	0.6
CTONG20265130	1.2	2.2	6.3	0.8	6	20.3
D3OST20005540	0.7	1.7	0.4	0.7	0.2	0.9
D3OST20037970	2.7	2.7	1.7	1.9	0.6	1.3
D9OST20031370	0.8	2.9	1.1	0.04	0.04	0.04
DFNES10001850				0.0		0
DFNES20031920	2.1	2.2	0.8	1.2	2.9	0.8
FCBBF10005060				0.9	0	1
FCBBF20032970	3.1	3.6	3.6	1.6	0.9	2
FCBBF20035260				0	0	0
FCBBF20054260	2	2	2.4			
FCBBF20071860	0.9	1.1	1.9	0	0	0.04
FCBBF30001840	1	1.6	1.5	2.5	0	0
FCBBF30016320	1	1.9	0.6	1.3	1.5	0.3
FCBBF30016570	2.4	1.8	1.7	0.4	0.2	0.4
FCBBF30033050	4.1	0	3.2	1	0	0.3
FCBBF30071520	2	0	1.2			
FCBBF30083820	2.9	3.5	1.4	2.2	1.6	0.5

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
FCBBF30215060				0.5	0.5	0.5
FCBBF30251420	0	2.6	0	0.3	0.1	0.6
FCBBF30252520	1	3.8	2.4	0.4	0	0
FCBBF30262360				0.0	0.04	0.04
FCBBF30266920				0.3	0.4	2
FCBBF30278630				1.3	3.6	0
FCBBF30285280	0.0		0	0	0	0
FCBBF40001420	0.3	0.7	0.3	0.1	0.7	0.1
FEBRA1C001880	0.5	0.4	0.4	0.4	0.4	0.5
FEBRA2C010120	4.2	6.4	3.5	0.7	0	0
FEBRA2C017050	0	0.8	0.8	0.04	0	0
FEBRA2C034360	0.8	0.9	0.7	0.1	0.1	0.1
FEBRA2C037260	1.2	1.4	0.9			
FEBRA2C037500	0.04	0	0.1	4.4	4	3.4
FEBRA2C082100	0.2	0.3	0.5	2.1	0.7	0.5
FEBRA2C095880	0.9	0	0.5	0.7	0.3	0.7
FEBRA2C167390	0.3	0	0	0.9	0.3	0.6
FEBRA2C175800	0.9	0	0	0.04	0	0
FEBRA2C225010	0.9	0.2	0.2	0	0	0
HCA5M100C0530	2.7	2.7	3.1	0.9	0.8	0.4
HCHON2J00226	0.1	0	0	0.8	0.6	0.9
HCHON2J008980	1.8	2.4	0.2			
HCHON2J009350	0	0	0			
HCHON2J010990				0.3	0.3	0.3
HCHON2J011160	0.04	0.2	0.04			
HCHON2J015230	2.6	2.3	2.4	1.2	1.7	0.6
HCHON2J022470	2	1.2	0.7	1.6	1.1	1.1
HCHON2J035130	1.9	2	2.4	1.3	0	2
HCHON2J043590	2.6	2.4	1.8	1.5	0.3	0.6
HCHON2J067220	1.5	2.1	2.3	2.1	0	0.9
HCHON2J076500	2.1	2.4	2.1	0	0.1	0
HEART20021840	0.6	0.4	0			
HEART20067870	0	0	0	0	0	0
HEART20083640	0.8	0.2	0.2			
HHDPC100C0650	1.4	1.4	1.1	0.7	0.4	0.3
HHDPC20034390	1.1	0.5	1.2	0.3	0.04	0.04
HHDPC20095280	0.8	0.7	0.5	0	0.5	0
HLUNG10000550	7.6	7	6.9	2.1	1.4	1
KIDNE20018970	1.5	1.2	0.9	1.4	0.9	0.9
KIDNE20028720	1.5	1.2	0			

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, cti, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; cti, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	cti	TNF_1h	TNF_3h	cti	Hp	Δ cagE
KIDNE20079440	1.4	1.8	0			
KIDNE20096470	2.1	2.6	2.3	1.3	1	0.7
KIDNE20106740	0.2	0.1	0	0	0	0
KIDNE20120090	0.2	0	0			
KIDNE20127750	1.9	0.6	0.4			
KIDNE20130450	0.9	0.9	1.3	0.1	0.8	0.4
KIDNE20132180				0.7	0	0
KIDNE20141190	0.1	0.2	0	0.4	0.3	0
KIDNE20148900	4.6	0	4.7			
KIDNE20163880	0.6	1.5	0	2.2	1.8	1.2
KIDNE20182690	0.5	0.4	3.9	2.5	3.1	3.1
LIVER10004790	1.5	3.3	1.6	0	0	0
LIVER20011130	2.4	0.8	0	0.2	1.9	0.2
LIVER20038540	0	5.1	0	1.2	4.9	0
LIVER20055440	0.5	0.5	0.4	0.3	0.1	0.1
LIVER20062510	1	1.1	1.2	0	0	0.9
LIVER20085800	0	0.8	0.5			
MAMGL10000830	5.4	4.3	0.1	0.6	0.6	0.7
MESAN20031900	0.7	0.3	0.4	0.1	0.1	0.1
MESAN20121130	2.6	2.8	2.2	0.1	0.04	0.04
MESAN20127350	1.6	0.7	0.3			
MESAN20130220	0.9	2.3	2.2			
MESAN20154010	2.6	2.2	2	2.9	2.4	2.5
MESAN20174170	0	0	0.7	0	0	0
NOVAR10001020				0.3	0.04	0.04
NT2NE20053580				0.8	0	0
NT2NE20089610	0.9	1.3	1.5	0.1	0.04	0.04
NT2NE20089970	0.7	0	0	0	0	0
NT2NE20146810				2.8	2.3	1.9
NT2NE20155110	2.5	2.6	2.9			
NT2NE20156260	1.3	1.3	1.7	0.3	0.1	1
NT2NE20158600	0.8	3.4	3			
NT2NE20172590				0	0.8	0
NT2NE20174920	1.8	1	1.1	1.4	0	0
NT2NE20181650	1	1.1	0.5	0.2	0.1	0.04
NT2RI20005750	0	0.4	0	0.6	0.04	0.8
NT2RI20009870	3	2.3	2.3	7.3	2.1	3.4
NT2RI20023160	3.5	1.1	2.8	1.7	0.4	1.8
NT2RI20040930	0.7	0.6	0.5	0.3	0.1	0.1
NT2RI20046080	1.8	1.8	1.5	1.2	0.8	0.9

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, cti, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; cti, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
NT2RI20055790	0.9	0.9	0.9	0.8	0.6	1
NT2RI20069730	2.4	2.1	1.7	2.1	1.4	1.4
NT2RI20203900	0	0	0	0	0	0
NT2RP70062230				1.8	0	1.5
NT2RP70102350	1.7	0.04	0.04			
NT2RP70110860	0	0	0.6	0	0	0
NT2RP70111320				3.2	4.4	2.8
NT2RP70130020	0	0	0	1	0	0.1
NT2RP70143480	1.2	2	1.7	0.8	1.1	0.6
NT2RP70150800				0.8	0.3	0.3
NT2RP70157890	4.6	1.1	0.3	2.2	1.8	0
NT2RP70169110	0.5	1.3	1.7	1	3.3	2.5
NT2RP70175670	0.3	0.1	1.4	4.3	3.3	3.3
NT2RP70188020	2.5	2.8	2.6	0	0	0
NT2RP70188710	0	0.1	0.2	4.3	2.8	2.9
NT2RP70190640				0.4	0.4	0.9
NTONG20029480	3.1	0.7	2.2			
NTONG20064840				1.5	1	1
NTONG20067090	2.5	2.1	2.3	0.4	0.1	0.2
NTONG20070340	0.1	0	0	6.3	1.3	0.7
NTONG20077560				0.5	0.5	0.5
NTONG20083650	2.9	2.9	2.7	2.5	2.5	1.9
NTONG20090680	2.1	2	2.4	2	1.3	1.6
OCBBF20005230	1.7	1.3	2.3	0.9	0.7	0.7
OCBBF20019380	0.6	0.6	0.5	0	0	0
OCBBF20020150	4.2	3.2	3	1	0	0.6
OCBBF20020830	2.7	2.7	1.3	4.4	2.3	2.1
OCBBF20039250	1	1.2	0.9	0.4	0.1	0.5
OCBBF20041680	1.4	0	0			
OCBBF20047570	0.04	0	0	0.3	0.2	0.6
OCBBF20051610	0	0.04	0.04	0	0	0
OCBBF20054200	0.4	0.3	0	0.04	0.04	0.04
OCBBF20061720	1.3	2	0.2	0.7	1.2	0
OCBBF20062140	3.3	3.1	5			
OCBBF20071960				0.1	0	0
OCBBF20072320	0.04	0	0.04	0.04	0.04	0.04
OCBBF20079310	0.04	0	0	0	0.04	1
OCBBF20081380	6.3	6.1	5.1	0.8	0.4	0.6
OCBBF20085200				0.1	0.5	1.3
OCBBF20094240	0.9	1.5	1.6	1.1	0.3	0

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
OC3BF20107920	2.9	2.9	2.6	2.6	0.7	0.3
OC3BF20127040	1.4	1.3	0.5	0.2	0.04	0
OC3BF20130110				3.2	2.4	1.8
OC3BF20139260	2.1	0.7	0.2			
OC3BF20164050	0.3	0.3	0.2	0.2	0	0.04
OC3BF20178990	2.1	0.7	0.2	0.9	0	0
OC3BF20180840	3.7	2.7	3.1	0.1	0.3	0.3
PEBLM10000240	2.1	2.2	1.6	0	0.3	0
PEBLM20013120	3.3	0.5	3			
PEBLM20024550	0.1	0	0	3	2.2	0.7
PEBLM20052820	1.9	2.1	2.2	1	0.6	0.8
PEBLM20074370	0.9	0.9	1.7	3.7	3.1	3
PERIC200002140	0.04	0.9	0.4	0.7	0.3	0.8
PERIC200004780	0	0.04	0.1	0.04	0	0.04
PLACE60003460	4.1	1.5	4.8	0.6	1.6	5.1
PLACE60136720	0.5	0.7	0.7	0.6	0.7	0.2
PLACE60155130	0.7	2.3	0			
PLACE60169420	1.2	1.4	1.6	0.6	0	0.8
PLACE60181070	42.3	10	28.2			
PROST10004800	3.1	3.2	1.8			
PROST20120160	0	0.6	0	0	0.3	0.9
PROST20144220	2.5	2.8	2.4	1.6	0.5	0.2
PROST20149160	0.7	0	0.4	1.6	0.6	0.6
PROST20149250	0	0.9	0.4	0	0	0
PROST20151240	1.3	0.7	0	0	1.2	0
PROST20153320	1.4	1.2	1.8	1.4	0.3	1.2
PROST20161950	0	0	0.6	2.2	1.4	1.2
PROST20189770	1.1	1.4	0.8	2.8	2.8	2.1
PUAEN20003740	3.1	0.5	2.8	1.4	0.5	2.4
PUAEN20011880	1.3	2.4	0.4	0.1	0.3	0
PUAEN20015260	0.04	0.04	7.4			
PUAEN20025680	1.9	1	2.3	3.1	0.9	1.1
PUAEN20040670	0.3	0.5	0.2	1.3	0.5	1
PUAEN20045250	1.8	1.6	1.6	1.9	1.6	1.1
PUAEN20078980	1.1	0.3	0.7	0.5	0	0.1
PUAEN20085150	2	1	2.3	1.6	1.1	0.2
SKMUS20018230	1.9	2.2	1.8	0.8	0.5	0.6
SKMUS20028210	1.6	2.7	2.2	0	0	1.3
SKMUS20031680	0.9	0	0	1.2	2.4	0.3
SKMUS20046670	0.3	0.3	0.3			

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, cti, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; cti, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	cti	TNF_1h	TNF_3h	cti	Hp	Δ cagE
SKNSH20062340				0.6	0.5	0
SKNSH20080430	1.1	2.6	0.5	0	1.3	0
SMINT20001760	1.8	1.5	0.7	0.3	0.1	0.3
SMINT20013480	1.3	2.1	0.9			
SMINT20014580	2.7	2.1	1.4	1.2	0	0.6
SMINT20033400	2.6	1.7	1.4			
SMINT20047810	2.2	0.7	0.5			
SMINT20051610	0.1	0.1	0.3	0.4	0.1	0.5
SMINT20056210				0.9	1.8	0
SMINT20060780	0.2	0.6	0.5	0.04	0.04	0.04
SMINT20080540				0	0	0
SMINT20105000				0	1.1	0.3
SMINT20108530	1.3	1.5	0	0.04	0.04	0.04
SMINT20122850	0.04	0.04	0.04	0.04	0.04	0.04
SMINT20122910				0.3	0.3	0.3
SMINT20153530	4.8	4.6	5.6	2.7	1.5	1.8
SMINT20161220	8.5	6.2	19.5	2	1.1	1
SMINT20163960	0.6	0.5	1.4	0	0	0
SMINT20164770	2.4	2.1	1.6	1.8	1.2	1
SMINT20168570	0	0	0			
SPLEN20008820	2.5	2.3	2.7	1.6	1.3	0.8
SPLEN20011410	0.4	0.4	0.1			
SPLEN20013540	1.6	0.9	1.1	2.4	1.4	1.8
SPLEN20019450	1	1.8	1.2	0.2	0.6	0.4
SPLEN20022230	4.5	6.2	3.9	1.4	1.1	1.6
SPLEN20040600	3.2	4.5	3.6	0	0	0
SPLEN20076530	0.04	0.04	0.04	0	0	0
SPLEN20101190	0.3	0.2	0.6	1.6	0	0
SPLEN20126190	2.5	3.4	2.8	5.2	3.5	3.1
SPLEN20152760	4.2	3	3.2	1.2	0.8	1.6
SPLEN20157300	0.4	0.5	2.5			
SPLEN20158990	1.9	0.9	2.6	1.1	1.1	1.3
SPLEN20163560	0.3	0.6	0.3	0	0	0
SPLEN20174260	0.4	0	0	0.3	0.1	0.1
SPLEN20211570	2.3	2.3	2.2	1	2.1	1.4
SPLEN20214580	0.04	0.6	0.9	1.4	1.3	2.6
SPLEN20245300	3.1	2.6	1.9	0.6	0	0.2
SPLEN20279950	0.8	2.1	0.3			
SPLEN20280660	0.6	0.5	1	0	0	0
SPLEN20283650	1.8	1	0.8	0.8	0	0

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
SPLEN20329240				0.2	0	0
STOMA20010250	2	0.9	1	0	0	0.7
STOMA20032890	0.9	1.5	0.4			
STOMA20048520	0.04	2	0.4	0	0.9	0
STOMA20057820	1.3	1	0	4.3	4.1	0
STOMA20062290	0.4	0.6	0.4	0.3	0.3	0.2
STOMA20076800	1.1	0.7	0.6	1.2	0.6	0.3
TESTI20001170	0	0	0	0.8	0.6	0.7
TESTI20002780				0	0	0
TESTI20004890	1.1	0.7	0.6	0	0.2	0.4
TESTI20011200	6.3	3.7	5.9	0.5	0.04	0.2
TESTI20018230	0	0	0	0.04	0.04	0.04
TESTI20035960	0.1	0	0	0.04	0.04	0.04
TESTI20038270				0	0	0
TESTI20044230	0	0	0	0.6	0.2	0.2
TESTI20046750	0.4	0.04	0.04	1	0.8	0
TESTI20060400	1.2	2	0.2	0.7	0.5	0.04
TESTI20066770	0	0	0	0.04	0.04	0.04
TESTI20076850	0	0.6	0	0.04	0.04	0.04
TESTI20083940	0.9	1.5	1.4	0	1.2	1.3
TESTI20087620	0.8	2.3	0.8	1.1	0.04	0.1
TESTI20098530				5.3	1.2	0
TESTI20105720	2.7	3.5	2.5	0.04	0.1	0.04
TESTI20108720	0.04	1.5	1.1	2.5	2.1	1.8
TESTI20123080				6	0	0
TESTI20128350				1.4	1.6	0
TESTI20136100	3.1	1.9	2.1			
TESTI20137670				0.4	0.4	0.4
TESTI20143240	0.2	0.1	0.1	0.3	0.04	0.3
TESTI20143620	0.04	0	0			
TESTI20156100	0.1	0.04	0.1			
TESTI20161970	1.2	0.7	0	1.1	0.4	1
TESTI20168480				0.5	5.7	0.5
TESTI20168960				0.5	0.5	0.5
TESTI20178160	0.04	0.04	0.04	0.04	0.04	0.04
TESTI20185810				0.9	0	0
TESTI20199170	0.7	0	0	0.9	0.8	0
TESTI20200260				0.3	0	0
TESTI20200710	3.9	2.6	2.4	2.5	3.5	2.9
TESTI20202650	0.04	0.04	0.04	1	1.2	0.3

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
TESTI20220100	0	5.7	0			
TESTI20224620				0	0	1.5
TESTI20229600	0	0	0			
TESTI20230850	0.04	0.04	0	0.04	0.04	0.04
TESTI20231920				0.5	0.5	0.5
TESTI20234140				1.8	0.3	0.3
TESTI20234270	2.6	2.8	2.9	0.5	0.04	0.3
TESTI20238000	0.2	0	0.04	0.04	0.04	0.04
TESTI20238610				0.04	0.04	0.04
TESTI20239510	0	0.2	0	0.04	0.2	1
TESTI20242990	1.8	2.1	1.8	0	0	0
TESTI20265250	2.1	1.6	1.9	1.5	0.8	0.4
TESTI20265370	0.04	0.04	0.04	0.04	0.04	0.04
TESTI20266740	0.2	0	0.7	0.04	0.04	0.04
TESTI20272390	1.3	1.2	0.8	0.2	0.2	0.4
TESTI20275030	0	0	0	0	0	0.3
TESTI20275620	1.3	0.04	0.7			
TESTI20277360	0	0	0			
TESTI20282540	0.04	0	0.1	0.2	0.04	0.3
TESTI20284880	0.4	0.2	0.1	0.04	0	0.1
TESTI20285830	0.04	0.04	0.04			
TESTI20288110				1.2	0	0
TESTI20289850	0.04	0	0	0.04	0.04	0.04
TESTI20307540				0.6	0.8	0
TESTI20308600				0.5	1.2	0.5
TESTI20311290	0	0	0	0	0	0.7
TESTI20317600	0	0	0	0.04	0.04	0.04
TESTI20319190	0.2	0	0	0.04	0.04	0.3
TESTI20332420	0.6	0.1	0.9			
TESTI20335200				0.9	1.4	0.9
TESTI20342430	0	2.8	0	0.6	0.6	0.5
TESTI20345060				0.1	0	0.04
TESTI20347300	0.9	0.6	1.4	0.04	0	0
TESTI20357960	1	1	1.7	2.7	1.3	1.7
TESTI20361140	0.04	0.04	0.04	0.2	0	0
TESTI20369220	0.04	0.04	0.04			
TESTI20369690	1.5	0	1.3	1.3	1.4	1
TESTI20370020	0.4	1.7	0.1			
TESTI20371030	1.3	1.3	1	0.8	0.5	0.5
TESTI20386230	2	0.2	0.3			

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*, ctl, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ctl	TNF_1h	TNF_3h	ctl	Hp	Δ cagE
TESTI20391210	0.6	2.3	4.9	3.1	0	2.4
TESTI20392090	0	0	0.04	0.04	0.04	0.7
TESTI20392250	9.3	7.8	3.8			
TESTI20392270	1.8	1.4	1.6	1.1	1.6	1.1
TESTI20401020	0.2	0.5	0.8	0	0	0
TESTI20401430	4.3	4.8	4.3			
TESTI20409440	1.4	0.5	0.3	0.5	0	0.3
TESTI20415640	0.8	2.5	1	0	0	0
TESTI20424000	0.2	0.04	0.04	0	0	0
TESTI20424730	1.8	0.7	2.9	3.8	0	3.3
TESTI20425070	2.3	2.4	2.6	1.9	1.4	1.2
TESTI20433130				0	0	0
TESTI20438570	0.8	0.6	0.6	0.8	0.6	1.2
TESTI20443090	0.1	0.1	0.1	0.3	0.5	0.6
TESTI20463520				0	0	0
TESTI20465520	0.6	0.6	0.5	0.2	0	0.1
TESTI20478010	0.9	1.7	0.7	0	0.3	0
TESTI20478180	0.04	0.04	0.04	0.04	0	0
THYMU20029100	1.9	1.2	2.3	2	2.9	2.5
THYMU20061700	0	0	0	0.7	0.2	0.2
THYMU20095960	2.9	2.4	0.5			
THYMU20111180	1.1	0.6	0.5	0	0	0
THYMU20118060	0.2	0	0.2	0.04	0.04	0.04
THYMU20130890	0.6	1.3	3.3			
THYMU20142040	1	1.1	0.7	1.3	1.1	1
THYMU20142970	4	3.5	3.8	1.6	2	0.6
THYMU20153160	1	0.7	1	0.1	0.1	0.04
THYMU20158250	10.4	7	5.5	1.1	0	0
THYMU20187720	3.2	3.2	2.8	2.4	2.2	2.3
THYMU20194360	1.8	2.1	1.7	0.4	0.3	1.3
THYMU20208300	1.9	1.9	1.6	0.3	0.2	0.3
THYMU20226600	3	0	1.4	1.1	0.3	2.6
THYMU20239000	2.1	2.3	2.8	1.4	0.8	1.1
THYMU20253250	1.1	0.3	0.3			
THYMU20272490	2.7	1.4	0.6	0.04	0.04	0.04
THYMU20284120	3.8	4.1	4	0.4	0.04	0.5
THYMU20286290	0	2.1	0.4	3.1	2.5	1.7
TKIDN10000010	2.2	2.2	2.5	1.2	1	1.1
TRACH20005020	0	0	0	2.8	0.9	0.5
TRACH20032720	0.1	0	0	0.6	0.04	0.1

EP 1 347 046 A1

Table 52 (continued)

Alteration of the expression level of each clone due to TNF- α stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*. ct1, TNF_1h, and TNF_3h in the column of THP-1, respectively, indicate the relative mRNA expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 1 hour, and in the cell stimulated with 10 ng/mL TNF- α for 3 hours; ct1, Hp, and Δ cagE in the column of MKN45 indicate the relative mRNA expression levels in MKN45 cultured without *Helicobacter pylori*, in the cells co-cultured with cag PAI-positive *Helicobacter pylori* (TN2) (at a ratio of MKN45 : TN2 = 1:100 cells (colonies)) for 3 hours, and in the cells co-cultured with the cagE mutant (TN2 Δ cagE) (at a ratio of MKN45 : TN2 Δ cagE = 1:100 cells (colonies)) for 3 hours, respectively. [ATAC-PCR]

Clone Name	THP-1			MKN45		
	ct1	TNF_1h	TNF_3h	ct1	Hp	Δ cagE
TRACH20041830				0.8	0.2	0.9
TRACH20060150	0.2	0.9	2			
TRACH20076760	5.1	4.9	4.5	0.6	0.5	0.4
TRACH20082780				0	0	0
TRACH20091230	0.4	0	0.2	2.1	1.1	1.2
TRACH20099340	1.8	3.8	4.9	1.9	2.5	0.9
TRACH20109650	3.5	3.3	3.5	3.7	3.7	3.4
TRACH20115740	0.04	0.04	0.04			
TRACH20134950	5.6	5	4	3.5	1.2	1.9
TRACH20135520	1	0.9	0.6	0.9	0.9	0.5
TRACH20153810	2.1	0	0			
TRACH20184490	2.2	3.2	2.8	1.6	0	0
TSTOM20001390	1.5	2.1	1.8	2.5	0.4	2.5
TSTOM20005690	1.3	0.8	1.1	0.3	0	0.1
UMVEN10001550	2.4	2.6	3.3	0.6	0	0.04
UMVEN20003540	5.2	3.9	4.9	3.1	2.4	2.8
UTERU20004240	0.04	0.2	0.1	0.04	0	0.04
UTERU20046980				0	0	0
UTERU20055930	2.5	3.6	2.9	2.3	1.6	2.5
UTERU20068990	0.04	1.3	0.04	0.1	0	0
UTERU20070810	2.7	1.9	2.4	1.9	1.3	1.1
UTERU20115740	3.1	3.2	5	2.3	1.9	0
UTERU20119060	0.8	1.9	0	1.9	0.3	1.6
UTERU20124070	2	2.7	1.8	2.8	2.1	1.8
UTERU20126880				0	2.2	0.1
UTERU20134910	2.5	2.7	2.3	2.9	1.4	1.3
UTERU20146680	0	0.1	0	0.5	0	0.04
UTERU20176130	2.9	1.3	1.6	1.9	0.6	0.8
UTERU20185230	3.1	3.2	1.8	1.6	1.1	0.6
UTERU20186740	1.9	1.4	0.7	0.04	0	0

Homology Search Result Data

[0322] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences.

[0323] In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared

[0324] Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

3NB6910001910//ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA LIGASE) (ALARS).//3.10E-20//

EP 1 347 046 A1

392aa//24%//067323
 3NB6920014080
 3NB6920014590//HOMEBOX PROTEIN DLX-6//1.00E-91//226aa//78%//Q98877
 ADIPS10000640//Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds.//1.60E-169//303aa//
 5 100%//AF222742
 ADIPS20004250//ZINC FINGER PROTEIN OZF//6.60E-27//223aa//32%//Q15072
 ADRGL10001470//CYTOCHROME P450 11B1 PRECURSOR (EC 1.14. 15.4) (CYPXIB1) (P450C11) (STEROID
 11-BETA-HYDROXYLASE).//1.60E-38//84aa//98%//P15538
 ADRGL20000640
 10 ADRGL20011190//spectrin, beta, non-erythrocytic 1 [Homo sapiens].//1.00E-36//250aa//38%//NP_003119
 ADRGL20012870
 ADRGL20013010
 ADRGL20013520
 ADRGL20018300//KINESIN LIGHT CHAIN (KLC).//1.20E-207//566aa//70%//Q07866
 15 ADRGL20018540
 ADRGL20028570//Rattus norvegicus MG87 mRNA, complete cds.//2.90E-69//250aa//53%//AF095741
 ADRGL20035850//CYTOCHROME P450 17 (EC 1.14. 99.9) (CYPXVII) (P450-C17) (STEROID 17-ALPHA-HY-
 DROXYLASE/17,20 LYASE).//7.30E-52//99aa//100%//P05093
 ADRGL20044590
 20 ADRGL20048330//Mus musculus mRNA for granuphilin-a, complete cds.//0//673aa//89%//AB025258
 ADRGL20061930//transposon-derived BusterI transposase-like protein//6.00E-65//500aa//33%//NP_067034
 ADRGL20067670
 ADRGL20068170
 ADRGL20068460
 25 ADRGL20073570
 ADRGL20076360
 ADRGL20078100//NADPH:ADRENODOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18. 1.2) (ADRENODOX-
 IN REDUCTASE) (FERREDOXIN-NADP(+) REDUCTASE).//3.10E-147//276aa//99%//P22570
 ADRGL20083310
 30 ASTRO10001650//DREBRIN E.//4.80E-293//540aa//99%//Q16643
 ASTRO20001410
 ASTRO20005330
 ASTRO20008010//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//6.00E-57//143aa//
 70%//Q03923
 35 ASTRO20012490
 ASTRO20027430//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//2. 20E-18//178aa//
 34%//Q15404
 ASTRO20032120
 ASTRO20033160//BRAIN MITOCHONDRIAL CARRIER PROTEIN-1.//2.70E-125//291aa//80%//095258
 40 ASTRO20055750//Human elastin gene, exon 1.//2.70E-293//654aa//88%//M17282
 ASTRO20058630
 ASTRO20064750//Homo sapiens BM-003 mRNA, complete cds.//6.10E-69//214aa//64%//AF208845
 ASTRO20072210//PERIAXIN.//2.10E-25//87aa//56%//Q63425
 ASTRO20084250//Ciona savignyi mRNA for PEM-3, complete cds.//3.50E-56//154aa//64%//AB001769
 45 ASTRO20100720
 ASTRO20105820//ACTIN INTERACTING PROTEIN 2.//2.60E-111//392aa//56%//P46681
 ASTRO20106150//H.sapiens mRNA for calpain-like protease.//1.80E-291//473aa//98%//Y10552
 ASTRO20108190//TUBERIN (TUBEROUS SCLEROSIS 2 PROTEIN).//5.30E-278//513aa//100%//P49815
 ASTRO20111490
 50 ASTRO20114370//Mus musculus SMAR1 mRNA, complete cds.//1.30E-213//461aa//89%//AF235503
 ASTRO20114610
 ASTRO20125520//dnaj protein [Schizosaccharomyces pombe]//7.80E-37//260aa//38%//CAB59885
 ASTRO20130500//UBIQUITIN-ACTIVATING ENZYME E1.//2.70E-157//815aa//42%//Q29504
 ASTRO20136710
 55 ASTRO20138020
 ASTRO20141350//Mus musculus mRNA for granuphilin-b, complete cds.//7.40E-12//169aa//30%//AB025259
 ASTRO20143630
 ASTRO20145760//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//1.60E-14//233aa//27%//P38584

EP 1 347 046 A1

ASTRO20152140
 ASTRO20155290
 ASTRO20166810
 ASTRO20168470//ZINC FINGER PROTEIN 135.//4.80E-103//289aa//59%//P52742
 5 ASTRO20173480
 ASTRO20181690//oocyte-specific protein P100//1.60E-70//554aa//36%//S23468
 ASTRO20190390
 BEAST20004540
 BGGI110000240
 10 BGGI110001930
 BGGI120006160//isomerase-like protein [Arabidopsis thaliana].//1.00E-52//187aa//47%//BAB00076
 BLADE20003400//ZINC FINGER PROTEIN 177.//2.50E-33//205aa//38%//Q13360
 BLADE20003890//ZINC FINGER PROTEIN 135.//1.50E-264//471aa//95%//P52742
 BLADE20004630
 15 BNGH420088500
 BRACE20003070//Rattus norvegicus neurabin mRNA, complete cds.//2.30E-40//172aa//46%//U72994
 BRACE20006400
 BRACE20011070//Mus musculus F-box protein FBX15 mRNA, partial cds.//9.60E-142//471aa//56%//AF176530
 BRACE20019540
 20 BRACE20027620//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE, INDUCIBLE (EC 3.1.2.2)
 (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (LONG CHAIN ACYL-COA HYDROLASE) (CTE-I)
 (LACH2) (ACH2).//2.70E-148//423aa//65%//088267
 BRACE20037660
 BRACE20038000//MAP kinase phosphatase [Drosophila melanogaster].//3.80E-8.3//426aa//42%//BAA89534
 25 BRACE20038470//Rattus norvegicus neurexophilin 4 (Nph4) mRNA, complete cds.//1.70E-57//109aa//98%//
 AF042714
 BRACE20038480//Human SEC14L mRNA, complete cds.//2.60E-93//179aa//99%//D67029
 BRACE20038850
 BRACE20039040
 30 BRACE20039440//Drosophila melanogaster CHARYBDE (charybde) mRNA, complete cds.//6.50E-17//142aa//
 35%//AF221109
 BRACE20039540//MHC class I chain-related gene A protein [Homo sapiens]//2.00E-116//246aa//90%//
 NP_000238
 BRACE20050900
 35 BRACE20051380
 BRACE20051690
 BRACE20052160//Xenopus laevis bicaudal-C (Bic-C) mRNA, complete cds.//2.10E-13//208aa//30%//AF224746
 BRACE20053280//Mus musculus PdZ-containing protein (PdZx) mRNA, complete cds.//5.20E-63//223aa//64%//
 AF229645
 40 BRACE20053480//Mus musculus erythroblast macrophage protein EMP mRNA, complete cds.//1.70E-133//
 145aa//97%//AF263247
 BRACE20053630//BRITTLE-1 PROTEIN PRECURSOR.//1.20E-24//208aa//31%//P29518
 BRACE20054500
 BRACE20055180
 45 BRACE20056810
 BRACE20057190//NUCLEOPLASMIN.//5.20E-42//215aa//45%//P05221
 BRACE20057420
 BRACE20057620//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BIND-
 ING PROTEIN) (EIF-4F 25 KDA SUBUNIT).//1.00E-22//60aa//73%//P48597
 50 BRACE20057730//toxin sensitivity protein KT12 homolog.//1.10E-10//173aa//26%//A64492
 BRACE20058580//Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds.//2.10E-178//358aa//96%//
 AB041533
 BRACE20058810
 BRACE20059370//PROTEIN 4.1 (BAND 4.1) (P4.1).//6.70E-52//400aa//32%//P11171
 55 BRACE20060550//ANKYRIN HOMOLOG PRECURSOR.//1.30E-14//139aa//44%//Q06527
 BRACE20060720
 BRACE20060840
 BRACE20060890//ZINC FINGER PROTEIN ZIC4 (ZINC FINGER PROTEIN OF THE CEREBELLUM 4).//4.00E-

EP 1 347 046 A1

131//264aa//87%//Q61467
 BRACE20061050
 BRACE20061740
 BRACE20062400
 5 BRACE20062640//HYPOTHETICAL 93.7 KDA PROTEIN F48E8.6 IN CHROMOSOME III.//9.10E-90//343aa//
 45%//Q09568
 BRACE20062740
 BRACE20063630
 BRACE20063780
 10 BRACE20063800
 BRACE20063930
 BRACE20064880//POLY(RC) BINDING PROTEIN 2 (PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLE-
 OPROTEIN X) (HNRNP X) (CTBP) (CBP).//1.80E-129//207aa//81%//Q61990
 BRACE20067430
 15 BRACE20068590//HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961.//2.70E-155//504aa//56%//Q9Y2G7
 BRACE20069090
 BRACE20081720
 BRACE20082950
 BRACE20090440
 20 BRACE20096200//Homo sapiens sir2-related protein type 7 (SIRT7) mRNA, complete cds.//1.00E-162//305aa//
 99%//AF233395
 BRACE20096540
 BRACE20097320
 BRACE20099570
 25 BRACE20101700
 BRACE20101710
 BRACE20106690
 BRACE20106840//Rattus norvegicus partial mRNA for CRM1 protein.//9.00E-59//120aa//100%//AJ238278
 BRACE20107530//Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, com-
 30 plete cds.//1.70E-48//108aa//91%//AF044574
 BRACE20108130//Homo sapiens RAB-like protein 2B (RABL2B) mRNA, complete cds.//1.60E-43//92aa//100%//
 AF095352
 BRACE20108880//MALEYLACETOACETATE ISOMERASE (EC 5.2.1.2) (MAAI) (GLUTATHIONE TRANS-
 FERASE ZETA 1) (EC 2.5.1.18).//5.90E-11//27aa//100%//043708
 35 BRACE20109370
 BRACE20109830
 BRACE20111830
 BRACE20114780
 BRACE20115450
 40 BRACE20115920//RHO-GTPASE-ACTIVATING PROTEIN 4 (RHO-GAP HEMATOPOIETIC PROTEIN C1) (P115)
 (KIAA0131).//9.70E-73//291aa//52%//P98171
 BRACE20116110
 BRACE20116460//ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34).//1.00E-20//
 45 48aa//100%//P30049
 BRACE20118360
 BRACE20121850
 BRACE20136240
 BRACE20141080
 BRACE20142320
 50 BRACE20142570
 BRACE20147800
 BRACE20148210
 BRACE20148240//Gsplp [Saccharomyces cerevisiae].//1.00E-05//75aa//35%//NP_013396
 BRACE20150310
 55 BRACE20151320//Drosophila melanogaster Oregon R cytoplasmic basic protein (deltex) mRNA, complete cds.//
 6.10E-35//202aa//41%//U09789
 BRACE20152870
 BRACE20153680//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//4.10E-107//209aa//

EP 1 347 046 A1

99%//AF078779
 BRACE20154120//Shb=Src homology 2 protein//2.60E-23//79aa//48%//AAB29780
 BRACE20163150
 BRACE20163350//MYELIN PO PROTEIN PRECURSOR//8.20E-08//92aa//33%//P20938
 5 BRACE20165830
 BRACE20171240
 BRACE20172980//translation initiation factor eIF3 [Schizosaccharomyces pombe]//5.60E-06//136aa//30%//
 CAB11250
 BRACE20175870
 10 BRACE20177200//RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN (RAN BINDING PROTEIN 1) (RANBP1)//
 9.90E-32//63aa//100%//P34022
 BRACE20179340
 BRACE20185680//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
 TIVATING ENZYME)//1.40E-16//94aa//40%//Q01576
 15 BRACE20188470//ATP-binding cassette, sub-family A member 8//1.70E-115//457aa//50%//NP_009099
 BRACE20190040
 BRACE20190440
 BRACE20192440//TRANSLATION INITIATION FACTOR IF-3//1.20E-09//161aa//26%//P47438
 BRACE20195100
 20 BRACE20201570
 BRACE20210140
 BRACE20220300
 BRACE20223280
 BRACE20223330
 25 BRACE20224480
 BRACE20224500
 BRACE20228480
 BRACE20229280
 BRACE20230700
 30 BRACE20232840//ATP-binding cassette, sub-family E, member 1//0//560aa//75%//NP_002931
 BRACE20235400
 BRACE20237270//Human WW domain binding protein-2 mRNA, complete cds//6.10E-21//50aa//88%//U79458
 BRACE20238000
 BRACE20240740
 35 BRACE20248260//H. sapiens PR264 mRNA//1.50E-13//78aa//48%//X62447
 BRACE20253160//putative trna-splicing endonuclease subunit [Schizosaccharomyces pombe]//1.10E-11//
 148aa//32%//CAA21061
 BRACE20253330//Homo sapiens Na+/H+ exchange regulatory co-factor (NHERF) mRNA, complete cds//5.50E-
 18//157aa//99%//AF036241
 40 BRACE20257100//transcription factor (SMIF gene)//2.00E-37//110aa//94%//NP_060873
 BRACE20262930
 BRACE20262940
 BRACE20266750
 BRACE20267250
 45 BRACE20269200
 BRACE20269710
 BRACE20273890//Human phosphotyrosine independent ligand p62B B-cell isoform for the Lck SH2 domain mR-
 NA partial cds//5.70E-25//100aa//65%//U46752
 BRACE20274080
 50 BRACE20276430//Homo sapiens retinoblastoma-associated protein RAP140 mRNA, complete cds//4.70E-106//
 203aa//100%//AF180425
 BRACE20283920
 BRACE20284100//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//7.20E-121//237aa//100%//
 AF022728
 55 BRACE20286360
 BRACE20287410
 BRALZ20013500//Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds//3.30E-06//122aa//
 32%//AF043498

EP 1 347 046 A1

BRALZ20014450
 BRALZ20017430//H.sapiens mRNA for protein phosphatase 5.//1.70E-41//99aa//87%//X89416
 BRALZ20018340//H.sapiens mRNA for glutamine transaminase K.//4.70E-93//114aa//98%//X82224
 BRALZ20019660
 5 BRALZ20054710//Mus musculus mRNA for cysteine and histidine-rich protein (Chrp gene).//1.70E-163//280aa//
 99%//AJ251516
 BRALZ20058880
 BRALZ20059500
 BRALZ20064740
 10 BRALZ20065600
 BRALZ20069760
 BRALZ20073760//MONOCYTE TO MACROPHAGE DIFFERENTIATION PROTEIN.//8.40E-41//76aa//69%//
 Q15546
 BRALZ20075450
 15 BRALZ20075760
 BRALZ20077900//anaphase-promoting complex 1; meiotic checkpoint regulator//3.00E-91//190aa//92%//
 NP_073153
 BRALZ20077930//Xenopus laevis 4g2 mRNA, complete cds.//1.20E-191//501aa//71%//AF182319
 BRALZ20080310
 20 BRALZ20088690
 BRAMY10001300//Homo sapiens MAGE-E1b mRNA, complete cds.//5.40E-78//140aa//97%//AB040528
 BRAMY10001570
 BRAMY20000520//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
 C2).//7.10E-70//293aa//53%//P07910
 25 BRAMY20000860
 BRAMY20002770
 BRAMY20004110
 BRAMY20011140
 BRAMY20025840//H.sapiens mRNA from TYL gene.//7.10E-103//198aa//98%//X99688
 30 BRAMY20039260
 BRAMY20045240
 BRAMY20054880//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.//1.40E-43//155aa//59%//AF102129
 BRAMY20060920//reduced in osteosclerosis transporter//1.50E-09//60aa//53%//NP_112471
 BRAMY20063970
 35 BRAMY20071850
 BRAMY20102080
 BRAMY20103570
 BRAMY20104640//Mus musculus mRNA for serine/threonine protein kinase.//1.80E-140//345aa//75%//AJ250840
 BRAMY20110640
 40 BRAMY20111960
 BRAMY20112800
 BRAMY20116790
 BRAMY20120910//GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (AES-VAES-2).//1.60E-
 97//188aa//100%//Q08117
 45 BRAMY20121190
 BRAMY20121620//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.80E-256//500aa//85%//
 AF055666
 BRAMY20124260//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//2.80E-286//
 55 554aa//92%//U87306
 BRAMY20134140//ATPase, H⁺ transporting, lysosomal (vacuolar proton pump) 9kD//4.60E-29//52aa//59%//
 NP_003936
 BRAMY20135900//CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN.//2.00E-07//146aa//23%//P55060
 BRAMY20136210
 BRAMY20137560
 55 BRAMY20144620
 BRAMY20147540
 BRAMY20148130
 BRAMY20152110

EP 1 347 046 A1

BRAMY20153110//TRYPTOPHAN 5-MONOOXYGENASE (EC 1.14.16.4) (TRYPTOPHAN 5-HYDROXYLASE)//
8.50E-58//201aa//58%//Q92142
BRAMY20157820//PUTATIVE KINESIN-LIKE PROTEIN C2F12.13.//1.10E-90//341aa//50%//O14343
BRAMY20160700
5 BRAMY20162510//MELANOMA-ASSOCIATED ANTIGEN B2 (MAGE-B2 ANTIGEN) (DAM6)//1.30E-33//209aa//
35%//O15479
BRAMY20163250
BRAMY20163270
BRAMY20167060
10 BRAMY20167710
BRAMY20168920
BRAMY20170140
BRAMY20174550//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochon-
drial protein, complete cds.//0//648aa//98%//AF047690
15 BRAMY20178640
BRAMY20181220
BRAMY20182730
BRAMY20183080
BRAMY20184670//Homo sapiens mRNA for ALEX1, complete cds.//6.40E-14//139aa//27%//AB039670
20 BRAMY20195090
BRAMY20196000
BRAMY20204450
BRAMY20205740
BRAMY20210400//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP150
25 mRNA, complete cds.//2.80E-16//141aa//39%//AF117756
BRAMY20211390//seven in absentia (Drosophila) homolog 1 [Homo sapiens]//3.70E-156//282aa//99%//
NP_003022
BRAMY20211420//Homo sapiens mRNA for LAK-4p, complete cds.//3.00E-31//224aa//33%//AB002405
BRAMY20213100//Xenopus laevis Mi-2 histone deacetylase complex protein 66 mRNA, complete cds.//2.10E-
30 66//394aa//44%//AF171099
BRAMY20215230
BRAMY20217460//Homo sapiens cardiac voltage gated potassium channel modulatory subunit mRNA, complete
cds, alternatively spliced.//3.70E-81//158aa//98%//AF295530
BRAMY20218250//putative four repeat ion channel [Rattus norvegicus]//0//588aa//99%//AF078779
35 BRAMY20218670
BRAMY20229800
BRAMY20229840
BRAMY20230600
BRAMY20231720
40 BRAMY20240040//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds.//3.20E-
301//642aa//90%//AF042800
BRAMY20242470//CORONIN-LIKE PROTEIN P57 (CORONIN 1A) //1.60E-70//210aa//66%//P31146
BRAMY20245300//Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA, complete
cds.//0//737aa//99%//AF304370
45 BRAMY20247110//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, com-
plete cds.//6.00E-117//366aa//63%//AF127084
BRAMY20247280
BRAMY20248490
BRAMY20250240
50 BRAMY20250320
BRAMY20252180
BRAMY20252720//Homo sapiens mRNA for thioredoxin reductase II alpha, partial cds.//1.60E-84//161aa//99%//
AB019694
BRAMY20260910//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//811aa//
55 99%//AF125158
BRAMY20261680
BRAMY20266850//Homo sapiens oxidation protection protein (OXR1) mRNA, complete cds. //4. 50E-57//193aa//
56%//AF309387

EP 1 347 046 A1

BRAMY20267130
 BRAMY20268990
 BRAMY20270730//Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and
 vasotocin genes, complete cds.//7.80E-155//398aa//66%/U90880
 5 BRAMY20271400//RHO-GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHOGEF) (RIP2).//0//946aa//80%/P97433
 BRAMY20273960
 BRAMY20277140
 BRAMY20277170//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.2 (KSHIIIA).//1.00E-290//538aa//
 10 97%/P22462
 BRAMY20280720
 BRAMY20284910
 BRAMY20285160//COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN].//1.90E-79//148aa//
 15 100%/P01024
 BRAMY20285930
 BRAMY20286820
 BRAWH10000930
 BRAWH20002320//Manduca sexta death-associated small cytoplasmic leucine-rich protein SCLP mRNA, com-
 plete cds.//3.50E-18//167aa//31%/AF250910 BRAWH20004600//Mus musculus mRNA for NAKAP95, complete
 20 cds.//8.40E-184//336aa//84%/AB028921
 BRAWH20011710//cytoplasmic linker 2//1.60E-96//316aa//59%/NP_034120 BRAWH20012390//Trichomonas
 vaginalis mRNA for centrin (cel gene).//4.70E-14//153aa//28%/AJ249457
 BRAWH20012410
 BRAWH20014920
 25 BRAWH20015350
 BRAWH20015890
 BRAWH20016620//Homo sapiens mRNA for MOK protein kinase, complete cds.//3.40E-82//160aa//99%/ARC22594
 BRAWH20016660
 30 BRAWH20016860
 BRAWH20017010//Homo sapiens testes development-related NYD-SP22 mRNA, complete cds. //1.00E-23//
 56aa//92%/AF367474
 BRAWH20018730//HYPOTHETICAL 56.4 KDA PROTEIN IN SRS2-SIP4 INTERGENIC REGION.//1.90E-46//
 503aa//31%/P47026
 35 BRAWH20028110//Homo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//9.40E-
 168//476aa//61%/AF005654
 BRAWH20029630//Homo sapiens bet3 (BET3) mRNA, complete cds.//2.40E-47//96aa//100%/AF041432
 BRAWH20030250
 BRAWH20064050//FIBULIN-1, ISOFORM C PRECURSOR.//6.30E-42//337aa//33%/P23144
 40 BRAWH20075700//ZINC FINGER PROTEIN ZFP-1 (MKR1 PROTEIN).//1.60E-159//332aa//84%/P08042
 BRAWH20096780//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.00E-140//514aa//52%/Q99676
 BRAWH20100690
 BRAWH20101360
 BRAWH20103180
 45 BRAWH20103290//GUANINE NUCLEOTIDE EXCHANGE FACTOR DBS (DBL'S BIG SISTER) (MCF2 TRANS-
 FORMING SEQUENCE-LIKE PROTEIN) (KIAA0362) (FRAGMENT).//0//756aa//99%/O15068
 BRAWH20105840//HYPOTHETICAL 27.0 KDA PROTEIN IN SPO0A-MMGA INTERGENIC REGION.//1.70E-21//
 156aa//32%/P54527
 BRAWH20106180
 50 BRAWH20107540
 BRAWH20110660
 BRAWH20110790
 BRAWH20110960//Homo sapiens mRNA for 26S proteasome subunit p40.5, complete cds.//1.50E-175//378aa//
 90%/AB009398
 55 BRAWH20111550
 BRAWH20112940//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDPACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE,N-ACETYL GALACTOSAM-
 INYLTRANSFERASE) (GALNAC-T1).//1.10E-59//369aa//36%/Q07537

EP 1 347 046 A1

BRAWH20113430//COLD-INDUCIBLE RNA-BINDING PROTEIN (GLYCINE-RICH RNA-BINDING PROTEIN CIRP) (A18 HNRNP) //9.30E-52//104aa//96%//Q14011
 BRAWH20114000//GLUTAMATE DEHYDROGENASE 1 PRECURSOR (EC 1.4.1.3) (GDH) //5.90E-233//426aa//98%//P00367
 5 BRAWH20117950//LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (PROLINE-BETA-NAPHTHYLAM-
 IDASE) //1.80E-78//364aa//42%//Q29550
 BRAWH20118230//BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
 (OP-1) //7.60E-74//85aa//98%//P18075
 10 BRAWH20121640//transporter protein; system N1 Na+ and H+-coupled glutamine transporter//1.00E-106//
 450aa//61%//NP_006832
 BRAWH20122580
 BRAWH20122770
 BRAWH20125380//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS) //6.40E-15//121aa//35%//
 Q57695
 15 BRAWH20126190
 BRAWH20126980
 BRAWH20128270//BH3 INTERACTING DOMAIN DEATH AGONIST (BID) //2.70E-100//195aa//99%//P55957
 BRAWH20132190//Homo sapiens putative N-acetyltransferase Camello 2 (CML2) mRNA, complete cds.//1.80E-
 17//110aa//44%//AF185571
 20 BRAWH20137480//actin binding LIM protein 1//2.80E-70//181aa//55%//NP_006710
 BRAWH20138660//Homo sapiens stonin 2 mRNA, complete cds.//1.50E-171//322aa//99%//AP255309
 BRAWH20139410
 BRAWH20142340
 BRAWH20147290
 25 BRAWH20149340//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP) (P140 RAS-GRF) //4.10E-129//
 290aa//83%//P28818
 BRAWH20155950
 BRAWH20158530
 BRAWH20160280
 30 BRAWH20162690
 BRAWH20164460//TAT-BINDING HOMOLOG 7 //1.60E-96//366aa//54%//P54816
 BRAWH20166790
 BRAWH20171030//Homo sapiens putative helicase RUVBL mRNA, complete cds.//2.80E-209//324aa//100%//
 AF218313
 35 BRAWH20173050
 BRAWH20182060
 BRAWH20185060
 BRCAN10001490//chromobox homolog 6//2.10E-40//82aa//100%//NP_055107
 BRCAN20003460//outer arm dynein intermediate chain 1//5.60E-57//159aa//49%//T02761
 40 BRCAN20006200
 BRCAN20006390
 BRCAN20054490//Sus scrofa mRNA for 54 kDa vacuolar H(+)-ATPase subunit, beta isoform.//1.00E-117//229aa//
 96%//AJ223758
 45 BRCAN20060190
 BRCAN20064010
 BRCAN20071190//FAF1 PROTEIN (FAS-ASSOCIATED FACTOR 1) //4.00E-225//433aa//96%//P54731
 BRCAN20091560//Xenopus laevis mRNA for Nfrl, complete cds.//1.20E-256//605aa//77%//D86491
 BRCAN20103740//P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RE-
 CEPTOR) //2.20E-18//60aa//78%//Q99572
 50 BRCAN20124080
 BRCAN20126130
 BRCAN20143700
 BRCAN20147880
 BRCAN20216690
 55 BRCAN20224720//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO) //4.40E-132//254aa//100%//
 P50336
 BRCAN20237240
 BRCAN20263400

EP 1 347 046 A1

BRCAN20273100
 BRCAN20273340
 BRCAN20273550
 BRCAN20273640//lymphocyte specific formin related protein//3.00E-80//350aa//56%//NP_062653
 5 BRCAN20275130
 BRCAN20279700//Homo sapiens copine I mRNA, complete cds.//2.10E-32//82aa//68%//U83246
 BRCAN20280210//H.sapiens HZF10 mRNA for zinc finger protein.//3.30E-54//219aa//49%//X78933
 BRCAN20280360//Homo sapiens phosphatidic acid phosphohydrolase type-2c mRNA, complete cds.//8.20E-22//
 213aa//28%//AF047760
 10 BRCAN20280400
 BRCAN20283190//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.20E-131//235aa//
 99%//014646
 BRCAN20283380//Mus musculus mRNA for serine hydrolase protein, isoform 2 (serh1 gene).//6.50E-45//103aa//
 80%//AJ245737
 15 BRCAN20284600
 BRCAN20285450
 BRCOC10000870
 BRCOC20001860//Homo sapiens endoplasmic reticulum alpha-mannosidase I mRNA, complete cds.//6.30E-
 154//282aa//99%//AF145732
 20 BRCOC20004040//Rattus norvegicus sphingosine 1-phosphate receptor Edg-8 (Edg-8) mRNA, complete cds.//
 4.80E-108//265aa//81%//AP233649.
 BRCOC20004870
 BRCOC20006370//PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR (C210RF3).//4.00E-67//
 144aa//88%//P53801
 25 BRCOC20008160//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//4.20E-155//777aa//
 40%//AB029290
 BRCOC20008500//Human ras inhibitor mRNA, 3' end.//4.60E-229//428aa//100%//M37190
 BRCOC20020850
 BRCOC20021550//Rattus norvegicus mRNA for Nadrin. complete cds.//1.90E-56//247aa//55%//AB042827
 30 BRCOC20023230
 BRCOC20026640
 BRCOC20027510//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//2.20E-18//178aa//
 34%//Q15404
 BRCOC20031000
 35 BRCOC20031250//TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM).//7.10E-38//92aa//82%//P48500
 BRCOC20031870
 BRCOC20035130//14-3-3 PROTEIN EPSILON (MITOCHONDRIAL IMPORT STIMULATION FACTOR L SUBU-
 NIT) (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1) (14-3-3E).//1.00E-29//71aa//88%//P42655
 BRCOC20037320//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.00E-75//
 40 937aa//26%//060100
 BRCOC20037400
 BRCOC20041750
 BRCOC20055420//GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE 2 (EC 2.3.1.97) (PEPTIDE N-
 MYRISTOYLTRANSFERASE 2) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE 2) (NMT 2).//
 45 7.90E-229//421aa//99%//060551
 BRCOC20059510//B. taurus myosin IB mRNA, complete CDS.//1.40E-29//117aa//53%//Z22852
 BRCOC20074760//CDC4-LIKE PROTEIN (FRAGMENT).//4.50E-90//366aa//48%//P50851
 BRCOC20077690
 BRCOC20078640
 50 BRCOC20090520
 BRCOC20091960//CDC42-binding protein kinase beta (DMPK-like) [Homo sapiens]//1.50E-71//140aa//100%//
 NP_006026
 BRCOC20093800
 BRCOC20099370//Homo sapiens SPG protein (SPG) mRNA, complete cds.//0//576aa//97%//AF302154
 55 BRCOC20101230//7.40E-32//227aa//35%//
 BRCOC20105100
 BRCOC20107300//Homo sapiens GTT1 mRNA, complete cds.//3.60E-44//90aa//98%//AF270647
 BRCOC20110100

EP 1 347 046 A1

BRCOC20114180
 BRCOC20117690
 BRCOC20119960
 BRCOC20121720
 5 BRCOC20122290
 BRCOC20128130
 BRCOC20134480
 BRCOC20135730
 BRCOC20136750
 10 BRCOC20144000//DNA REPAIR PROTEIN RAD8.//5.50E-14//111aa//36%//P36607
 BRCOC20147480
 BRCOC20148330
 BRCOC20155970
 BRCOC20158240
 15 BRCOC20176520//Rattus norvegicus mRNA for type II brain 4.1, complete cds.//2.30E-127//269aa//79%//
 AB032827
 BRCOC20178270//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.90E-101//272aa//64%//
 P51522
 BRCOC20178560//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//9.50E-130//
 20 247aa//85%//P48059
 BRHIP10001290//Homo sapiens GalNAc-T9 mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltrans-
 ferase, complete cds.//1.10E-108//299aa//63%//AB040672
 BRHIP10001740
 BRHIP20000870
 25 BRHIP20001630
 BRHIP20003120//Homo sapiens reticulon gene family protein (RTN3) mRNA, complete cds.//2.20E-92//190aa//
 98%//AF059524
 BRHIP20005340//GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID
 DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR).//2.10E-157//407aa//77%//Q16666
 30 BRHIP20005530//UBIQUITIN-ACTIVATING ENZYME E1 1.//1.00E-59//318aa//41%//Q02053
 BRHIP20096170//Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds.//9.70E-
 35//174aa//39%//AF084523
 BRHIP20096850//ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE)
 (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).//1.60E-166//423aa//69%//P25409
 35 BRHIP20103090//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45
 SUBUNIT).//2.00E-12//82aa//47%//P40682
 BRHIP20104440
 BRHIP20105710
 BRHIP20106100//GAR2 PROTEIN.//1.50E-19//199aa//31%//P41891
 40 BRHIP20107440
 BRHIP20110800
 BRHIP20111200
 BRHIP20115080//DYNAMIN 2 (DYNAMIN UDNM).//4.80E-63//123aa//95%//P39054
 BRHIP20115760
 45 BRHIP20118380
 BRHIP20118910
 BRHIP20119330//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//6.80E-207//651aa//
 54%//Q05481
 BRHIP20121410
 50 BRHIP20123140
 BRHIP20129720
 BRHIP20132860//Homo sapiens rhophilin-like protein mRNA, complete cds.//5.40E-144//298aa//93%//AF268032
 BRHIP20135100
 BRHIP20137230//Homo sapiens mRNA for paralemin.//1.70E-37//352aa//35%//Y16278
 55 BRHIP20139720
 BRHIP20140630
 BRHIP20142850
 BRHIP20143730

EP 1 347 046 A1

BRHIP20143860
 BRHIP20149540
 BRHIP20153560
 BRHIP20153600//Xenopus laevis RRM-containing protein SEB-4 mRNA, complete cds.//1.50E-72//148aa//93%//
 5 AF223427
 BRHIP20167880//Mus musculus left-right dynein (Lrd) mRNA, complete cds.//8.10E-22//119aa//54%//AF183144
 BRHIP20169680
 BRHIP20169900
 BRHIP20170100
 10 BRHIP20173150
 BRHIP20174040//CGMP-DEPENDENT 3', 5' -CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CYCLIC GMP
 STIMULATED PHOSPHODIESTERASE) (CGS-PDE).//0//857aa//99%//000408 BRHIP20175420//Mus musculus
 partial mRNA for stretch responsive protein 278 (sr278 gene).//6.60E-36//170aa//50%//AJ250191
 BRHIP20176420//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
 15 C2).//9.30E-68//292aa//52%//P07910
 BRHIP20179200
 BRHIP20180140
 BRHIP20183690
 BRHIP20186120
 20 BRHIP20186500
 BRHIP20189980//FLAGELLAR WD-REPEAT PROTEIN PF20.//2.90E-41//210aa//46%//P93107
 BRHIP20190070
 BRHIP20191490//interferon, alpha-inducible protein 27//2.60E-36//92aa//95%//NP_005523
 BRHIP20191770
 25 BRHIP20191860//TRANSCRIPTION FACTOR 4 (IMMUNOGLOBULIN TRANSCRIPTION FACTOR 2) (ITF-2)
 (SL3-3 ENHANCER FACTOR 2) (SEF-2).//0//569aa//99%//P15884
 BRHIP20194940//Homo sapiens A-kinase anchoring protein 220 mRNA, complete cds.//1.30E-23//190aa//37%//
 AF176555
 BRHIP20195890//FORKHEAD BOX PROTEIN D2 (FORKHEAD-RELATED PROTEIN FKHL17) (FORKHEAD-
 30 RELATED TRANSCRIPTION FACTOR 9) (FREAC-9).//9.10E-07//104aa//31%//060548
 BRHIP20196410
 BRHIP20198190
 BRHIP20205090
 BRHIP20207430
 35 BRHIP20207990
 BRHIP20208270
 BRHIP20208420
 BRHIP20208590
 BRHIP20214950
 40 BRHIP20217620
 BRHIP20218580//Mus musculus betaPix-b mRNA, complete cds.//5.10E-100//196aa//94%//AF247654
 BRHIP20222280//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.70E-217//505aa//
 75%//Q03923
 BRHIP20227080
 45 BRHIP20230710
 BRHIP20232290
 BRHIP20233090
 BRHIP20234380
 BRHIP20236950
 50 BRHIP20238600//WD-REPEAT PROTEIN SAZD.//3.30E-95//182aa//99%//Q12788
 BRHIP20238690
 BRHIP20238880
 BRHIP20240460
 BRHIP20243470//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PRO-
 55 TEIN) (35 KDA LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN).
 (LECTIN L-29).//1.10E-16//114aa//42%//P38486
 BRHIP20249110//hexokinase 1//0//912aa//71%//NP_000179
 BRHIP20252450//Mus musculus Syne-1B mRNA, partial cds.//1.40E-159//980aa//33%//AF281870

EP 1 347 046 A1

BRHIP20253660//Rattus norvegicus mRNA for Proline Rich Synapse Associated Protein 1A (ProSAP1A gene).//
1.90E-120//239aa//92%//AJ249562
BRHIP20254480
BRHIP20277620
5 BRHIP20283030//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//1.40E-88//
881aa//29%//P33450
BRHIP20284800
BRHIP20285830//TYPE III INTERMEDIATE FILAMENT.//8.20E-10//88aa//35%//P23729
BRHIP20285930//Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.//3.30E-08//104aa//32%//
10 AF029213
BRHIP30001110
BRHIP30004570//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//3.60E-32//281aa//31%//
Q01102
15 BRHIP30004880//H.sapiens mRNA for titin protein (clone hh1-hh54).//9.60E-85//812aa//26%//X90568
BRHSSN1C000920
BRSSN2C003120//METABOTROPIC GLUTAMATE RECEPTOR PRECURSOR.//7.00E-08//257aa//22%//P91685
BRSSN2C006340
BRSSN2C013420//histone deacetylase 6 [Homo sapiens] //0//811aa//99%//NP_006035
20 BRSSN2C014260//RIBONUCLE INHIBITOR//1.70E-10//195aa//29%//P29315
BRSSN2C015030
BRSSN2C015790//ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC).//9.00E-102//352aa//53%//P00860
BRSSN2C018690//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.30E-41//88aa//100%//AF155103
BRSSN2C021600//RING CANAL PROTEIN (KELCH PROTEIN).//3.60E-59//510aa//31%//Q04652
25 BRSSN2C023570
BRSSN2C033200//RAL GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR-LIKE 2 (RALGDS-LIKE FAC-
TOR) (RAS-ASSOCIATED PROTEIN RAB2L).//3.90E-18//458aa//25%//O15211
BRSSN2C033410
BRSSN2C039370//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.
30 16).//2.50E-38//94aa//52%//P17097
BRSSN2C043040
BRSSN2C046570
BRSSN2C046790//ZINC FINGER PROTEIN 135.//8.60E-81//231aa//60%//P52742
BRSSN2C046860
35 BRSSN2C066110//Homo sapiens mRNA for mucolipidin, short form (ML4 gene).//1.70E-26//121aa//49%//
AJ293659
BRSSN2C097020
BRSSN2C101100//GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) (AES-1/AES-2).//2.50E-
10//70aa//51%//Q08117
40 BRSSN2C105870
BRSSN2C105960
BRSSN2C108300
BRSSN2C117990
BRSSN2C120810//SERINE PROTEASE HEPsin (EC 3.4.21.-) (TRANSMEMBRANE PROTEASE, SERINE 1).//
45 9.80E-144//254aa//100%//P05981
BRSSN2C121030
BRSSN2C137020
BRSSN2C142940
BRSSN2C146100//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (ADENYLATE CYCLASE TYPE III)
50 (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
CYCLASE).//0//389aa//90%//P21932
BRSSN2C151990
BRSSN2C152380
BRSSN2C159070
55 BRSSN2C159820
BRSSN2C169050
BRSSN2C176820//Mus musculus p300 transcriptional cofactor JMY mRNA, complete cds.//8.50E-297//640aa//
89%//AF201390

EP 1 347 046 A1

BRSSN20177570
 BRSSN20187310//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2)//3.20E-
 26//306aa//30%//P16157
 BRSTN10000830
 BRSTN20000580
 BRSTN20002200
 BRSTN20005360//TRANSLATION INITIATION FACTOR IF-2//1.20E-07//205aa//26%//060841
 BRTHA20000570
 BRTHA20004740//HYPOTHETICAL 41.6 KDA PROTEIN IN IMP1-HLJ1 INTERGENIC REGION (RF1095)//
 1.60E-16//310aa//27%//P28625
 BRTHA20046290//NOVEL ANTIGEN 2 (NAG-2) (TSPAN-4)//7.30E-84//153aa//100%//014817
 BRTHA20046390
 BRTHA20046420
 CD34C30001250
 CD34C30003140
 CD34C30004240//H. sapiens graf gene//1.10E-140//270aa//100%//Y10388
 CD34C30004940
 COLON10001350//IG ALPHA-1 CHAIN C REGION//1.70E-196//353aa//99%//P01876
 COLON20043180
 COLON20093370
 CTONG10000100//GUFA PROTEIN//2.10E-31//156aa//45%//Q06916
 CTONG10000220//Mus musculus cerebellar postnatal development protein-1 (Cpd1) mRNA, partial cds//1.80E-
 101//220aa//90%//U89345
 CTONG10000620
 CTONG10000930
 CTONG10000940//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4
 INHIBITOR C) (P18-INK4C)//7.20E-13//131aa//35%//Q60772
 CTONG10001650
 CTONG10002770//PLECTIN//12.00E-49//284aa//28%//P30427
 CTONG20002180
 CTONG20004690//CYTOCHROME B561 (CYTOCHROME B-561)//2.80E-50//101aa//100%//P49447
 CTONG20009770//26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE
 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN)//0//908aa//99%//Q13200
 CTONG20014280//Xenopus laevis fizzly mRNA, complete cds//2.00E-82//479aa//38%//AF034578
 CTONG20027090
 CTONG20028410
 CTONG20038890
 CTONG20049410
 CTONG20050280//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//8.00E-149//490aa//55%//P16415
 CTONG20052650//BYSTIN//5.10E-60//120aa//99%//Q13895
 CTONG20052900//FASCIN (ACTIN BUNDLING PROTEIN)//7.30E-257//437aa//98%//Q16658
 CTONG20075860//Homo sapiens mRNA for SPIN protein//3.90E-123//204aa//69%//Y14946
 CTONG20076130//ZINC FINGER PROTEIN 185 (LIM-DOMAIN PROTEIN ZNF185) (P1-A)//1.10E-158//327aa//
 89%//015231
 CTONG20077790
 CTONG20082690
 CTONG20085950//ZINC FINGER PROTEIN 191//5.80E-91//346aa//53%//014754
 CTONG20091080//HOMEBOX PROTEIN DLX-1//1.00E-54//134aa//84%//Q64317
 CTONG20091320
 CTONG20092570//Rattus norvegicus neural membrane protein 35 mRNA, complete cds//1.00E-55//300aa//
 49%//AF044201
 CTONG20092580
 CTONG20092680//Rattus norvegicus protein associating with small stress protein PASS1 (Pass1) mRNA, com-
 plete cds//1.40E-11//98aa//40%//AF168362
 CTONG20092700//Mus musculus transcriptional repressor RP58 (rp58) mRNA, complete cds//6.60E-18//162aa//
 35%//AF140224
 CTONG20093950//Mus musculus zfh-4 mRNA for zinc-finger homeodomain protein 4, complete cds//0//473aa//
 90%//AB024499

EP 1 347 046 A1

CTONG20095270
 CTONG20095290
 CTONG20095340//PROBABLE CATION-TRANSPORTING ATPASE WO8D2.5 IN CHROMOSOME IV (EC
 3.6.1.-)//3. 90E-134//500aa//37%//Q27533
 5 CTONG20096430
 CTONG20096750
 CTONG20097660
 CTONG20098440
 CTONG20099380
 10 CTONG20099550//TRICHOHYALIN//4.20E-16//534aa//25%//Q07283
 CTONG20099630
 CTONG20100240//Mus musculus radial spokehead-L protein (Rshl1) mRNA, complete cds. //1.60E-185//520aa//
 63%//AF329192
 CTONG20101480
 15 CTONG20103480
 CTONG20105080
 CTONG20105660
 CTONG20106230
 CTONG20106520//THREONINE SYNTHASE (EC 4.2.99.2)//6.70E-77//347aa//40%//Q42598
 20 CTONG20108210
 CTONG20114290//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT)//1.30E-75//
 937aa//27%//060100
 CTONG20114740//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//1.70E-37//72aa//100%//AF155114
 CTONG20118150//HYPOTHETICAL 100.6 KDA TRP-ASP REPEATS CONTAINING PROTEIN C1672.07 IN
 25 CHROMOSOME III.//2.10E-150//910aa//36%//014053
 CTONG20118250//CARBONIC ANHYDRASE (EC 4.2.1.1) (CARBONATE DEHYDRATASE)//3.30E-88//257aa//
 62%//Q92051
 CTONG20119200//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//1.00E-18//41aa//100%//AF155114
 CTONG20120770
 30 CTONG20121010//ZINC FINGER PROTEIN 29 (ZFP-29)//7.80E-131//380aa//58%//Q07230
 CTONG20121580//KINESIN-LIKE PROTEIN KIF1A.//3.50E-148//395aa//59%//P33173
 CTONG20124010
 CTONG20124220//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULA-
 TORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1)//0//691aa//98%//P36956
 35 CTONG20124470
 CTONG20124730
 CTONG20125540//PTB-ASSOCIATED SPLICING FACTOR (PSF)//6.90E-07//144aa//29%//P23246
 CTONG20125640//60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)//7.50E-137//306aa//89%//P05388
 CTONG20126070
 40 CTONG20127450//H.sapiens mRNA for Ndr protein kinase.//4.50E-11//37aa//89%//Z35102
 CTONG20128430//Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds. //8. 40E-127//
 616aa//40%//U83115
 CTONG20128470
 CTONG20129960//Mus musculus F-box protein FBX18 mRNA, partial cds.//0//905aa//92%//AF184275
 45 CTONG20131490
 CTONG20131560//NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK (DESMOYOKIN)
 (FRAGMENTS)//0//632aa//99%//Q09666
 CTONG20132220
 CTONG20133390//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
 50 CTONG20133480
 CTONG20133520//ZINC FINGER PROTEIN 228.//1.50E-163//670aa//50%//Q9UJU3
 CTONG20136300
 CTONG20138030
 CTONG20139070
 55 CTONG20139340
 CTONG20139860//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.//
 3.50E-17//162aa//36%//AF121775
 CTONG20140320

EP 1 347 046 A1

CTONG20140580//HepA-related protein//8.80E-61//345aa//42%//NP_054859
 CTONG20141650
 CTONG20143690
 CTONG20146300
 5 CTONG20146970
 CTONG20147050
 CTONG20149460//RING CANAL PROTEIN (KELCH PROTEIN)//1.20E-56//556aa//27%//Q04652
 CTONG20149950
 CTONG20150910
 10 CTONG20153300//H.sapiens mRNA for tre oncogene (clone 210)//4.80E-214//259aa//78%//X63546
 CTONG20153580//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds//
 4.80E-37//325aa//28%//AF186273
 CTONG20155180
 CTONG20155400
 15 CTONG20156780//Rattus norvegicus PGC1 mRNA for PPAR gamma coactivator, complete cds//1.80E-72//
 176aa//46%//AB025784
 CTONG20158040//UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23) (ANTIGEN X)
 (AGX) (AGX-1) (SPERM-ASSOCIATED ANTIGEN 2)//4.90E-126//376aa//61%//Q16222
 CTONG20158150
 20 CTONG20158660//Rattus norvegicus mRNA for seven transmembrane receptor, complete cds//5.90E-99//
 632aa//36%//AB019120
 CTONG20159530//GLYPICAN-1 PRECURSOR//3.40E-113//222aa//100%//P35052
 CTONG20160560
 CTONG20161850
 25 CTONG20162170
 CTONG20163550
 CTONG20164990
 CTONG20165050
 CTONG20186320//RING CANAL PROTEIN (KELCH PROTEIN)//3.70E-19//290aa//26%//Q04652
 30 CTONG20200310//mitotic control protein dis3 homolog//1.20E-113//655aa//36%//JE0110
 CTONG20265130
 CTONG20267700
 CTONG20273610
 D3OST1000090
 35 D3OST10002670
 D3OST10002700
 D3OST20006180//Drosophila melanogaster slingshot mRNA, complete cds//9.20E-114//358aa//56%//AB036834
 D3OST20006540
 D3OST20007340
 40 D3OST20013280//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC)//1.10E-48//103aa//99%//015511
 D3OST20024170
 D3OST20024360//Homo sapiens neuroendocrine differentiation factor mRNA, complete cds//4.70E-35//80aa//
 100%//AF219226
 D3OST20024520
 45 D3OST20036070
 D3OST20037970
 D3OST20038560
 D3OST30002580
 D3OST30002910
 50 D6OST20003580//H.sapiens mRNA for aminopeptidase P-like//7.40E-70//103aa//99%//X95762
 D6OST20004450
 D6OST20005070
 D9OST20000310
 D9OST20002780
 55 D9OST20015470//Mus musculus MPS1 gene and mRNA, 3' end//4.60E-147//329aa//79%//L20315
 D9OST20023970//CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KDA SYNOVIAL PROTEIN)
 (YKL-40) (CHITINASE-3 LIKE 1)//1.30E-17//44aa//90%//P36222
 D9OST20026730//Homo sapiens caspase recruitment domain protein 7 mRNA, complete cds//2.40E-141//

EP 1 347 046 A1

524aa//40%//AF298548
D9OST20031370//Homo sapiens mRNA for partial putative TCPTP-interacting protein (ptpip5 gene).//3.40E-39//
176aa//48%//AJ242719
D9OST20033970//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.50E-152//541aa//
5 52%//Q05481
D9OST20035800
D9OST20035940//BRAIN MITOCHONDRIAL CARRIER PROTEIN-1.//9.10E-93//216aa//80%//095258
D9OST20040180//OLFACTORY RECEPTOR-LIKE PROTEIN OLF4.//1.20E-106//301aa//64%//Q95157
DFNES10000030
10 DFNES10001850
DFNES20001530//ATAXIN 7 (SPINOCEREBELLAR ATAXIA TYPE 7 PROTEIN).//2.30E-25//98aa//57%//015265
DFNES20010910
DFNES20014040//TRICHOHYALIN. //1.70E-17//380aa//26%//P37709
DFNES20025880
15 DFNES20031920//Drosophila melanogaster mRNA for fucosyltransferase homologue (FucTB gene).//8.40E-18//
133aa//36%//AJ302046
DFNES20037420//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN
GST1-HS).//1.00E-274//499aa//99%//P15170
DFNES20055270
20 DFNES20071130//PHOSPHOTRIESTERASE RELATED PROTEIN (PARATHION HYDROLASE-RELATED PRO-
TEIN) //4.40E-141//233aa//86%//Q60866
DFNES20082800
FCBBF10000240
FCBBF10000380
25 FCBBF10000630//Homo sapiens huntingtin interacting protein HYPB mRNA, partial cds.//3.70E-16//36aa//100%//
AF019610
FCBBF10000770//Homo sapiens REC8 mRNA, partial cds.//6.10E-266//528aa//96%//AF132734
FCBBF10001150//Homo sapiens protocadherin beta 14 (PCDH-beta14) mRNA, complete cds.//4.10E-308//
717aa//79%//AF152493
30 FCBBP10001210//Homo sapiens mRNA for SHPS-1, complete cds.//6.90E-22//135aa//43%//D86043
FCBBF10001550
FCBBF10001710//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.90E-131//397aa//59%//
P51522
FCBBF10001820//CITRATE LYASE BETA CHAIN (EC 4.1.3.6) (CITRASE) (CITRYL-COA LYASE SUBUNIT) (EC
4.1.3.34) //3.70E-32//294aa//27%//053078
35 FCBBF10002430
FCBBF10002700
FCBBF10002800
FCBBF10003220
40 FCBBF10003670//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCO-
SYLASE) (GUANINE INSERTION ENZYME).//2.60E-195//308aa//100%//P54578
FCBBF10003740
FCBBF10003760
FCBBF10003770//Homo sapiens mRNA for GRIP1 protein.//0//572aa//99%//AJ133439
45 FCBBF10004120
FCBBF10004370//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAG-
MENT) //3.30E-96//292aa//52%//Q06730
FCBBF10005060//CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP).//8.40E-51//260aa//41%//
P10123
50 FCBBF10005460//Mus musculus putative neuronal cell adhesion molecule (Punc) mRNA, complete cds.//9.20E-
275//484aa//94%//AF026465
FCBBF10005500
FCBBF10005740//MITOCHONDRIAL CARRIER PROTEIN YMC2 PRECURSOR.//1.10E-27//194aa//38%//
P38087
55 FCBBF20006780
FCBBF20014270//ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (EN-
DOZEPINE) (EP).//1.40E-34//85aa//81%//P45882
FCBBF20023700

EP 1 347 046 A1

FCBBF20032970
 FCBBF20035280
 FCBBF20042170//Homo sapiens NIBAN mRNA, complete cds.//1.90E-177//345aa//100%//AB050477
 FCBBF20042560
 5 FCBBF20049300//NEUR OLFACOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL)
 (1B426B). //7.70E-64//187aa//63%//Q62609
 FCBBF20051220
 FCBBF20054280
 FCBBF20056370
 10 FCBBF20059090//ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7) (FRAGMENT).//2.00E-08//
 96aa//34%//P15621
 FCBBF20064520//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HNRNP C1 AND HNRNP
 C2).//5.50E-70//293aa//53%//P07910
 FCBBF20067810//SP00B-ASSOCIATED GTP-BINDING PROTEIN.//1.30E-51//275aa//42%//P20964
 15 FCBBF20068820//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.50E-74//216aa//62%//
 P51522
 FCBBF20071860
 FCBBF20072650
 FCBBF20075560
 20 FCBBF20076330
 FCBBF30001840
 FCBBF30007680//Homo sapiens general transcription factor 2-i (GTF2I) mRNA, alternatively spliced product,
 complete cds.//4.80E-56//141aa//72%//AF038968
 FCBBF30008470
 25 FCBBF30010810//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//7.10E-173//436aa//
 70%//Q03923
 FCBBF30012350//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMA CHAIN (CAM-
 KINASE II GAMMA CHAIN) (EC 2.7.1.123) (CAMK-II, GAMMA SUBUNIT). //8. 80E-143//291aa//92%//P11730
 FCBBF30012810//Homo sapiens ubiquitin-specific processing protease mRNA, complete cds.//1.10E-123//
 30 450aa//49%//AF229438
 FCBBF30013770//Rattus norvegicus dnchc2 mRNA for cytoplasmic dynein heavy chain. complete cds.//0//806aa//
 93%//AB041881
 FCBBF30015940//Chlamydomonas reinhardtii dhc1 gene for 1-alpha dynein heavy chain.//4.90E-228//831aa//
 52%//AJ243806
 35 FCBBF30016320
 FCBBF30016570
 FCBBF30018550//Homo sapiens putative zinc finger protein mRNA, complete cds.//9.40E-90//560aa//35%//
 AF251039
 FCBBF30019120
 40 FCBBF30024750//SEMAPHORIN 4F PRECURSOR (SEMAPHORIN W) (SEMA W).//2.00E-73//129aa//100%//
 095754
 FCBBF30025560//NERVOUS-SYSTEM SPECIFIC OCTAMER-BINDING TRANSCRIPTION FACTOR N-OCT 3
 (BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 2) (BRN-2 PROTEIN) [CONTAINS: N-OCT 5A; N-OCT
 5B].//4.30E-171//203aa//100%//P20265
 45 FCBBF30028180
 FCBBF30033050
 FCBBF30039020//GROWTH-ARREST-SPECIFIC PROTEIN 2.//1.80E-68//194aa//64%//043903
 FCBBF30049550//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0//1016aa//
 99%//Q01484
 50 FCBBF30052180
 FCBBF30054440
 FCBBF30057290//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
 cds.//8.90E-258//642aa//68%//AB021644
 FCBBF30062880
 55 FCBBF30070770
 FCBBF30071520
 FCBBF30078290
 FCBBF30083620//PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX).//5.80E-146//344aa//77%//

EP 1 347 046 A1

P51805

FCBBF30083820//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//1.50E-14//142aa//38%//AF159567

FCBBF30086440

5 FCBBF30090690//Homo sapiens HT017 mRNA, complete cds.//8.60E-541/311aa/138%//AF225421

FCBBF30095260

FCBBF30123470

FCBBF30129630//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//9.50E-98//228aa//73%//Q03923

10 FCBBF30170590

FCBBF30172550

FCBBF30175310//ETHANOLAMINEPHOSPHOTRANSFERASE (EC 2.7.8.1) (ETHPT).//2.10E-38//401aa//28%//P22140

FCBBF30178730

15 FCBBF30189490

FCBBF30190850//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//6.10E-30//275aa//31%//P16581

FCBBF30195640//Homo sapiens ALR-like protein mRNA, complete cds.//9.10E-188//331aa//99%//AF264750

20 FCBBF30199610

FCBBF30215060

FCBBF30225660

FCBBF30233680

FCBBF30238870//PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2).//0//641aa//99%//Q99435

25 FCBBF30240020

FCBBF30240960//ZINC FINGER PROTEIN 136.//8.30E-131//338aa//65%//P52737

FCBBF30242250

FCBBF30243640//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//6.40E-53//102aa//100%//P55345

30 FCBBF30246230//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//7.10E-17//141aa//40%//AF159567

FCBBF30246630//H.sapiens mRNA for ZYG homologue.//4.80E-60//562aa//29%//X99802

FCBBF30247930//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//2.70E-73//162aa//87%//AF177477

35 FCBBF30250730//TRICHOHYALIN.//1.30E-10//240aa//27%//P22793

FCBBF30251420

FCBBF30252520//Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds.//2.50E-47//103aa//98%//U90030

40 FCBBF30252800//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN CAP43).//1.30E-134//260aa//97%//Q92597

FCBBF30252850//Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA, complete cds.//2.90E-46//185aa//50%//AF022770

45 FCBBF30262360

FCBBF30262510

FCBBF30266780

FCBBF30266920

FCBBF30278630

50 FCBBF30279030//Homo sapiens BNPI mRNA for brain-specific Na-dependent inorganic phosphate cotransporter, complete cds.//2.40E-120//222aa//100%//AB032436

FCBBF30281880//regulator of G-protein signalling 7 [Homo sapiens].//2.00E-05//100aa//33%//NP_002915

FCBBF30284720

FCBBF30285280

55 FCBBF40001420

FCBBF40001730//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1).//4.20E-120//265aa//84%//P25388

FCBBF40005480

EP 1 347 046 A1

FEBRA10001880//Homo sapiens serine/threonine kinase mRNA, complete cds.//4.60E-106//344aa//53%//
 AF005046
 FEBRA10001900
 FEBRA20002100//D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER).//2.00E-13//159aa//27%//
 5 052733
 FEBRA20003210
 FEBRA20004620//RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP).//1.50E-46//208aa//143%//P47736
 FEBRA20007620//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 SPBC16H5.10C.//2.30E-126//692aa//39%//042945
 10 FEBRA20009090
 FEBRA20010120//CLEAVAGE STIMULATION FACTOR, 64 KDA SUBUNIT (CSTF 64 KDA SUBUNIT) (CF-1 64
 KDA SUBUNIT).//1.10E-73//137aa//97%//P33240
 FEBRA20017050
 FEBRA20018280
 15 FEBRA20018690//ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7) (FRAGMENT).//2.00E-08//
 96aa//34%//P15621
 FEBRA20024100//Rattus norvegicus myosin heavy chain Myr 8 mRNA, complete cds.//0//863aa//78%//AF209114
 FEBRA20025270
 FEBRA20025520
 20 FEBRA20026110//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-21//810aa//
 48%//Q05481
 FEBRA20026280
 FEBRA20027810
 FEBRA20029860
 25 FEBRA20034360
 FEBRA20034680//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-93//481aa//35%//
 P51523
 FEBRA20037260
 FEBRA20037500
 30 FEBRA20040530//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.30E-115//335aa//54%//
 P51523
 FEBRA20042190
 FEBRA20052910
 FEBRA20060610
 35 FEBRA20072120
 FEBRA20079310
 FEBRA20080810//Rattus norvegicus mRNA for peptide/histidine transporter, complete cds.//1.30E-107//239aa//
 E7%//AB000280
 FEBRA20082010//ZINC FINGER PROTEIN 195.//0//482aa//99%//014628
 40 FEBRA20082100
 FEBRA20086620//NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL)
 (1B426B).//3.80E-165//453aa//65%//Q62609
 FEBRA20088360//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE
 CHAIN) (100 KDA COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN AL-
 45 PHA C SUBUNIT).//5.60E-05//58aa//53%//P17427
 FEBRA20090290
 FEBRA20092890//Rattus norvegicus neural cell adhesion protein BIG-2 precursor (BIG-2) mRNA, complete cds.//
 0//697aa//93%//U35371
 FEBRA20093520
 50 FEBRA20095140
 FEBRA20095880
 FEBRA20097310//Human Hsp27 ERE-TATA-binding protein (HET) mRNA, complete cds.//0//597aa//97%//
 U72355
 FEBRA20098460
 55 FEBRA20111460
 FEBRA20113560//R. norvegicus mRNA for DRM protein.//5.10E-65//157aa//80%//Y10019
 FEBRA20125070
 FEBRA20130190//UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3//8.20E-65//345aa//42%//

EP 1 347 046 A1

NP_055071

FEBRA20132740//Homo sapiens mRNA for CDEP, complete cds.//3.70E-16//40aa//92%//AB008430

FEBRA20140100//RER1 PROTEIN.//3.20E-106//196aa//99%//015258

FEBRA20144170//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//1.30E-269//495aa//99%//Q15349

FEBRA20145780

FEBRA20161120

FEBRA20166540

FEBRA20167390//Mus musculus ST6GalNAc V mRNA for GD1 alpha synthase, complete cds.//9.40E-64//134aa//91%//AB030836

FEBRA20171380//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//6.30E-127//415aa//48%//Q06730

FEBRA20174410//Mus musculus mRNA for nuclear protein ZAP, complete cds.//2.30E-193//543aa//69%//AB033168

FEBRA20176800

FEBRA20184330//Rattus norvegicus glutamate receptor interacting protein 2 (GRIP2) mRNA, complete cds.//8.10E-72//161aa//88%//AF072509

FEBRA20192420

FEBRA20195820//ZINC FINGER PROTEIN 132.//2.60E-47//134aa//63%//P52740

FEBRA20196370

FEBRA20196630//RNA helicase-related protein//0//317aa//100%//NP_031398

FEBRA20197110

FEBRA20204000

FEBRA20204060

FEBRA20211710

FEBRA20214970

FEBRA20215500//Mus musculus Nupl (nupl) mRNA, complete cds.//1.80E-38//146aa//64%//U94988

FEBRA20216360

FEBRA20222040

FEBRA20223220//Homo sapiens mRNA for fibulin-4.//9.20E-110//202aa//100%//AJ132819

FEBRA20225040//high-glucose-regulated protein 8//1.40E-110//514aa//51%//NP_057342

FEBRA20226010

FEBRA20229560

FEBRA20229630

FEBRA20232850

FEBRA20233770//NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4).//6.30E-62//164aa//81%//Q99743

FEBRA20235500//P3 PROTEIN.//5.20E-74//391aa//39%//P09131

FEBRA20237640//Rattus norvegicus neurabin mRNA, complete cds.//9.10E-29//172aa//46%//U72994

FEHRT20003250//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//2.20E-146//269aa//100%//P42356

FELNG20002410

HCASM10000500//TOPOISOMERASE 1-RELATED PROTEIN TRF5.//3.70E-09//193aa//22%//P48561

HCHON10001760//histone deacetylase 5//1.00E-133//320aa//67%//NP_005465 HCHON20000380

HCHON20001560//TRANSCRIPTION FACTOR-LIKE PROTEIN MORF4.//7.20E-116//235aa//93%//Q9Y690

HCHON20002260

HCHON20003220//10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (10-FTHFDH) (FBP-CI).//2.30E-302//731aa//72%//P28037

HCHON20003440//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//1.30E-64//155aa//87%//AF084530

HCHON20007380//Homo sapiens mRNA for HELG protein.//3.90E-129//331aa//76%//AJ277291

HCHON20007510//rab6 GTPase activating protein (GAP and centrosome-associated)//0//765aa//62%//NP_036329

HCHON20008150

HCHON20008180

HCHON20008320//ZINC FINGER PROTEIN 135.//2.20E-130//345aa//62%//P52742

HCHON20008980

HCHON20009350

EP 1 347 046 A1

HCHON20009560//ZINC FINGER PROTEIN 74.//1.50E-22//113aa//46%//Q16587
 HCHON20010990
 HCHON20011160
 HCHON20014970
 5 HCHON20015230//Homo sapiens nuclear pore-associated protein (NPAP60L) mRNA, complete cds.//1.40E-78//
 158aa//97%//AF107840
 HCHON20015350//PUTATIVE RRNA METHYLTRANSFERASE SPB1 (EC 2.1.1.-).//1.90E-117//771 aa//36%//
 P25582
 HCHON20015980//Homo sapiens integrin alpha 11 subunit precursor (ITGA11) mRNA, complete cds.//1.00E-227//
 10 419aa//99%//AF137378
 HCHON20016040//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3)
 (IGF-BINDING PROTEIN 3).//2.00E-21//45aa//97%//P17936
 HCHON20016650//Mus musculus seven-pass transmembrane receptor precursor (Celsr1) mRNA, complete cds.//
 6.20E-27//343aa//27%//AF031572
 15 HCHON20022470
 HCHON20035130//ZINC FINGER PROTEIN 22 (ZINC FINGER PROTEIN KOX15) (FRAGMENT).//1.10E-18//
 64aa//56%//P17026
 HCHON20036420//Homo sapiens mRNA for PED phosphoprotein.//1.30E-64//130aa//100%//Y13736
 HCHON20036760
 20 HCHON20040020//TNF-INDUCIBLE PROTEIN CG12_1.//8.80E-40//302aa//36%//095236
 HCHON20043590
 HCHON20059870//Hypothetical protein.//4.20E-204//667aa//56%//AL163279
 HCHON20064590//ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M).//5.00E-38//654aa//27%//P01023
 HCHON20067220
 25 HCHON20067700//Homo sapiens gremlin mRNA, complete cds.//5.70E-76//106aa//99%//AF045800
 HCHON20068410//Drosophila melanogaster microtubule associated protein (asp) mRNA, complete cds.//8.10E-
 47//803aa//27%//U95171
 HCHON20068710
 HCHON20074820
 30 HCHON20076500
 HCHON20086720//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3)
 (IGF-BINDING PROTEIN 3).//4.10E-113//205aa//100%//P17936
 HCHON20097490//dedicator of cyto-kinesis 1//1.00E-154//860aa//37%//NP_001371
 HCHON20100740//LACTADHERIN PRECURSOR (MILK FAT GLOBULE-EGF FACTOR 8) (MFG-E8) (HMFG)
 35 (BREAST EPITHELIAL ANTIGEN BA46) (MFGM) [CONTAINS: MEDIN].//1.60E-205//363aa//99%//Q08431
 HEART20003060//BASIGIN PRECURSOR (LEUKOCYTE ACTIVATION ANTIGEN M6) (COLLAGENASE STIM-
 ULATORY FACTOR) (EXTRACELLULAR MATRIX METALLOPROTEINASE INDUCER) (EMMPRIN) (5F7)
 (CD147 ANTIGEN).//1.30E-132//248aa//100%//P35613
 HEART20005410
 40 HEART20017730//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//2.40E-25//
 368aa//30%//Q01484
 HEART20021840
 HEART20025980//Homo sapiens smoothelin large isoform L2 (SMTN) mRNA, complete cds.//9.00E-152//223aa//
 97%//AF064238
 45 HEART20034320//ENDOGLUCANASE Z PRECURSOR (EC 3.2.1.4) (ENDO-1, 4-BETA-GLUCANASE) (THER-
 MOACTIVE CELLULASE) (AVICELASE I).//1.20E-64//480aa//32%//P23659
 HEART20037810
 HEART20049400
 HEART20049410//Homo sapiens cerberus-related protein (CER1) gene, complete cds.//1.10E-12//144aa//29%//
 50 AF090189
 HEART200498C0
 HEART20061950//Homo sapiens mRNA for myopodin.//1.30E-28//327aa//35%//AJ010482
 HEART20063340
 HEART20067870
 55 HEART20067890
 HEART20072310
 HEART20074430
 HEART20077670//Mus musculus mRNA for E-MAP-115 protein.//1.70E-50//363aa//41%//Y15197

EP 1 347 046 A1

HEART20083640//Mus musculus Xin mRNA, complete cds.//3.10E-63//272aa//58%//AP051945
HEART20089940
HEART20090000//Rattus norvegicus PIPP mRNA for proline-rich inositol polyphosphate 5-phosphatase, complete
cds.//0//639aa//91%//AB032551
5 HEART20095990
HHDPC10000650
HHDPC10000830//HYPOTHETICAL 24.9 KDA PROTEIN C16C10.7 IN CHROMOSOME III.//1.50E-23//56aa//
60%//Q09463
HHDPC20001040
10 HHDPC20006920
HHDPC20014320//ADAM 12 PRECURSOR (EC 3.4.24.-) (A DISINTEGRIN AND METALLOPROTEINASE DO-
MAIN 12) (MELTRIN ALPHA).//1.20E-14//139aa//38%//043184
HHDPC20030490//LIPOPOLYSACCHARIDE-INDUCED TUMOR NECROSIS FACTOR-ALPHA FACTOR
(LPS-INDUCED TNF-ALPHA FACTOR) (P53-INDUCED PROTEIN 7).//1.90E-69//134aa//95%//Q99732
15 HHDPC20031130//Kruppel-type zinc finger (C2H2) [Homo sapiens]//3.30E-196//607aa//57%//NP_005806
HHDPC20034390
HHDPC20034720//CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4 (INTRACELLULAR CHLORIDE ION
CHANNEL PROTEIN P64H1).//1.50E-121//213aa//99%//Q9Y696 HHDPC20057420//Mus musculus proline-rich
protein (Bprp) mRNA, complete cds.//5.40E-45//143aa//69%//AF085348
20 HHDPC20057940
HHDPC20064600//SUPPRESSOR PROTEIN SRP40.//8.00E-05//175aa//24%//P32583
HHDPC20068620//Ig kappa chain precursor V region (0-81VL) - human (fragment)//8.10E-06//132aa//31%//
S22658
HHDPC20084140//Homo sapiens polyadenylate binding protein-interacting protein-1 (PAIP1) mRNA, complete
25 cds.//8.10E-12//230aa//23%//AF013758
HHDPC20091140//Homo sapiens gremlin mRNA, complete cds.//2.20E-60//105aa//100%//AF045800
HHDPC20091780//coagulation factor V (proaccelerin, labile factor)//2.00E-26//170aa//40%//NP_000121
HHDPC20092080//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3)
(IGF-BINDING PROTEIN 3).//3.30E-100//185aa//94%//P17936
30 HHDPC20095280
HLUNG10000550
HLUNG20016330//Homo sapiens actin filament associated protein (AFAP) mRNA, complete cds.//6.70E-130//
531aa//49%//AF188700
HLUNG20016770
35 HLUNG20017120//PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2).//8.40E-11//82aa//40%//Q53915
HLUNG20023340//Mus musculus SLM-1 (S1m1) mRNA, complete cds.//8.80E-141//270aa//95%//AF098796
HLUNG20033780//Rho guanine nucleotide exchange factor 5//6.00E-60//440aa//38%//NP_005426
HLUNG20084390
40 IMR3220002430//CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT) (RETINOBLAST-
OMA BINDING PROTEIN P48) (RETINOBLASTOMA-BINDING PROTEIN 4) (MSI1 PROTEIN HOMOLOG).//
7.10E-09//303aa//24%//Q09028
KIDNE20002520//glutamyl tRNA synthetase homolog//9.90E-156//290aa//100%//T00743
KIDNE20003940//RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOS-
PHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT
45 PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).//1.80E-151//582aa//51%//
Q06496
KIDNE20006780
KIDNE20007210//Xenopus laevis mRNA for RPA interacting protein alpha (ripalpha gene).//8.30E-17//104aa//
47%//AJ243177
50 KIDNE20007770//CARCINOEMBRYONIC ANTIGEN CGM6 PRECURSOR (NONSPECIFIC CROSS-REACTING
ANTIGEN NCA-95) (ANTIGEN CD67) (CD66B ANTIGEN).//1.20E-17//326aa//27%//P31997
KIDNE20008010//Homo sapiens mRNA for putative protein kinase (WNK1 gene).//2.50E-25//460aa//29%//
AJ296290
KIDNE20009470
55 KIDNE20011170
KIDNE20011400
KIDNE20013730
KIDNE20017130//Oreochromis niloticus sex-determining protein DMO mRNA, complete cds.//5.10E-43//252aa//

EP 1 347 046 A1

43%//AF203490
 KIDNE20018730
 KIDNE20018970
 KIDNE20020150//HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2)//9.90E-251//458aa//98%//
 5 P08107
 KIDNE20021680//SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE PRECURSOR (EC 1.1.1.35)
 (HCDH)//7.10E-141//273aa//98%//Q16836
 KIDNE20021910//Homo sapiens MRS1 mRNA, complete cds//2.30E-30//339aa//27%//AF093239
 KIDNE20021980
 10 KIDNE20022620//like-glycosyltransferase//8.50E-253//633aa//70%//NP_004728
 KIDNE20024830//Homo sapiens copine I mRNA, complete cds//1.30E-46//134aa//47%//U83246
 KIDNE20027250//ZINC FINGER PROTEIN 41 (ZFP-41) (CTFIN92) (FRAGMENT)//3.80E-55//105aa//91%//
 Q02526
 KIDNE20027950//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.
 15 16)//2.40E-40//82aa//100%//P17097
 KIDNE20028390//GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.10)//16.00E-70//85aa//
 90%//P43424
 KIDNE20028720//Mus musculus Ac39/physophilin mRNA, complete cds//2.70E-130//345aa//68%//U21549
 KIDNE20028830
 20 KIDNE20029800
 KIDNE20067330
 KIDNE20079440
 KIDNE20096280
 KIDNE20096470
 25 KIDNE20100070//Rattus norvegicus kidney-specific protein (KS) mRNA, complete cds. //1.20E-253//572aa//77%//
 AF062389
 KIDNE20100840
 KIDNE20101370//GOLGIN-95 //3.40E-20//76aa//68%//Q08379
 KIDNE20101510//UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)//0//
 30 519aa//95%//P07911
 KIDNE20102650
 KIDNE20102710//Mus musculus mRNA for Shank3b protein (shank3 gene)//1.20E-81//203aa//71%//AJ245904
 KIDNE20104300
 KIDNE20106740
 35 KIDNE20107390//Homo sapiens CHRAC17 (CHRAC17) mRNA, complete cds//1.50E-40//105aa//86%//
 AF226077
 KIDNE20107500
 KIDNE20107620//Rattus norvegicus protein kinase WNK1 (WNK1) mRNA, complete cds//8.70E-140//266aa//
 74%//AF227741
 40 KIDNE20109730//Mus musculus orphan transporter isoform B9 (Xtrp2) mRNA, alternatively spliced, complete
 cds//8.70E-34//103aa//65%//AF075266
 KIDNE20109890//Rattus norvegicus TGF-beta resistance-associated protein (TRAG) mRNA, complete cds//
 2.60E-141//774aa//37%//AF305813
 KIDNE20112000
 45 KIDNE20115080//Homo sapiens mRNA for hNBL4, complete cds//6.20E-115//226aa//96%//AB030240
 KIDNE20118580//actin interacting protein [Arabidopsis thaliana]//5.00E-34//140aa//56%//CAB16815
 KIDNE20120090
 KIDNE20121880//Mus musculus claudin-19 mRNA, partial cds//6.10E-97//193aa//95%//AF249889
 KIDNE20122910
 50 KIDNE20124400//Homo sapiens mRNA for ALEX1, complete cds//1.10E-18//167aa//28%//AB039670
 KIDNE20125630
 KIDNE20126010
 KIDNE20126130
 KIDNE20127100//Drosophila melanogaster Diablo (dbo) mRNA, complete cds//1.10E-10//254aa//26%//
 55 AF237711
 KIDNE20127450
 KIDNE20127750//Homo sapiens partial mRNA for transport-secretion protein 2.1 (ITS-2, 1 gene) //6.50E-45//
 178aa//46%//AJ278475

EP 1 347 046 A1

KIDNE20130450
 KIDNE20131580//Homo sapiens mRNA for LAK-4p, complete cds.//1.80E-111//211aa//100%//AB002405
 KIDNE20132180
 KIDNE20137340//HYPOTHETICAL 49.1 KDA PROTEIN C11D3.06 IN CHROMOSOME I.//5.80E-13//149aa//
 5 30%//Q10085
 KIDNE20138010
 KIDNE20141190
 KIDNE20144890
 KIDNE20148900
 10 KIDNE20163880
 KIDNE20180710
 KIDNE20181660
 KIDNE20182690//Homo sapiens mRNA for RERE, complete cds.//3.50E-222//401aa//99%//AB036737
 KIDNE20186780
 15 KIDNE20190740//Rattus norvegicus SNIP-b mRNA, complete cds.//6.70E-20//51aa//92%//AF156982
 LIVER10001260
 LIVER10004790
 LIVER20002160//HEAT SHOCK COGNATE 71 KDA PROTEIN.//0//585aa//95%//P11142
 LIVER20011130//Homo sapiens F-box protein FBL9 mRNA, partial cds.//5.50E-107//210aa//99%//AF176701
 20 LIVER20011910
 LIVER20028420
 LIVER20035110
 LIVER20035680
 LIVER20038540
 25 LIVER20045650
 LIVER20055200//Homo sapiens leucocyte immunoglobulin-like receptor-8 (LIR-8) mRNA. complete cds.//2.50E-
 43//132aa//71%//AF025534
 LIVER20055440//Homo sapiens Rho GAP p190-A mRNA, complete cds.//2.90E-101//195aa//98%//AF159851
 LIVER20059810//UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE
 30 4-EPIMERASE).//1.60E-15//39aa//100%//Q14376
 LIVER20062510
 LIVER20064100//Ciona intestinalis mRNA for myoplasmin-C1, complete cds.//2.90E-14//167aa//26%//D42167
 LIVER20064690//PLASMA SERINE PROTEASE INHIBITOR PRECURSOR (PCI) (PROTEIN C INHIBITOR)
 (PLASMINOGEN ACTIVATOR INHIBITOR-3) (PAI3)//1.70E-146//319aa//89%//P05154
 35 LIVER20075680
 LIVER20080530//Drosophila melanogaster forked mRNA for large Forked protein, complete cds.//1.10E-11//
 198aa//32%//D21203
 LIVER20084730
 LIVER20085800
 40 LIVER20087060//Mus musculus putative purine nucleotide binding protein mRNA, complete cds.//2.70E-233//
 619aa//70%//U44731
 LIVER20087510
 LIVER20091180
 MAMGL10000830//Drosophila melanogaster L82B (L82) mRNA, complete cds.//3.00E-27//231aa//38%//
 45 AF125385
 MESAN10001260//Drosophila melanogaster Crossveinless 2 (CV-2) mRNA, complete cds.//6.50E-104//628aa//
 35%//AF288223
 MESAN20004570//MEDIAN BODY PROTEIN.//3.00E-07//343aa//23%//Q08014
 MESAN20014500//Drosophila melanogaster Dispatched (dispatched) mRNA, complete cds.//1.60E-46//225aa//
 50 37%//AF200691
 MESAN20025190//Mus musculus cell cycle checkpoint control protein Mrad9 gene, complete cds.//7.30E-19//
 43aa//97%//AF045662
 MESAN20027090
 MESAN20029400
 55 MESAN20031900//Homo sapiens mRNA for zinc-binding protein (Rbcc728 gene).//2.90E-161//724aa//43%//
 AJ272269
 MESAN20035290
 MESAN20036460

EP 1 347 046 A1

MESAN20038510
 MESAN20089360
 MESAN20101140//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//2.30E-25//
 52aa//98%//P48059
 5 MESAN20103120//Homo sapiens sodium/calcium exchanger NCKX3 (SLC24A3) mRNA, complete cds.//4.10E-
 66//289aa//37%//AF169257
 MESAN20106640
 MESAN20115970
 MESAN20121130
 10 MESAN20125860//MELANOTRANSFERRIN PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN P97).//
 1.30E-40//81aa//100%//P08582
 MESAN20127350//myelin expression factor-3//2.80E-15//227aa//29%//JE0163
 MESAN20130220//Homo sapiens testis-specific chromodomain Y-like protein (CDYL) mRNA, alternatively proc-
 essed, complete cds.//2.10E-126//319aa//63%//AF081258
 15 MESAN20132110
 MESAN20136110//Ciona savignyi mRNA for PEM-3, complete cds.//1.90E-85//236aa//65%//AB001769
 MESAN20138450
 MESAN20139360
 MESAN20141920//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 20 cds.//0//691aa//97%//U53445
 MESAN20152770
 MESAN20153910
 MESAN20154010//Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds.//9.10E-60//
 69aa//100%//AJ224326
 25 MESAN20157080
 MESAN20161590
 MESAN20164090
 MESAN20171520//Homo sapiens TNF intracellular domain-interacting protein mRNA, complete cds. //9. 30E-30//
 198aa//40%//AF168676
 30 MESAN20174170//REGULATOR OF G-PROTEIN SIGNALING 4 (RGS4) (RGP4).//1.80E-39//80aa//98%//
 P49798
 MESAN20182090
 MESAN20186700
 NESOP10001080
 35 NOVAR10000150
 NOVAR10000910//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//6.00E-199//392aa//98%//
 P23508
 NOVAR10001020
 NOVAR20000380
 40 NOVAR20003520
 NT2NE20003740
 NT2NE20010050
 NT2NE20010210
 NT2NE20010400//Homo sapiens GL013 mRNA, complete cds.//2.90E-51//223aa//60%//AF267859
 45 NT2NE20010490//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.30E-194//464aa//
 72%//Q03923
 NT2NE20015240
 NT2NE20021620//Saccharomyces cerevisiae Vps9p (VPS9) ger. complete cds.//1.00E-13//250aa//24%//
 U20373
 50 NT2NE20043780
 NT2NE20053580
 NT2NE20068130//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (S-LAYER LAYER PROTEIN B) (S-LAYER
 PROTEIN 1) //2.50E-34//377aa//40%//Q06852
 NT2NE20072200
 55 NT2NE20074250
 NT2NE20080170//HUNTINGTIN-ASSOCIATED PROTEIN-INTERACTING PROTEIN (DUO PROTEIN) (KALI-
 RIN) (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10) //6.60E-57//661aa//27%//P97924
 NT2NE20089610

EP 1 347 046 A1

NT2NE20089970//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.60E-29//77aa//81%//Q05481
 NT2NE20108540
 NT2NE20110360
 5 NT2NE20118960//DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KDA SBJUNIT PRECURSOR (EC 2.4.1.119) (RIBOPHORIN II).//9.30E-274//562aa//94%//P04844
 NT2NE20122430//GLYOXYLATE-INDUCED PROTEIN.//7.70E-25//144aa//38%//P30147
 NT2NE20124480
 NT2NE20125050//Gallus gallus mRNA for avena, complete cds.//5.80E-199//468aa//84%//AB017437
 10 NT2NE20130190
 NT2NE20131890
 NT2NE20132170//Rattus norvegicus lysosomal amino acid transporter 1 mRNA, complete cds.//3.70E-97//357aa//52%//AF361239
 NT2NE20142210//SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM).//3.00E-24//660aa//26%//Q61079
 15 NT2NE20146810
 NT2NE20152750
 NT2NE20155110
 NT2NE20156260
 20 NT2NE20157470//COMPLEMENT C2 PRECURSOR (EC 3.4.21.43) (C3/C5 CONVERTASE).//6.60E-138//256aa//100%//P06681
 NT2NE20158600//erythroid ankyrin - Synechocystis sp. (strain PCC 6803).//7.00E-13//160aa//31%//S74626
 NT2NE20159740
 NT2NE20172590
 25 NT2NE20174800
 NT2NE20174920
 NT2NE20177520//Guinea pig mRNA for decay-accelerating factor (isoform GDab-SEC), complete cds.//1.70E-15//273aa//28%//D49421
 NT2NE20181650//Shb=Src homology 2 protein//2.90E-36//115aa//43%//AAB29780
 30 NT2NE20183760
 NT2NE20184900//Mus musculus mRNA for transcription factor CA150b, complete cds.//8.60E-29//98aa//55%//AB023485
 NT2NE20187390
 NT2RI20C01330//Homo sapiens KE03 protein mRNA, partial cds.//3.40E-103//339aa//57%//AF064604
 35 NT2RI20C03480//GLYPICAN-2 PRECURSOR (CEREBROGLYCAN) (HSPG M13).//1.80E-261//581aa//82%//P51653
 NT2RI20C05750//Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds.//8.90E-139//272aa//95%//AF084464
 NT2RI20C09370//lunatic fringe precursor [Mus musculus]//5.50E-123//237aa//91%//U94351
 40 NT2RI20C22600
 NT2RI20C23160
 NT2RI20C23590
 NT2RI20C23910//Homo sapiens TMTSP mRNA for transmembrane molecule with thrombospondin module, complete cds.//0.480aa//96%//AB044385
 45 NT2RI20C25400//Mouse mRNA for P24 protein, complete cds.//9.70E-94//196aa//91%//D83206
 NT2RI20C25640
 NT2RI20C28470
 NT2RI20C36670
 NT2RI20C40930//MITOCHONDRIAL CARRIER PROTEIN YMC2 PRECURSOR.//1.10E-27//194aa//38%//P38087
 50 NT2RI20C40990//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//2.40E-25//368aa//30%//Q01484
 NT2RI20C41380//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN, TYPE A) (NMMHC-A).//8.10E-10//322aa//21%//P35579
 55 NT2RI20C46080
 NT2RI20C48440//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN).//2.10E-171//316aa//100%//P04899
 NT2RI20C50960//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//5.40E-

EP 1 347 046 A1

164//496aa//61%//AF033120
 NT2RI20054050//Drosophila melanogaster Abnormal X segregation (Axs) gene, complete cds.//2.40E-83//487aa//
 37%//AF101361
 NT2RI20055790
 5 NT2RI20056700//NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL)
 (1B426B).//3.40E-237//439aa//97%//Q62609
 NT2RI20069730
 NT2RI20076290
 NT2RI20086220
 10 NT2RI20091730
 NT2RI20091940//CORNICHON-LIKE PROTEIN.//9.70E-73//159aa//81%//035089
 NT2RI20198260
 NT2RI20203900
 NT2RI20207030
 15 NT2RI20216250
 NT2RI20240080//SMALL GLUTAMINE-RICH TETRATRICOPEPTIDE REPEAT-CONTAINING PROTEIN.//
 1.30E-86//311aa//58%//043765
 NT2RI20244600//Homo sapiens mRNA for sphingosine-1-phosphatase (ORF1).//2.60E-50//273aa//36%//
 AJ293294
 20 NT2RI20244960
 NT2RI20250750
 NT2RI20252550
 NT2RI20273230//PUTATIVE HELICASE YGR271W.//1.10E-14//152aa//38%//P53327
 NT2RP60000770//Homo sapiens mRNA for ZAC zinc finger protein.//5.80E-179//325aa//98%//AJ006354
 25 NT2RP60000850//Bos taurus RPGR-interacting protein-1 (RPGRIP1) mRNA, complete cds.//2.10E-139//751aa//
 38%//AF227258
 NT2RP70010740
 NT2RP70027380//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//7.40E-31//203aa//
 36%//P15882
 30 NT2RP70032610//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON- NEU-
 RAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//4.40E-180//387aa//88%//P06733
 NT2RP70036880//Gtpase activating protein for Yptlp; Gyplp [Saccharomyce scerevisiae].//2.00E-66//250aa//
 50%//NP_014713
 NT2RP70037240//H.sapiens E-MAP-115 mRNA.//1.10E-79//475aa//41%//X73882
 35 NT2RP70043480//ZINC FINGER PROTEIN 93 (ZINC FINGER PROTEIN HTF34) (FRAGMENT).//0//588aa//
 91%//P35789
 NT2RP70044280//CTD-BINDING SR-LIKE PROTEIN RA4 (FRAGMENT).//1.20E-11//190aa//31%//095104
 NT2RP70045590//PUTATIVE ENDONUCLEASE C1F12. 06C (EC 3.1.-.-).//3.60E-34//246aa//36%//Q10348
 NT2RP70056750
 40 NT2RP70062230//NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NF-H).//
 2.50E-29//622aa//29%//P19246
 NT2RP70063950//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.90E-13//417aa//26%//P52734
 NT2RP70072690
 45 NT2RP70075240
 NT2RP70077660
 NT2RP70078420//Drosophila melanogaster Centaurin Gamma 1A (ceng1A) mRNA, complete cds.//1.00E-120//
 700aa//40%//AF254741
 NT2RP70080850
 50 NT2RP70081610//Mus musculus 101F6 protein mRNA, complete cds.//5.20E-52//214aa//50%//AF131206
 NT2RP70085440
 NT2RP70102350//Mus musculus mRNA for Olig3 bHLH protein, complete cds.//1.90E-134//257aa//98%//
 AB038698
 NT2RP70105210
 55 NT2RP70110860
 NT2RP70111320
 NT2RP70122910
 NT2RP70125160

EP 1 347 046 A1

NT2RP70130020
 NT2RP70133740//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//2.60E-136//267aa//94%//
 015127
 NT2RP70134990
 5 NT2RP70137290
 NT2RP70137640
 NT2RP70143480
 NT2RP70147210
 NT2RP70150800
 10 NT2RP70157890//zinc finger protein 267; zinc finger (C2H2) [Homo sapiens]//1.60E-125//228aa//99%//
 NP_003405
 NT2RP70159960//Rattus norvegicus p135 SynGAP mRNA, partial cds.//4.80E-60//177aa//69%//AF053938
 NT2RP70169110
 NT2RP70175670
 15 NT2RP70179710
 NT2RP70181970
 NT2RP70188020
 NT2RP70188710
 NT2RP70190640
 20 NT2RP70192730//LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC
 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTER-
 YL ESTERASE).//3.00E-181//323aa//99%//P38571
 NT2RP70194450
 NT2RP70195430//PUTATIVE NADP-DEPENDENT OXIDOREDUCTASE IN TEHB-RHSE INTERGENIC REGION
 25 (EC 1.1.1.1) //1.10E-57//349aa//38%//P76113
 NT2RP70198350//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//2.60E-111//213aa//98%//P51858
 NT2RP70203790
 NTONG20009770//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-
 CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.30E-304//599aa//92%//
 P42675
 30 NTONG20013620//Homo sapiens hydroxysteroid sulfotransferase SULT2B1b (HSST2) mRNA, complete cds.//
 6.10E-82//151aa//100%//U92315
 NTONG20015870//KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4).//3.30E-132//489aa//
 54%//P19013
 35 NTONG20028070//CYR61 PROTEIN PRECURSOR (GIG1 PROTEIN) (INSULIN-LIKE GROWTH FACTOR-
 BINDING PROTEIN 10).//1.60E-65//133aa//92%//000622
 NTONG20029480//Mus musculus Xin mRNA, complete cds.//7.20E-93//409aa//54%//AF051945
 NTONG20029700//Homo sapiens laminin alpha 3b chain mRNA, partial cds.//6.60E-230//425aa//92%//AF005258
 NTONG20046140//Homo sapiens mRNA for MNK1, complete cds.//5.70E-89//177aa//98%//AB000409
 40 NTONG20048060
 NTONG20049910
 NTONG20050620
 NTONG20050860
 NTONG20051530//KUPFFER CELL RECEPTOR.//6.30E-85//391aa//45%//P70194
 45 NTONG20052650//Gallus gallus Xin mRNA, complete cds.//5.40E-146//768aa//40%//AF051944
 NTONG20056570//CORONIN-LIKE PROTEIN P57.//2.20E-121//356aa//62%//Q92176
 NTONG20061870
 NTONG20063010//Mus musculus EF-9 mRNA, partial cds.//1.70E-78//154aa//92%//U72678
 NTONG20064400//REPETIN.//2.20E-107//446aa//50%//P97347
 50 NTONG20064840//Mus musculus spl mRNA for synaptotagmin-like protein 1, complete cds.//2.60E-128//258aa//
 90%//AB050741
 NTONG20065010
 NTONG20066460//Mus musculus Gd mRNA for gasdermin, complete cds.//8.30E-207//446aa//88%//AB033595
 NTONG20067090//Mus musculus mRNA for Sh3yl1, complete cds.//2.00E-63//136aa//91%//D85926
 55 NTONG20067830//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//1.10E-
 24//227aa//34%//P16157
 NTONG20070200//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-134//352aa//65%//
 P51522

EP 1 347 046 A1

NTONG20070340//collagen alpha 1 (IX) chain//1.50E-43//220aa//45%//S42617
 NTONG20075220//Rattus norvegicus SNIP-a mRNA, complete cds//1.80E-121//436aa//41%//AF156981
 NTONG20076930//ALPHA-1-INHIBITOR III PRECURSOR//1.20E-124//513aa//47%//P14046
 NTONG20077560
 5 NTONG20083650
 NTONG20088620//Homo sapiens genethonin 3 mRNA, partial cds//4.90E-202//390aa//99%//AF177292
 NTONG20090600//SYNAPSIN I (BRAIN-PROTEIN 4.1)//2.10E-07//198aa//29%//P17600
 NTONG20090680
 NTONG20092290
 10 NTONG20092330//BESTROPHIN (VITELLIFORM MACULAR DYSTROPHY PROTEIN) (TU15B)//1.40E-135//
 414aa//59%//O76090
 OCBBF10000540//Mus musculus rjs (rjs) mRNA, complete cds//4.00E-14//105aa//36%//AF061529
 OCBBF10001750//Mus musculus mRNA for sprouty-4, complete cds//1.50E-159//300aa//92%//AB019280
 OCBBF10001850//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//8.90E-166//605aa//51%//
 15 P51523
 OCBBP20005230
 OCBBF20006770//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)//2.50E-287//693aa//
 84%//Q13428
 OCBBF20013890
 20 OCBBF20019380//seizure related gene 6//6.00E-170//336aa//90%//NP_067261
 OCBBF20019830
 OCBBF20020150
 OCBBF20020830//Homo sapiens Pumilio 1 (PUMH1) mRNA, complete cds//0//814aa//99%//AF315592
 OCBBF20022900//Homo sapiens SCHIP-1 mRNA, complete cds//2.80E-250//469aa//99%//AF145713
 25 OCBBF20023570
 OCBBF20026630
 OCBBF20028050//Homo sapiens B2 gene partial cDNA, clone B2E//7.70E-38//246aa//33%//AJ002220
 OCBBF20028650//DOSAGE COMPENSATION REGULATOR (MALE-LESS PROTEIN) (NO ACTION POTEN-
 TIAL PROTEIN)//1.40E-50//160aa//47%//P24785
 30 OCBBF20029800
 OCBBF20030280//Rattus norvegicus hfb2 mRNA, complete cds//5.20E-63//175aa//68%//AF031483
 OCBBF20030910//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA)//2.90E-146//279aa//
 98%//P55786
 OCBBP20032460
 35 OCBBF20035930//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA)//7.80E-135//264aa//96%//
 P81126
 OCBBF20037440//ZINC-FINGER PROTEIN HT2A (72 KDA TAT-INTERACTING PROTEIN)//2.10E-08//80aa//
 40%//Q13049
 OCBBF20039250//Homo sapiens breast cancer metastasis-suppressor 1 (BRMS1) mRNA, complete cds//2.20E-
 40 55//188aa//56%//AF159141
 OCBBF20041680
 OCBBF20045330
 OCBBF20046120//zinc finger protein 16 (KOX 9)//1.00E-131//350aa//59%//NP_008889
 OCBBF20046470//ARFAPTIN 1//5.80E-114//229aa//97%//P53367
 45 OCBBF20046690//PROBABLE CATION-TRANSPORTING ATPASE WO8D2.5 IN CHROMOSOME IV (EC
 3.6.1.-). //4.20E-105//249aa//39%//Q27533
 OCBBF20047570
 OCBBF20048660
 OCBBF20049300//ZINC FINGER PROTEIN 184 (FRAGMENT)//7.10E-141//566aa//45%//Q99676
 50 OCBBF20049840//Homo sapiens mRNA for neurabin II protein//4.90E-166//808aa//47%//AJ401189
 OCBBF20050770//CARNITINE O-PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC
 2.3.1.21) (CPT I) (CPTI-L)//3.10E-211//653aa//56%//P32198
 OCBBF20051610
 OCBBF20053430//Mus musculus MAST205 protein kinase mRNA, complete cds//0//498aa//94%//U02313
 55 OCBBF20053490//MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE)
 (PMI) (PHOSPHOHEXOMUTASE)//1.10E-24//52aa//100%//P34949
 OCBBF20053730//85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2 (EC 3.1.1.4) (IPLA2) (CAI- PLA2)//
 0//636aa//91%//O60733

EP 1 347 046 A1

OCBBF20054200//DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA.//1.10E-27//97aa//54%//P21461
 OCBBF20054760//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RE-
 CEPTOR INTERACTING PROTEIN).//4.00E-122//230aa//97%//Q13546
 OCBBF20059560//Homo sapiens (clone D320) C219-reactive peptide mRNA, partial cds.//6.70E-39//140aa//
 5 62%//L34688
 OCBBF20060300
 OCBBF20061720
 OCBBF20062140
 OCBBF20062410
 10 OCBBF20063320
 OCBBF20066390//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-63//173aa//65%//
 P51523
 OCBBF20068490//Mus musculus RW1 protein mRNA, complete cds.//4.60E-40//310aa//37%//AF060565
 OCBBF20071210//M-PHASE PHOSPHOPROTEIN 9 (FRAGMENT).//1.80E-96//184aa//100%//Q99550
 15 OCBBF20071840//ZINC FINGER PROTEIN 135.//1.00E-139//416aa//57%//P52742
 OCBBF20071960//Coturnix coturnix japonica qMEF2D gene.//6.50E-06//124aa//31%//AJ002238
 OCBBF20072240//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//7.60E-165//
 354aa//83%//AF097645
 OCBBF20072320
 20 OCBBF20073540//Homo sapiens p30 DBC mRNA, complete cds.//4.00E-65//146aa//91%//AF293335
 OCBBF20074140
 OCBBF20076220
 OCBBF20078920//Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds.//3.10E-67//152aa//92%//
 U91543
 25 OCBBF20079310
 OCBBF20079460
 OCBBF20080050//RTOA PROTEIN (RATIO-A).//3.50E-07//191aa//32%//P54681
 OCBBF20080410//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.90E-145//445aa//51%//P28160
 OCBBF20081380
 30 OCBBF20082830//NDRG1 PROTEIN (DIFFERENTIATION-RELATED GENE 1 PROTEIN) (DRG1) (REDUCING
 AGENTS AND TUNICAMYCIN-RESPONSIVE PROTEIN) (RTP) (NICKEL- SPECIFIC INDUCTION PROTEIN
 CAP43).//3.10E-190//282aa//99%//Q92597
 OCBBF20084660
 OCBBF20085200
 35 OCBBF20086400//Mus musculus ADP-ribosylation factor-like membrane-associated protein (Arm1) mRNA, com-
 plete cds.//2.10E-114//244aa//87%//AF205936
 OCBBF20086910//Mus musculus mSox5L mRNA, complete cds.//9.30E-253//528aa//91%//AB006330
 OCBBF20087010
 OCBBF20088140
 40 OCBBF20088220
 OCBBF20091150
 OCBBF20094240
 OCBBF20097720
 OCBBF20100400
 45 OCBBF20103130
 OCBBF20104040
 OCBBF20105570
 OCBBF20107090//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds.//2.60E-77//359aa//49%//
 AF029343
 50 OCBBF20107920
 OCBBF20108190//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//2.90E-151//429aa//61%//P16415
 OCBBF20108430//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CY-
 CLASE-INHIBITING G ALPHA PROTEIN).//2.10E-171//316aa//100%//P04899
 OCBBF20108580//APICAL-LIKE PROTEIN (APXL PROTEIN).//1.00E-196//376aa//100%//Q13796
 55 OCBBF20108630//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE TRANS-
 PORTER 1) (ATP-BINDING CASSETTE 1).//1.00E-63//268aa//46%//P41233
 OCBBF20109310
 OCBBF20111770

EP 1 347 046 A1

OCBBF20116850//Mus musculus Isr(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds.//2.10E-88//285aa//57%//AB024538

OCBBF20118970

OCBBF20120390//SODIUM-DEPENDENT PROLINE TRANSPORTER (FRAGMENT).//0//636aa//100%//Q99884

5 OCBBF20121390//RING CANAL PROTEIN (KELCH PROTEIN).//7.80E-28//220aa//31%//Q04652

OCBBF20122620

OCBBF20124360//Homo sapiens mRNA for Misshapen/NIK-related kinase MINK-1, complete cds.//2.70E-98//185aa//100%//AB035698

OCBBF20125530//Mus musculus PRAJA1 (Praj1) mRNA, complete cds.//3.60E-110//281aa//77%//U06944

10 OCBBF20126780

OCBBF20127040//Drosophila melanogaster woc gene, exons 1-11.//1.10E-09//284aa//24%//AJ276394

OCBBF20127140//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1 (TRANS-DUCIN BETA CHAIN 1).//5.50E-63//119aa//100%//P04901

OCBBF20127550

15 OCBBF20128120//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//1.20E-205//397aa//93%//AB032401

OCBBF20129360//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//1.00E-130//461aa//36%//P51178

OCBBF20130110

20 OCBBF20130910

OCBBF20132850//Homo sapiens brain tumor associated protein NAG14 (NAG14) mRNA, complete cds.//3.80E-24//399aa//27%//AF196976

OCBBF20139260

OCBBF20140640

25 OCBBF20140890

OCBBF20145760//GLYPICAN-1 PRECURSOR.//3.40E-118//222aa//100%//P35052

OCBBF20148280//Mus musculus mlt 1 gene, complete cds.//1.70E-151//502aa//63%//AB032418

OCRRF20148730//RING CANAL PROTEIN (KELCH PROTEIN).//2.90E-43//509aa//26%//Q04652

OCRRF20149280//Mus musculus WAVE-1 mRNA, complete cds.//4.30E-07//210aa//29%//AF290877

30 OCBBF20151150

OCBBF20153340//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//0//701aa//93%//AF076183

OCBBF20153350//G PROTEIN PATHWAY SUPPRESSOR2 (GPS2 PROTEIN).//1.20E-49//103aa//99%//Q13227

OCBBF20155060//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//1.90E-67//307aa//37%//P33450

35 OCBBF20164050

OCBBF20164670

OCBBF20170690

OCBBF20173060

40 OCBBF20173250

OCBBF20173980//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//3.70E-211//531aa//70%//AF050219

OCBBF201781501//Plasmodium falciparum ADA2-like protein gene, partial cds.//2.20E-19//322aa//27%//AF184590

45 OCBBF20178880//11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH).//3.90E-37//101aa//78%//Q92781

OCBBF20178990

OCBBF20180120//Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds.//1.50E-272//320aa//89%//AF154121

50 OCBBF20180840

OCBBF20186870

OCBBF20188730

OCBBF20189560

PANCR10000910//ATP-binding cassette, sub-family A member 8//2.00E-17//230aa//30%//NP_009099

55 PEBLM10000240

PEBLM10000710//leptin receptor//2.10E-29//69aa//91%//U66496

PEBLM20013120//Homo sapiens rhotekin mRNA, partial cds.//4.10E-25//164aa//36%//AF290512

PEBLM20024320//zinc resistance protein homolog //3.80E-28//139aa//45%//T27544

EP 1 347 046 A1

PEBLM20024550
 PEBLM20040150
 PEBLM20042900
 5 PEBLM20044520//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4)
 (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//2.40E-54//331aa//39%//P53010
 PEBLM20052820//PROTEIN PHOSPHATASE 2C HOMOLOG 3 (EC 3.1.3.16) (PP2C-3).//7.60E-09//96aa//36%//
 Q09173
 PEBLM20060310
 10 PEBLM20060360//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
 (FRAGMENT).//5.10E-12//57aa//56%//Q06730
 PEBLM20060490//polymerase (RNA) III (DNA directed) (39kD) [Homo sapiens]//1.50E-72//143aa//100%//
 NP_006457
 PEBLM20071880
 PEBLM20072960
 15 PEBLM20074370
 PEBLM20075980//Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds.//2.30E-69//
 285aa//52%//AF302046
 PEBLM20078320//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.00E-184//543aa//59%//
 P51523
 20 PEBLM20085760//Homo sapiens mRNA for TOLLIP protein.//1.10E-106//153aa//98%//AJ242972
 PERIC10000250//DNA TOPOISOMERASE III BETA-1 (EC 5.99.1.2).//1.20E-138//271aa//94%//095985
 PERIC20002140
 PERIC20003860
 25 PERIC20003870//Mus musculus transcriptional activator alpha-NAC (Naca) gene, complete cds.//1.20E-152//
 956aa//43%//U48363
 PERIC20004220
 PERIC20004780//Rattus norvegicus Jun dimerization protein 1 (jdp-1) gene, complete cds.//2.00E-15//73aa//
 49%//U53450
 30 PLACE50000660//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//1.60E-12//200aa//27%//
 Q63009
 PLACE60003480//Rattus norvegicus protein associating with small stress protein PASS1 (Pass1) mRNA, com-
 plete cds.//4.60E-119//255aa//82%//AF168362
 PLACE60004630
 PLACE60060420//60S RIBOSOMAL PROTEIN L44 (L36A).//1.70E-29//58aa//100%//P09896
 35 PLACE60079250//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//979aa//61%//
 AB029290
 PLACE60086400
 PLACE60119750
 PLACE60121080
 40 PLACE60136500
 PLACE60136720
 PLACE60138830
 PLACE60153220
 PLACE60155130
 45 PLACE60161600
 PLACE60169420
 PLACE60177140//PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR).//9.90E-
 135//257aa//99%//P43119
 PLACE60181070
 50 PLACE60187690
 PLACE60188340
 PROST10003220//HOMEBOX PROTEIN HOX-A2.//5.00E-69//139aa//95%//043364
 PROST10004800
 PROST20005050
 55 PROST20005670
 PROST20021010
 PROST20024890
 PROST20029270

EP 1 347 046 A1

PROST20047270
 PROST20047390//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//5.70E-52//427aa//31%//
 P51523
 PROST20050670
 5 PROST20052280
 PROST20057930
 PROST20059040
 PROST20066880//Mus musculus zinc finger protein 276 C2H2 type (Zfp276) mRNA, complete cds.//9.80E-101//
 192aa//94%//AF178935
 10 PROST20079500
 PROST20083600//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, com-
 plete cds.//1.40E-101//243aa//83%//AF026954
 PROST20087700
 PROST20097950
 15 PROST20100460//Homo sapiens secretory mucin MUC6 (MUC6) mRNA, partial cds.//3.10E-216//421aa//98%//
 U97698
 PROST20104000//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//1.40E-20//128aa//39%//
 Q62203
 PROST20107820//Human C3f mRNA, complete cds.//9.90E-140//252aa//100%//U72515
 20 PROST20111050
 PROST20112970
 PROST20114390
 PROST20116600
 PROST20120050
 25 PROST20120160
 PROST20121900
 PROST20123530
 PROST20127400
 PROST20127800
 30 PROST20130530
 PROST20132600
 PROST20133270
 PROST20144220
 PROST20146010
 35 PROST20149160
 PROST20149250
 PROST20151240
 PROST20152460
 PROST20153320
 40 PROST20159240//Homo sapiens Opa-interacting protein OIP2 mRNA, partial cds.//1.10E-19//46aa//100%//
 AF025438
 PROST20161950//Mus musculus RalGDS-like protein 3 mRNA, complete cds.//8.30E-88//205aa//85%//
 AF237669
 PROST20164440
 45 PROST20166680
 PROST20168290
 PROST20169800//CYTOCHROME P450 4F2 (EC 1.14.13.30) (CYP1VF2) (LEUKOTRIENE-B4 OMEGA- HY-
 DROXYLASE) (LEUKOTRIENE-B4 20-MONOOXYGENASE) (CYTOCHROME P450- LTB-OMEGA)//6.30E-
 188//507aa//66%//P78329
 50 PROST20170980
 PROST20171280//hematopoietic zinc finger//2.00E-70//380aa//50%//NP_038894
 PROST20175290
 PROST20176170//Homo sapiens ENIGMA protein mRNA, complete cds.//2.60E-156//270aa//98%//AF265209
 PROST20178360
 55 PROST20185830//NITROGEN REGULATORY PROTEIN AREA//5.50E-07//141aa//28%//013412
 PROST20189770//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//5.00E-155//459aa//53%//
 P51523
 PROST20191640//Mus musculus UbcM4-interacting protein 4 mRNA, complete cds.//1.50E-91//279aa//57%//

EP 1 347 046 A1

AF360998
 PUAEN10000850
 PUAEN20003740
 PUAEN20011880//Mus musculus mRNA for MIWI (piwi), complete cds.//2.70E-190//670aa//51%//AB032604
 5 PUAEN20015260//Rattus norvegicus inositol polyphosphate multikinase (Ipmk) mRNA, complete cds.//2.40E-111//246aa//85%//AY014898
 PUAEN20015860//Mus musculus PDZ-RGS3 protein mRNA, complete cds.//1.50E-205//469aa//82%//AF350047
 PUAEN20018820//C-ETS-2 PROTEIN.//7.90E-261//469aa//99%//P15036
 PUAEN20025680
 10 PUAEN20027580
 PUAEN20030180//CARBONIC ANHYDRASE XII PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE XII) (CA-XII) (TUMOR ANTIGEN HOM-RCC-3.1.3).//7.60E-148//259aa//95%//043570
 PUAEN20040670//Mus musculus neuronal protein 4.1 mRNA, complete cds.//0//733aa//93%//AF061283
 PUAEN20044000
 15 PUAEN20045110
 PUAEN20045250
 PUAEN20051100//Mus musculus otogelin mRNA, complete cds.//2.60E-89//368aa//43%//U96411
 PUAEN20052470
 PUAEN20055020//Homo sapiens goodpasture antigen-binding protein (COL4A3BP) mRNA, complete cds.//0//624aa//100%//AF136450
 20 PUAEN20078980//faciogenital dysplasia homolog//1.00E-19//200aa//39%//NP_032027
 PUAEN20081230
 PUAEN20083140//Homo sapiens SWAP-70 mRNA, complete cds.//2.70E-280//451aa//99%//AF210818
 PUAEN20085150
 25 PUAEN20108240//Drosophila melanogaster ankyrin 2 (Ank2) mRNA, complete cds.//5.00E-22//200aa..35%//AF190635
 RECTM10001410
 RECTM20003490
 RECTM20005100
 30 SALGL10001710//Homo sapiens mRNA for C110RF25 gene.//1.80E-88//455aa//41%//AJ300461
 SKMUS20001980//Mus musculus N-RAP mRNA, complete cds.//1.40E-63//141aa//88%//U76618
 SKMUS20003610//PUTATIVE MITOCHONDRIAL CARRIER PROTEIN PET8.//7.40E-59//274aa//47%//P38921
 SKMUS20007010//VESTIGIAL PROTEIN.//2.70E-14//209aa//32%//Q26366
 SKMUS20007800//PROSTAGLANDIN TRANSPORTER (PGT) (MATRIN F/G).//4.20E-47//274aa//36%//Q00910
 35 SKMUS20011640
 SKMUS20012010
 SKMUS20016220//Mus musculus N-RAP mRNA, complete cds.//1.80E-85//352aa//47%//U76618
 SKMUS20018230//Homo sapiens MYPT2 mRNA, complete cds.//8.10E-13//107aa//40%//AB003062
 SKMUS20018500//Homo sapiens t(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA, complete cds.//2.30E-131//268aa//94%//L49054
 40 SKMUS20020840
 SKMUS20021530//Homo sapiens SPG protein (SPG) mRNA, complete cds.//1.50E-278//506aa//99%//AF302154
 SKMUS20024750//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.90E-21//203aa//33%//Q15404
 45 SKMUS20028210
 SKMUS20028400//Mus musculus YIP1B (Yiplb) mRNA, complete cds.//2.90E-53//142aa//74%//AF217188
 SKMUS20029200//Homo sapiens ASB-1 protein mRNA, complete cds.//1.20E-45//302aa//39%//AF156777
 SKMUS20031680
 SKMUS20046670
 50 SKMUS20048970//ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1).//8.00E-181//263aa//99%//P02568
 SKMUS20049030//H.sapiens mRNA for nebulin.//3.50E-148//286aa//99%//X83957
 SKMUS20077400
 SKMUS20084740
 SKNMC20006220
 55 SKNSH20008190//ZINC FINGER PROTEIN 133.//2.80E-165//503aa//56%//P52736
 SKNSH20020540
 SKNSH20028660
 SKNSH20031740

EP 1 347 046 A1

SKNSH20034660
 SKNSH20051940
 SKNSH20062340
 SKNSH20063040//Homo sapiens tetraspan NET-4 mRNA, complete cds.//1.00E-20//177aa//41%//AF065389
 5 SKNSH20080430
 SKNSH20087770
 SKNSH20089400//Homo sapiens Rad51-interacting protein mRNA, complete cds.//2.20E-172//292aa//93%//
 AF006259
 SKNSH20091970
 10 SMINT20001760//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.40E-37//138aa//37%//P51522
 SMINT20005410
 SMINT20008240
 SMINT20009840//IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).//9.00E-54//117aa//90%//
 P06309
 15 SMINT20011140
 SMINT20011580
 SMINT20011990
 SMINT20013480
 SMINT20014580
 20 SMINT20015590
 SMINT20022020
 SMINT20023280
 SMINT20024570//tektin A1//6. 90E-26//124aa//45%//M97188
 SMINT20026890//SMOOTHELIN.//3.10E-278//611aa//88%//P53814
 25 SMINT20028820//Homo sapiens mRNA for F5-2, complete cds.//2.40E-83//162aa//98%//AB020739
 SMINT20029760
 SMINT20033170
 SMINT20033400
 SMINT20035690
 30 SMINT20040860
 SMINT20042990
 SMINT20047810
 SMINT20049090//Homo sapiens mRNA for partial putative mitogen-activated protein kinase kinase kinase.//
 2.20E-32//69aa//98%//AJ242724
 35 SMINT20050750//SPARC PRECURSOR (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OS-
 TEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40).//4.20E-111//259aa//82%//P09486
 SMINT20051610//Mus musculus ES18 mRNA, complete cds.//6.90E-235//485aa//88%//AF083929
 SMINT20053300//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.//7.00E-
 20//44aa//100%//AF218421
 40 SMINT20053870
 SMINT20056210
 SMINT20058000
 SMINT20060780
 SMINT20065960
 45 SMINT20068010
 SMINT20071400
 SMINT20073650//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
 SMINT20076470
 SMINT20080540
 50 SMINT20089170
 SMINT20092330
 SMINT20092720
 SMINT20095050
 SMINT20098320
 55 SMINT20100680
 SMINT20101440//Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds.//
 1.70E-96//182aa//100%//U78556
 SMINT20102780//NICOTINATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.11) (NAPRTASE).//5.30E-05//

EP 1 347 046 A1

123aa//33%//P18133
 SMINT20103690
 SMINT20105000
 SMINT20105330//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOS-
 5 IDASE) //1.00E-54//138aa//78%//P16278
 SMINT20106290//FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA GLYCOSYLA-
 SE) //7.00E-07//214aa//32%//050606
 SMINT20106720//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//3.30E-235//477aa//89%//
 Y14737
 10 SMINT20108530
 SMINT20109970
 SMINT20110330
 SMINT20110660//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//
 1.20E-33//68aa//100%//AF177145
 15 SMINT20112730//IG ALPHA-1 CHAIN C REGION.//1.70E-196//353aa//99%//P01876
 SMINT20115880//Kruppel associated box (KRAB) zinc finger 1 [Rattus norvegicus]//1.50E-42//211aa//45%//
 NP_062566
 SMINT20121220//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE
 B) (NMMHC-B) //1.00E-18//493aa//24%//P35580
 20 SMINT20121950//HYPOTHETICAL 70.2 KDA PROTEIN C22E12.10C IN CHROMOSOME I.//5.70E-16//90aa//
 45%//Q10361
 SMINT20122850
 SMINT20122910//Mus musculus StAR-related protein 1-4E mRNA, partial cds.//1.50E-77//170aa//82%//
 AY007808
 25 SMINT20127350//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (U1 SNRNP 70 KDA) (SNRP70) //
 3.50E-14.185aa//32%//P08621
 SMINT20127930//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
 SMINT20130320//Rattus norvegicus MHC class II transactivator type IV (CIITA) mRNA, complete cds.//2.50E-33//
 645aa//26%//AF251307
 30 SMINT20131810
 SMINT20132280
 SMINT20136130//IG LAMBDA CHAIN C REGIONS.//4.00E-51//105aa//95%//P01842
 SMINT20138900//DESMIN.//7.20E-203//425aa//94%//P17661
 SMINT20144430//IG LAMBDA CHAIN V-I REGION BL2 PRECURSOR.//3.80E-55//130aa//83%//P06316
 35 SMINT20144800//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.60E-139//354aa//70%//U71363
 SMINT20144890
 SMINT20152940//Mus musculus ATP-dependent zinc metalloprotease (Afg311) mRNA, complete cds; nuclear
 gene for mitochondrial product.//1.10E-52//75aa//84%//AF329695
 SMINT20153260//EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) //
 3.50E-274//476aa//98%//Q16610
 40 SMINT20153530
 SMINT2015454 CHANNEL PROTEIN P64.//1.10E-135//419aa//68%//P35526
 SMINT20155180//Homo sapiens GBAS (GBAS) mRNA, complete cds.//6.70E-115//142aa//97%//AF029786
 SMINT20157450
 45 SMINT20158100
 SMINT20161220
 SMINT20162860
 SMINT20163960
 SMINT20164400
 50 SMINT20164770
 SMINT20168570//Homo sapiens mRNA for stabilin-1 (stab1 gene).//5.50E-61//128aa//98%//AJ275213
 SMINT20173190
 SMINT20173240
 SMINT20174360//RHYTHMICALLY EXPRESSED GENE 2 PROTEIN (DREG-2) //6.90E-24//242aa//28%//
 Q94915
 55 SMINT20177360//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLIC-
 ING COMPONENT 35 KDA) (PR264 PROTEIN).//6.40E-37//82aa//92%//P30352
 SMINT20178550

EP 1 347 046 A1

SMINT20179740//IG MU CHAIN C REGION.//8.50E-248//454aa//99%//P01871
 SMINT20183530//GCN20 PROTEIN.//5.50E-118//410aa//52%//P43535
 SMINT20190170//IG ALPHA-1 CHAIN C REGION.//8.50E-199//353aa//100%//P01876
 5 SMINT20191420//AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE ISO-
 FORM M).//5.40E-214//401aa//97%//P23109
 SMINT20191530//PUTATIVE ATP-DEPENDENT RNA HELICASE DBP73D.//5.00E-85//547aa//42%//P26802
 SMINT20192000
 SPLEN10000830
 SPLEN20000640
 10 SPLEN20002220
 SPLEN20003070
 SPLEN20006070//ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).//1.50E-81//
 788aa//30%//P16157
 SPLEN20008390//Human placenta (Diff48) mRNA, complete cds.//4.60E-108//337aa//60%//U49187
 15 SPLEN20008740//IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA
 POLYMERASE I SUPPRESSOR PROTEIN).//5.50E-12//490aa//22%//Q02821
 SPLEN20008820
 SPLEN20011410//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)
 (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)
 20 (P50-RHOGAP).//1.50E-21//183aa//34%//Q07960
 SPLEN20013540
 SPLEN20016260
 SPLEN20019450
 SPLEN20020070
 25 SPLEN20021660//GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYL-
 TRANSFERASE) (GGT).//9.00E-23//167aa//33%//P07314
 SPLEN20022230
 SPLEN20023140
 SPLEN20026950//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).//0//766aa//
 30 81%//P51531
 SPLEN20027440//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).//6.10E-25//
 368aa//30%//Q01484
 SPLEN20029310
 SPLEN20031600
 35 SPLEN20032040
 SPLEN20032190
 SPLEN20033960
 SPLEN20039240//HEAT SHOCK 70 KDA PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2).//9.80E-112//213aa//
 40 100%//P08107
 SPLEN20040600
 SPLEN20054290//Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and
 vasotocin genes, complete cds.//4.20E-180//448aa//71%//U90880
 SPLEN20076530
 SPLEN20077500//Mus musculus Niban mRNA, complete cds.//1.30E-39//351aa//31%//AB049355
 45 SPLEN20079260//ZINC FINGER PROTEIN 132.//6.30E-117//320aa//61%//P52740
 SPLEN20079510
 SPLEN20084600//RING CANAL PROTEIN (KELCH PROTEIN).//5.20E-58//558aa//29%//Q04652
 SPLEN20095410//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.50E-83//236aa//58%//Q99676
 SPLEN20095550
 50 SPLEN20095810
 SPLEN20097330
 SPLEN20099700//TAT-BINDING HOMOLOG 7.//1.50E-142//553aa//48%//P54816
 SPLEN20101190
 SPLEN20103950//40S RIBOSOMAL PROTEIN S17.//7.10E-22//49aa//100%//P06584
 55 SPLEN20106250
 SPLEN20117660//Homo sapiens BCL-6 corepressor (BCOR) mRNA, complete cds; alternatively spliced.//1.30E-
 38//139aa//61%//AF317391
 SPLEN20118300//Rattus norvegicus amino acid transport system A3 (Ata3) mRNA, complete cds.//1.70E-20//

EP 1 347 046 A1

210aa//28%//AF295535
 SPLEN20119810
 SPLEN20121750//Danio rerio uridine kinase mRNA, complete cds.//1.60E-29//130aa//50%//AF195851
 SPLEN20126190
 5 SPLEN20128000//Xenopus laevis XMAB21 (Xmab-21) mRNA, complete cds.//6.80E-12//287aa//24%//AF040992
 SPLEN20129610
 SPLEN20140800//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-145//586aa//47%//
 P51523
 SPLEN20141360
 10 SPLEN20141990
 SPLEN20142100//Rattus norvegicus alpha D integrin mRNA, complete cds.//7.10E-37//105aa//76%//AF021334
 SPLEN20143180//Mus musculus EWS/FLI1 activated transcript 2 (EAT-2) mRNA, complete cds.//2.50E-45//
 132aa//65%//AF020263
 SPLEN20144520
 15 SPLEN20145720//Rattus norvegicus nuclear GTPase PIKE mRNA, complete cds.//2.00E-24//120aa//45%//
 AF280816
 SPLEN20146450//H.sapiens mRNA for plakophilin 2a and b.//1.20E-08//87aa//42%//X97675
 SPLEN20146690
 SPLEN20147110//cyclin-E binding protein 1//0//580aa//58%//NP_057407
 20 SPLEN20147390//ZINC FINGER PROTEIN 136.//1.40E-105//417aa//49%//P52737
 SPLEN20149110
 SPLEN20149190
 SPLEN20149240//Cricetulus longicaudatus arginine N-methyltransferase p82 isoform mRNA, complete cds, al-
 ternatively spliced.//3.50E-259//525aa//86%//AF336043
 25 SPLEN20150940//Mus musculus histone deacetylase mHDA1 mRNA, complete cds.//4.20E-187//550aa//51%//
 AF006602
 SPLEN20151210//protein tyrosine phosphatase, non-receptor type 13(APO-1/CD95 (Fas)-associated phos-
 phatase)//3.00E-25//250aa//29%//NP_006255
 SPLEN20152610
 30 SPLEN20152760
 SPLEN20157300
 SPLEN20157880//Homo sapiens Ig superfamily receptor LNIR precursor, mRNA, complete cds.//1.70E-05//
 137aa//29%//AF160477
 SPLEN20158900
 35 SPLEN20158990
 SPLEN20160450//Homo sapiens mRNA for Hrs, complete cds.//5.60E-28//59aa//100%//D84064
 SPLEN20160690
 SPLEN20160980
 SPLEN20162680//NUCLEAR PROTEIN SNF7.//4.20E-11//189aa//25%//P39929
 40 SPLEN20163560
 SPLEN20165310//Homo sapiens mRNA for immunoglobulin lambda heavy chain. //4.90E-230//477aa//88%//
 Y14737
 SPLEN20166270
 SPLEN20167200//Mus musculus MPS1 gene and mRNA, 3'end.//1.50E-15//46aa//84%//L20315
 45 SPLEN20169220
 SPLEN20169720
 SPLEN20170310//Homo sapiens Asef mRNA for APC-stimulated guanine nucleotide exchange factor, complete
 cds.//8.40E-95//305aa//62%//AB042199
 SPLEN20171210
 50 SPLEN20171470
 SPLEN20171890
 SPLEN20172120
 SPLEN20173510//Xenopus laevis putative N-terminal acetyltransferase mRNA, complete cds.//3.90E-210//
 413aa//66%//AF247679
 55 SPLEN20174260
 SPLEN20176200
 SPLEN20179180//Homo sapiens EH domain containing 2 (EHD2) mRNA, complete cds.//1.10E-181//340aa//
 94%//AF181263

EP 1 347 046 A1

SPLEN20179810//Mus musculus pecanex 1 mRNA, complete cds.//3.80E-131//534aa//51%//AF096286
 SPLEN20181810//Mus musculus faciogenital dysplasia protein 2 (Fgd2) mRNA, complete cds.//6.60E-68//144aa//
 66%//AF017368
 SPLEN20186430//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//2.20E-163//226aa//96%//P35414
 5 SPLEN20193110
 SPLEN20194050//Homo sapiens HOTTTL protein mRNA, complete cds.//9.50E-135//264aa//93%//AF078842
 SPLEN20198110
 SPLEN20204170
 SPLEN20211220
 10 SPLEN20211570
 SPLEN20211940
 SPLEN20212730//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (M-TYPE).//1.70E-137//255aa//98%//P17655
 SPLEN20212950
 15 SPLEN20213830
 SPLEN20214400
 SPLEN20214580//Mus musculus mdg1-1 mRNA, complete cds.//1.40E-16//39aa//94%//AF190624
 SPLEN20222270//Mus musculus adaptor protein (Dok1) mRNA, complete cds.//1.10E-42//123aa//61%//AF179242
 SPLEN20225220
 20 SPLEN20242320
 SPLEN20242730
 SPLEN20243830//TRANSCRIPTION INITIATION FACTOR TFIID, 135 KDA SUBUNIT (TAFII-135) (TAFII135)
 (TAFII 130) (TAFII130).//4.70E-38//98aa//87%//000268
 SPLEN20245300//ADP-ribosylation factor binding protein GGA1//3.00E-39//120aa//76%//NP_037497
 25 SPLEN20249560
 SPLEN20250170//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.40E-51//488aa//27%//P52734
 SPLEN20250390//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU-TYPE). //3.00E-55//115aa//94%//P07384
 30 SPLEN20252190//ZINC FINGER PROTEIN 135.//6.00E-89//303aa//52%//P52742
 SPLEN2026440
 SPLEN20264110
 SPLEN20267650//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.20E-90//410aa//45%//Q99676
 SPLEN20273950
 35 SPLEN20279950
 SPLEN20280660
 SPLEN20283650//Mus musculus ras activator RasGRP (Rasgrp) mRNA, complete cds.//9.80E-54//182aa//57%//
 AF106070
 SPLEN20284240//Homo sapiens hOBDFP mRNA for osteoblast differentiation promoting factor, complete cds.//
 40 9.80E-93//177aa//98%//AB048363
 SPLEN20292950//ATP-binding cassette, sub-family A member 8 //3.30E-211//469aa//64%//NP_009099
 SPLEN20293800
 SPLEN20303970
 SPLEN20304950//Homo sapiens CAGH32 mRNA, partial cds.//9.60E-44//86aa//98%//U80743
 45 SPLEN20305620//DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE
 OXIDASE) (FRAGMENT).//3.60E-59//124aa//96%//Q02127
 SPLEN20329240
 STOMA20001830//IG ALPHA-1 CHAIN C REGION.//2.10E-196//353aa//99%//P01876
 STOMA20005390//IG ALPHA-1 CHAIN C REGION.//7.90E-197//353aa//100%//P01876
 50 STOMA20005670//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.90E-216//478aa//83%//
 Y14737
 STOMA20006400//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
 hinge isolate Lib-A2.//8.40E-214//377aa//100%//AJ390247
 STOMA20005780
 55 STOMA20005860//Homo sapiens TOB3 mRNA, complete cds.//1.80E-74//159aa//97%//AF343078
 STOMA20009880//MYOCILIN PRECURSOR (TRABECULAR MESHWORK-INDUCED GLUCOCORTICOID RE-
 SPONSIVE PROTEIN) //1.00E-196//405aa//91%//Q99972
 STOMA20010250//Homo sapiens RNA-binding protein (RBMS3) mRNA, complete cds.//7.70E-46//116aa//86%//

EP 1 347 046 A1

AF023259
STOMA20013890
STOMA20026880
STOMA20032890//ZINC FINGER PROTEIN CKR1 //5.80E-30//162aa//38%//P30373
5 STOMA20034770//IG ALPHA-1 CHAIN C REGION //4.40E-196//353aa//99%//P01876
STOMA20036460
STOMA20046680//FOSB PROTEIN (G0/G1 SWITCH REGULATORY PROTEIN 3) //4.10E-14//36aa//100%//
P53539
STOMA20048520
10 STOMA20048840
STOMA20051200
STOMA20056640//Ig lambda chain V region //6.80E-54//150aa//73%//S23626
STOMA20056670//IG ALPHA-1 CHAIN C REGION //7.90E-197//353aa//100%//P01876
STOMA20057820
15 STOMA20062130//IG KAPPA CHAIN V-III REGION HAH PRECURSOR //3.10E-53//129aa//80%//P18135
STOMA20062290
STOMA20063250//TRANSCRIPTION FACTOR COE3 (EARLY B-CELL FACTOR 3) (EBF-3) (OLF-1/EBF-LIKE
2) (OE-2) (O/E-2) //7.50E-50//105aa//93%//008791
STOMA20063980
20 STOMA20064470//PLACENTAL RIBONUCLEASE INHIBITOR (RIBONUCLEASE/ANGIOGENIN INHIBITOR)
(RAI) (RI) //3.60E-14//262aa//30%//P13489
STOMA20067800
STOMA20069040
STOMA20072690
25 STOMA20076800
STOMA20077450//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN) //2.70E-228//430aa//97%//P22314
STOMA20080500//ATP-binding cassette, sub-family A, member 7, isoform a //1.00E-297//538aa//94%//
NP_061985
STOMA20083610//IG ALPHA-1 CHAIN C REGION //7.90E-197//353aa//100%//P01876
30 STOMA20085140
STOMA20088380//IG ALPHA-1 CHAIN C REGION //2.10E-196//352aa//100%//P01876
STOMA20092530//Homo sapiens mRNA for immunoglobulin lambda heavy chain //3.10E-239//477aa//91%//
Y14737
STOMA20092560
35 STOMA20092890
SYNOV20001520//Homo sapiens kappa 1 immunoglobulin light chain mRNA, complete cds //5.50E-107//236aa//
E61113887
SYNOV20001730//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
rity-determining regions mRNA, complete cds //2.60E-226//479aa//86%//M87789
40 SYNOV20002510//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
intron splice Kp-25 //6.60E-214//377aa//100%//AJ390254
SYNOV20002790//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
rity-determining regions mRNA, complete cds //1.30E-238//476aa//91%//M87789
SYNOV20002970//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
45 rity-determining regions mRNA, complete cds //7.00E-226//476aa//86%//M87789
SYNOV20003970
SYNOV20004260//Homo sapiens mRNA for immunoglobulin lambda heavy chain //1.10E-225//477aa//86%//
Y14737
50 SYNOV20007000//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
rity-determining regions mRNA, complete cds //4.00E-239//478aa//91%//M87789
SYNOV20008240//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
rity-determining regions mRNA, complete cds //4.10E-237//479aa//90%//M87789
SYNOV20009230//IG ALPHA-1 CHAIN C REGION //7.90E-197//353aa//100%//P01876
SYNOV20010880//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
55 rity-determining regions mRNA, complete cds //1.60E-233//476aa//89%//M87789
SYNOV20011110//Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementa-
rity-determining regions mRNA, complete cds //6.90E-235//476aa//89%//M87789
SYNOV20013000//Ig gamma =immunoglobulin heavy chain [rats, humanized lympholytic MoAb CAMPATH-1H,

EP 1 347 046 A1

mRNA, 1465 nt.//7.70E-220//472aa//86%//S79307
 SYNOV20013560//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.40E-234//477aa//89%//Y14737
 SYNOV20013900//Homo sapiens mRNA for immunoglobulin kappa heavy chain.//3.50E-231//476aa//89%//Y14735
 SYNOV20017080
 SYNOV30001840
 TBAES20000590
 TBAES20002550//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.10E-310//586aa//89%//009175
 TBAES20003150//CYTOCHROME P450 4A1 (EC 1.14.15.3) (CYP1A1) (LAURIC ACID OMEGA- HYDROXYLASE) (P450-LA-OMEGA 1) (P452).//1.40E-82//323aa//44%//P08516
 TBAES20003770//SPERM-SPECIFIC ANTIGEN 2 (CLEAVAGE SIGNAL-1 PROTEIN) (CS-1).//1.90E-122//249aa//97%//P28290
 TCOLN20001390
 TESOP20000900
 TESOP20003120
 TESOP20004000//CATHEPSIN B PRECURSOR (EC 3.4.22.1) (CATHEPSIN B1) (APP SECRETASE).//3.30E-111//194aa//98%//P07858
 TESOP20005270//MONOAMINE-SULFATING PHENOL SULFOTRANSFERASE (EC 2.8.2.1) (SULFOTRANSFERASE, MONOAMINE-PREFERRING) (M-PST) (THERMOLABILE PHENOL SULFOTRANSFERASE) (TL-PST) (PLACENTAL ESTROGEN SULFOTRANSFERASE) (CATECHOLAMINE-SULFATING PHENOL SULFOTRANSFERASE) (HAST3).//3.40E-47//92aa//100%//P50224
 TESOP20005690//Mus musculus p53 apoptosis-associated target (Perp) mRNA, complete cds.//2.30E-53//113aa//91%//AF249870
 TESTI10000940
 TESTI20001000//FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA GLYCOSYLASE) //7.80E-06//238aa//28%//P74290
 TESTI20001170
 TESTI20001720
 TESTI20002720//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//1.70E-18//237aa//29%//P38584
 TESTI20002780//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.90E-11//140aa//36%//P08678
 TESTI20004890
 TESTI20011200
 TESTI20017950
 TESTI20018230
 TESTI20023510
 TESTI20029930
 TESTI20030310
 TESTI20030890
 TESTI20031270//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//7.30E-52//146aa//71%//Q13829
 TESTI20031810
 TESTI20035960//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.70E-67//329aa//40%//Q00808
 TESTI20036380//DRA PROTEIN (DOWN-REGULATED IN ADENOMA).//6.40E-46//243aa//35%//P40879
 TESTI20037560
 TESTI20038270
 TESTI20039400//EBNA-1 NUCLEAR PROTEIN.//3.60E-43//298aa//43%//P03211
 TESTI20041690//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//1.00E-12//341aa//21%//Q62318
 TESTI20044230//Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.//1.70E-94//291aa//64%//AF042180
 TESTI20044310//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.70E-06//118aa//32%//Q15404
 TESTI20046750
 TESTI20057750
 TESTI20060400//Columba livia mRNA for 5'-nucleotidase.//3.80E-115//328aa//66%//AJ131243

EP 1 347 046 A1

TESTI20061110//Xenopus laevis katanin p60 mRNA, partial cds.//1.80E-170//489aa//66%//AF177942
 TESTI20063830//Drosophila melanogaster nuclear fallout (nuf) mRNA, nuf-1 allele, complete cds.//2.10E-34//
 371aa//29%//AF045015
 TESTI20066670//probable acyl-CoA dehydrogenase //1.90E-72//222aa//60%//D75616
 5 TESTI20066770
 TESTI20067200//PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-3 (HOMEODOMAIN PROTEIN PBX3)//
 4.20E-132//352aa//71%//P40426
 TESTI20076850
 TESTI20082330//helicase II homolog//4.10E-44//775aa//25%//T13889
 10 TESTI20083200//Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX) mRNA, complete cds.//
 1.00E-41//131aa//58%//AF165519
 TESTI20083940
 TESTI20086210
 TESTI20087620
 15 TESTI20088220//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.50E-175//633aa//
 48%//Q05481
 TESTI20094020
 TESTI20094120
 TESTI20094230//Strongylocentrotus purpuratus tektin A1 mRNA, complete cds//4.50E-64//252aa//50%//M97188
 20 TESTI20094470//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//1.40E-183//318aa//99%//
 000321
 TESTI20098350
 TESTI20098530
 TESTI20102800
 25 TESTI20105720
 TESTI20108720//PROTEIN PHOSPHATASE 2C BETA ISOFORM (EC 3.1.3.16) (PP2C-BETA) (IA) (PROTEIN
 PHOSPHATASE 1B).//3.30E-49//249aa//46%//P36993
 TESTI20110280
 TESTI20112940
 30 TESTI20114070
 TESTI20116650
 TESTI20116830//Homo sapiens liprin-beta2 mRNA, partial cds.//8.20E-17//50aa//92%//AF034803
 TESTI20121550//NUCLEOPORIN-LIKE PROTEIN RIP (REV INTERACTING PROTEIN) (REV/REX ACTIVATION
 DOMAIN-BINDING PROTEIN).//1.60E-152//363aa//85%//P52594
 35 TESTI20122310
 TESTI20123080
 TESTI20123560
 TESTI20127760
 TESTI20128350
 40 TESTI20129150
 TESTI20129220
 TESTI20130010//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.10E-63//173aa//65%//P51523
 TESTI20130120
 TESTI20135660
 45 TESTI20136100//ZINC/CADMIUM RESISTANCE PROTEIN.//3.70E-12//101aa//35%//P20107
 TESTI20136710
 TESTI20136990
 TESTI20137370
 TESTI20137670
 50 TESTI20143240
 TESTI20143390//Mus musculus testicular condensin enzyme (AMAC1) mRNA, complete cds.//1.60E-51//
 123aa//79%//AF016712
 TESTI20143620
 TESTI20148000//PROTEIN DISULFIDE ISOMERASE (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA
 55 SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (RETINA COGNIN) (R-COGNIN).//2.80E-
 75//493aa//34%//P09102
 TESTI20152460//ML02 PROTEIN.//9.60E-42//170aa//40%//Q09329
 TESTI20155900

EP 1 347 046 A1

TESTI20156100//KRUPPEL-LIKE FACTOR 4 (EPITHELIAL ZINC-FINGER PROTEIN EZF).//2.30E-32//254aa//
 32%//043474
 TESTI20157100
 TESTI20157520
 5 TESTI20159140
 TESTI20161970
 TESTI20164100
 TESTI20168480//H.sapiens mRNA for titin protein (clone hh1-hh54).//6.30E-48//393aa//31%//X90568
 TESTI20168630
 10 TESTI20168960
 TESTI20169960
 TESTI20170350
 TESTI20171020
 TESTI20178160
 15 TESTI20179320
 TESTI20183370
 TESTI20184620//OXYSTEROL-BINDING PROTEIN.//6.20E-27//181aa//28%//P16258
 TESTI20185650//Xenopus laevis ubiquitin-like fusion protein mRNA, complete cds.//2.90E-129//543aa//46%//
 L08474
 20 TESTI20185810
 TESTI20189410//Mus musculus axotrophin mRNA, complete cds.//7.50E-43//142aa//57%//AF155739
 TESTI20192280
 TESTI20192800//Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16 mRNA, complete cds.//
 2.40E-23//164aa//41%//AF121775
 25 TESTI20193360
 TESTI20194300
 TESTI20194810
 TESTI20197940
 TESTI20199170
 30 TESTI20199750//TRICHOHYALIN.//8.80E-59//547aa//30%//P37709
 TESTI20200260
 TESTI20200710//Mus musculus epithelial protein lost in neoplasm-a (Eplin) mRNA, complete cds.//4.40E-40//
 212aa//42%//AF307844
 TESTI20202650
 35 TESTI20203440
 TESTI20204450//M.musculus of DNA encoding DNA-binding protein.//1.90E-58//477aa//32%//Z54200
 TESTI20208400//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NU-
 CLEOLAR PROTEIN P120).//1.70E-16//181aa//33%//P46087
 TESTI20208710
 40 TESTI20209460
 TESTI20209810
 TESTI20209990
 TESTI20211160
 TESTI20211220
 45 TESTI20211240
 TESTI20213150
 TESTI20213580
 TESTI20214250//MITOCHONDRIAL CARRIER PROTEIN PMT.//1.10E-34//242aa//36%//P32332
 TESTI20215990//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.10E-
 39//375aa//28%//AF186273
 50 TESTI20216370//LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ES-MALE) (ESTERASE-31).//
 1.50E-60//164aa//68%//Q63880
 TESTI20220100
 TESTI20220650
 55 TESTI20224620
 TESTI20226230//Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds.//8.90E-111//371aa//59%//AF102129
 TESTI20226490
 TESTI20229600//Drosophila melanogaster SP2353 mRNA, complete cds.//8.30E-117//607aa//33%//AF239610

EP 1 347 046 A1

TESTI20230250
 TESTI20230850//CIRCADIAN LOCOMOTOR OUTPUT CYCLES KAPUT PROTEIN (MCLOCK).//1.00E-23//
 186aa//30%//008785
 TESTI20231920
 5 TESTI20231940//Human OB binding protein-2 (OB-BP2) mRNA, complete cds.//4.60E-14//140aa//36%//U71383
 TESTI20232140//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//2.50E-90//388aa//47%//
 P10895
 TESTI20234140
 10 TESTI20234270
 TESTI20234360//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA-INTERACTING 1 (EC 5.2.1.8).//5.90E-
 66//128aa//98%//Q13526
 TESTI20237520//poly(A)-specific ribonuclease (deadenylation nuclease)//1.10E-34//311aa//26%//NP_002573
 TESTI20238000
 15 TESTI20238610//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)
 (DAM10).//6.80E-69//268aa//51%//P43366
 TESTI20239470
 TESTI20239510//ubiquitin specific protease 6//5.60E-43//182aa//50%//NP_004496
 TESTI20240090
 20 TESTI20241530
 TESTI20241920
 TESTI20242830
 TESTI20242990
 TESTI20244190//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
 25 hinge, isolate Lib-A2.//8.40E-214//377aa//100%//AJ390247
 TESTI20244760
 TESTI20249990//ATAXIN 7 (SPINOCEREBELLAR ATAXIA TYPE 7 PROTEIN).//7.30E-49//388aa//37%//015265
 TESTI20254220
 30 TESTI20254540//Homo sapiens hepatocellular carcinoma-associated antigen 59 mRNA, complete cds.//1.60E-
 100//197aa//98%//AF218421
 TESTI20254860//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//1.20E-35//564aa//28%//P70211
 TESTI20255820
 TESTI20258460//Homo sapiens OSBP-related protein 4 mRNA, complete cds.//8.20E-196//369aa//99%//
 AF323731
 35 TESTI20262330
 TESTI20262910
 TESTI20265250
 TESTI20265370
 TESTI20265970
 40 TESTI20266740//Homo sapiens topoisomerase-related function protein (TRF4-1) mRNA, partial cds.//2.70E-105//
 278aa//71%//AF089896
 TESTI20269570
 TESTI20271850
 TESTI20272060
 45 TESTI20272390
 TESTI20272960//Mus musculus gene for odorant receptor MOR83, complete cds.//3.30E-84//306aa//50%//
 AB030894
 TESTI20275030
 TESTI20275620
 50 TESTI20277360
 TESTI20278200
 TESTI20278400//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.50E-11//604aa//21%//P25386
 TESTI20280980
 TESTI20282540
 55 TESTI20284880
 TESTI20285830
 TESTI20288110
 TESTI20288910//Mus musculus endophilin II mRNA, complete cds.//2.10E-110//225aa//92%//U58885

EP 1 347 046 A1

TESTI20289850
 TESTI20291310
 TESTI20291620
 TESTI20291960//RHOMBROID PROTEIN (VEINLET PROTEIN).//2.00E-40//230aa//38%//P20350
 5 TESTI20294700
 TESTI20297850
 TESTI20301360
 TESTI20303220//Rattus norvegicus neural cell adhesion protein BIG-2 precursor (BIG-2) mRNA, complete cds.//
 0//807aa//94%//U35371
 10 TESTI20303360
 TESTI20303420
 TESTI20305540//M.musculus mRNA for IB3/5-polypeptide.//1.30E-183//684aa//56%//X79131
 TESTI20305560
 TESTI20307540
 15 TESTI20307700
 TESTI20308600
 TESTI20309170//Mucor circinelloides crgA gene for carotenoid regulatory protein.//3.10E-41//198aa//40%//
 AJ250998
 TESTI20310070
 20 TESTI20311290
 TESTI20314180//TRYPSIN I-P1 PRECURSOR (EC 3.4.21.4)//2.10E-25//86aa//40%//Q90627
 TESTI20316870//Homo sapiens mRNA for cartilage-associated protein (CASP).//4.90E-106//199aa//99%//
 AJ006470
 TESTI20317600
 25 TESTI20318090//ZINC FINGER PROTEIN 135.//2.00E-56//208aa//50%//P52742
 TESTI20319190
 TESTI20320440//THIOREDOXIN.//4.30E-32//103aa//63%//P50413
 TESTI20320670//Rattus norvegicus mRNA for type A/B hnRNP protein p40.//2.20E-170//337aa//91%//AJ238854
 TESTI20326810//RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN (RAN BINDING PROTEIN 1) (RANBP1).//
 30 2.00E-33//66aa//100%//P34022
 TESTI20327680
 TESTI20327740
 TESTI20328280
 TESTI20330310
 35 TESTI20332420//Mus musculus cell cycle checkpoint control protein Mrad9 gene, complete cds.//5.80E-20//
 246aa//28%//AP045662
 TESTI20333000
 TESTI20333950
 TESTI20334410//Sus scrofa RNA helicase (RHIV-1) mRNA, complete cds.//4.40E-58//281aa//33%//AF181119
 40 TESTI20335050//Homo sapiens cell cycle checkpoint protein CHFR mRNA, complete cds.//6.00E-188//333aa//
 99%//AF170724
 TESTI20335200//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//
 8.10E-20//87aa//50%//P13688
 TESTI20336410
 45 TESTI20337100
 TESTI20342430
 TESTI20343070
 TESTI20343570//TRIPEPTIDYL-PEPTIDASE II (EC 3.4.14.10) (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE).//
 2.00E-75//201aa//75%//P29144
 50 TESTI20345060
 TESTI20347180//Mus musculus membrane protein TMS-2 mRNA, complete cds.//6.00E-35//186aa//41%//
 AF181685
 TESTI20347300
 TESTI20347740
 55 TESTI20347770
 TESTI20351830
 TESTI20352620//PROACTIVATOR POLYPEPTIDE PRECURSOR [CONTAINS: SAPOSIN A (PROTEIN A); SA-
 POSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1) (SAP-1) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SA-

EP 1 347 046 A1

POSIN C (CO-BETA-GLUCOSIDASE) (A1 ACTIVATOR) (GLUCOSYLCERAMIDASE ACTIVATOR) (SPHINGOL-
IPID ACTIVATOR PROTEIN 2) (SAP-2); SAPOSIN D (PROTEIN C) (COMPONENT C)]//1.30E-52//240aa//44%//
P07602

TESTI20355020//Drosophila sp. His (his) mRNA, complete cds.//9.80E-30//416aa//28%//S79915

TESTI20357750

TESTI20357930

TESTI20357960

TESTI20358980//Volvox carteri mRNA for hydroxyproline-rich glycoprotein (HRGP gene).//2.90E-37//155aa//
50%//AJ242540

TESTI20361140

TESTI20366910//Homo sapiens mRNA for thioredoxin reductase II beta, complete cds.//2.00E-233//442aa//93%//
AB019695

TESTI20367360

TESTI20368330//M-PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48).//2.10E-258//473aa//99%//P30307

TESTI20369130

TESTI20369220

TESTI20369650//Homo sapiens mRNA for HsGAK, complete cds.//2.40E-269//493aa//99%//D88435

TESTI20369690

TESTI20370020

TESTI20370550

TESTI20370810//Homo sapiens mRNA for LAK-4p, complete cds.//1.10E-74//385aa//38%//AB002405

TESTI20371030//TIP ELONGATION ABERRANT PROTEIN 1 (CELL POLARITY PROTEIN TEA1).//7.80E-23//
243aa//29%//P87061

TESTI20371060

TESTI20373820

TESTI20375340//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.80E-68//273aa//45%//
P10895

TESTI20377230

TESTI20378190//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.30E-114//323aa//
52%//Q05481

TESTI20378450

TESTI20380650

TESTI20381040

TESTI20382750//Homo sapiens hook1 protein (HOOK1) mRNA, complete cds.//2.60E-96//195aa//99%//
AF044923

TESTI20383880//Homo sapiens gamma cysteine string protein mRNA, partial cds.//6.50E-61//109aa//100%//
AF368277

TESTI20385960//Homo sapiens mRNA for RET finger protein-like 3.//4.80E-156//288aa//100%//AJ010232

TESTI20386230

TESTI20386440

TESTI20388580

TESTI20390260

TESTI20390410

TESTI20391130

TESTI20391210

TESTI20391770

TESTI20392090

TESTI20392250//Homo sapiens VAV-3 protein mRNA, complete cds.//9.80E-145//268aa//98%//AF067817

TESTI20392270

TESTI20392760//PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.//5.70E-22//226aa//31%//
P36047

TESTI20393530//MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR (PTP).//9.00E-34//
105aa//68%//P12234

TESTI20396130

TESTI20397760//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIB (EC 3.6.1.-).//1.60E-109//221aa//
90%//P98195

TESTI20400940//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//4.70E-16//669aa//23%//Q02224

EP 1 347 046 A1

TESTI20401020//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.//5.80E-64//234aa//56%//AF004161
 TESTI20401280
 TESTI20401430
 5 TESTI20404240//INTERFERON-RELATED DEVELOPMENTAL REGULATOR 2 (SKMC15 PROTEIN).//4.60E-36//46aa//93%//Q12894
 TESTI20406420
 TESTI20408150
 TESTI20408970//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KDA) (P145).//4.30E-16//264aa//30%//P52591
 10 TESTI20409440
 TESTI20409890//GCD14 PROTEIN.//2.30E-46//263aa//40%//P46959
 TESTI20413300
 TESTI20415170
 15 TESTI20415640
 TESTI20416640//CHOLINE/ETHANOLAMINE KINASE [INCLUDES: CHOLINE KINASE (EC 2.7.1.32) (CK); ETHANOLAMINE KINASE (EC 2.7.1.82) (EK)].//2.10E-77//139aa//100%//Q9Y259
 TESTI20417300//DYNEIN BETA CHAIN, CILIARY.//6.80E-129//552aa//45%//P39057
 TESTI20419560
 20 TESTI20420620//TRANSCRIPTION INITIATION FACTOR TFIID 70 KDA SUBUNIT (TAFII-70) (TAFII-80) (TAFII80).//0//526aa//99%//P49848
 TESTI204214
 TESTI20422640
 TESTI20423020
 25 TESTI20424000
 TESTI20424730
 TESTI20425070
 TESTI20427830
 TESTI20428060
 30 TESTI20429280
 TESTI20429580
 TESTI20432750//Mus musculus pantothenate kinase 1 beta (panK1beta mRNA, complete cds.//9.70E-165//363aa//82%//AF200357
 TESTI20432820//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.00E-173//403aa//75%//P28160
 35 TESTI20433130
 TESTI20436560//LAMIN C.//9.20E-235//453aa//99%//P02546
 TESTI20438570//Homo sapiens nlp mRNA, complete cds.//2.70E-43//146aa//60%//AB017800
 TESTI20438660
 TESTI20441940//Human K-C1 cotransporter (hKCC1) mRNA, complete cds.//5.50E-139//264aa//99%//U55054
 40 TESTI20442760//Homo sapiens Ig-like membrane protein (IGSF3) mRNA, complete cds.//0//545aa//93%//AF031174
 TESTI20443090//DNA REPAIR PROTEIN RAD51 HOMOLOG 4 (R51H3) (TRAD).//2.70E-68//141aa//100%//075771
 TESTI20444130
 45 TESTI20444180
 TESTI20447540
 TESTI20449200//METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.//9.00E-173//313aa//99%//Q14831
 TESTI20451710
 50 TESTI20451990
 TESTI20455090//KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 18).//1.20E-76//199aa//80%//P05783
 TESTI20455620//HEAT SHOCK-RELATED 70 KDA PROTEIN 2 (HEAT SHOCK 70 KDA PROTEIN 2).//4.80E-218//336aa//99%//P54652
 55 TESTI20456110//52 KDA RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//9.40E-75//382aa//43%//P19474
 TESTI20458190
 TESTI20463520

EP 1 347 046 A1

TESTI20463580//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.50E-17//190aa//28%//Q13107

TESTI20465350//2'. 3' -CYCLIC NUCLEOTIDE 3' -PHOSPHODIESTERASE (EC 3.1.4.37) (CNP) (CNPASE).//2.20E-123//231aa//100%//P09543

TESTI20465520

TESTI20465690//Homo sapiens Borg4 mRNA, complete cds.//2.00E-152//235aa//99%//AB042237

TESTI20467210//Homo sapiens mRNA for HELG protein.//2.00E-166//368aa//83%//AJ277291

TESTI20467320//Mus musculus WAVE-1 mRNA, complete cds.//1.20E-111//233aa//88%//AF290877

TESTI20467970

TESTI20468630

TESTI20471410//PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A).//1.30E-210//382aa//99%//P35813

TESTI20471470

TESTI20471530

TESTI20472120

TESTI20473420

TESTI20473830//Columba livia mRNA for 5'-nucleotidase.//2.00E-14//75aa//49%//AJ131243

TESTI20477920

TESTI20478010

TESTI20478180

TESTI20478850

TESTI20479300

THYMU10005360//Human T cell receptor beta chain (TCRB) mRNA, VNDNJC region, 5'end.//1.20E-130//270aa//91%//L07294

THYMU10005540//Homo sapiens mRNA for immunoglobulin lambda heavy chain.//1.20E-237//479aa//90%//Y14737

THYMU20000570

THYMU20011950

THYMU20015210

THYMU20018190

THYMU20023380//Homo sapiens m6A methyltransferase (MT-A70) gene, complete cds.//1.20E-38//86aa//100%//AF014837

THYMU20027560

THYMU20029100

THYMU20032870

THYMU20039810//MPS1 protein.//2.60E-283//646aa//77%//I52603

THYMU20045120

THYMU20058070

THYMU20061700

THYMU20066100

THYMU20070360

THYMU20075320

THYMU20081490//Homo sapiens ICB-1 mRNA, complete cds.//1.50E-23//267aa//33%//AF044896

THYMU20095960

THYMU20100410

THYMU20101610

THYMU20101920

THYMU20105190//MYOSIN I ALPHA (MMI-ALPHA).//7.50E-54//282aa//45%//P46735

THYMU20106710//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//1.20E-54//113aa//98%//AE000660

THYMU20108310//Mouse NCBP-29 mRNA for PW29, complete cds.//7.70E-93//102aa//99%//D49429

THYMU20111180

THYMU20111420

THYMU20111830//protease, serine, 16 (thymus).//1.40E-129//175aa//98%//NP_005856

THYMU20114470

THYMU20115850

THYMU20118060

EP 1 347 046 A1

THYMU20118520//Xenopus laevis ubiquitin-like fusion protein mRNA, complete cds//3.00E-42//109aa//77%//
 L08475
 THYMU20119390
 THYMU20122730//target of myb1 (chicken) homolog//1.00E-122//233aa//100%//NP_005479
 5 THYMU20126900//UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22) (UDP-GLC DEHYDROGENASE)
 (UDP-GLCDH) (UDPGDH)//1.40E-229//341aa//99%//060701
 THYMU20128070
 THYMU20128260
 10 THYMU20130890//40S RIBOSOMAL PROTEIN S16//1.90E-28//125aa//57%//P17008
 THYMU20141670
 THYMU20142040//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//2.60E-12//155aa//32%//
 P70315
 THYMU20142970
 15 THYMU20143270//Homo sapiens HSNFRK (HSNFRK) mRNA, complete cds//5.40E-171//321aa//100%//
 AF226044
 THYMU20147770//Homo sapiens mRNA for immunoglobulin lambda heavy chain//5.40E-235//477aa//89%//
 Y14737
 THYMU20153160
 THYMU20158250
 20 THYMU20159430//IG ALPHA-1 CHAIN C REGION//7.90E-197//353aa//100%//P01876
 THYMU20161640//Mus musculus p53 apoptosis-associated target (Perp) mRNA, complete cds//1.40E-92//
 188aa//89%//AF249870
 THYMU20162190
 25 THYMU20169680//DIACYLGLYCEROL KINASE, ZETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- ZETA)
 (DAG KINASE ZETA)//1.40E-64//124aa//99%//Q13574
 THYMU20172150//CORONIN-LIKE PROTEIN P57 (CORONIN 1A)//1.60E-49//96aa//100%//P31146
 THYMU20173980
 THYMU20180280//RED PROTEIN (RER PROTEIN) (IK FACTOR) (CYTOKINE IK)//2.60E-40//83aa//96%//
 Q13123
 30 THYMU20186390
 THYMU20186730
 THYMU20187720
 THYMU20193640//HETEROGENE NUCLEAR RIBONUCLEOPROTEIN L (HNRNP L)//1.70E-82//157aa//99%//
 P14866
 35 THYMU20194360
 THYMU20194420
 THYMU20195990
 THYMU20201980//Mus musculus faciogenital dysplasia protein 2 (Fgd2) mRNA, complete cds//2.90E-122//
 259aa//86%//AF017368
 40 THYMU20202890//PROTEIN KINASE CLK3 (EC 2.7.1.-)//1.10E-204//367aa//99%//035492
 THYMU20204160
 THYMU20204990
 THYMU20208300
 THYMU20209590//DYNAMIN 2//2.10E-189//363aa//97%//P50570
 45 THYMU20215090
 THYMU20215970
 THYMU20216840
 THYMU20222890
 THYMU20226600
 50 THYMU20228540
 THYMU20229220
 THYMU20232090//SYNTAXIN BINDING PROTEIN 2 (UNC-18 HOMOLOG 2) (UNC-18B)//2.10E-54//112aa//
 99%//Q15833
 THYMU20235760
 55 THYMU20239000//collagen alpha 1(XI) chain //1.70E-37//579aa//33%//S18251
 THYMU20239430
 THYMU20240710//Halocynthia roretzi mRNA for HrPET-3, complete cds//5.60E-54//155aa//44%//AB029335
 THYMU20241210//Homo sapiens mRNA for nuclear protein, NP220, complete cds//2.00E-58//117aa//100%//

EP 1 347 046 A1

D83032

THYMU20241850//HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DX BETA CHAIN PRECURSOR.//4.40E-141//261aa//100%//P05538

THYMU20246840

5 THYMU20247480//ZINC FINGER PROTEIN 135.//1.20E-97//191aa//90%//P52742

THYMU20250420

THYMU20251890

THYMU20253250

THYMU20255570

10 THYMU20255720

THYMU20259090

THYMU20265300

THYMU20271250

THYMU20272490

15 THYMU20277390

THYMU20279750

THYMU20283790

THYMU20284120

THYMU20286290

20 THYMU20286320

TKIDN10000010//translocase of inner mitochondrial membrane 23 (yeast) homolog//6.30E-67//133aa//98%//NP_006318

TKIDN20004640//GALACTOKINASE 2 (EC 2.7.1.6).//5.10E-99//200aa//97%//Q01415

TKIDN20005210

25 TKIDN20030590

TKIDN20030620

TKIDN20047480//MITOGEN-ACTIVATED PROTEIN KINASE 12 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL-REGULATED KINASE 6) (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-ACTIVATED PROTEIN KINASE-3) (MITOGEN-ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP KINASE P38 GAMMA).//2.20E-52//104aa//100%//P53778

30 TOVAR20004760

TOVAR20005750

TRACH20002870//CLAUDIN-6.//1.30E-27//175aa//42%//Q9Z262

TRACH20003590//CYTOCHROME P450 4A4 (EC 1.14.14.1) (CYP1A4) (PROSTAGLANDIN OMEGA-HYDROXYLASE) (P450-P-2).//1.50E-138//493aa//49%//P10611

35 TRACH20005020

TRACH20005400//Mus musculus GTPase Rab37 (Rab37) mRNA, complete cds.//3.30E-109//223aa//93%//AF233582

TRACH20007020//TRICHOHYALIN.//5.60E-24//532aa//23%//P37709

40 TRACH20016210//ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.65) (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 6) (FUCT-VI).//5.00E-192//254aa//99%//P51993

TRACH20019960//SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN PRECURSOR (EC 3.6.1.37) (SODIUM PUMP) (NA+/K+ ATPASE).//9.50E-185//410aa//84%//P05023

TRACH20027840

45 TRACH20028030//Mus musculus mmDNAJA4 mRNA for mmDj4, complete cds.//8.50E-205//397aa//92%//AB032401

TRACH20029540

TRACH20032720

TRACH20033230//MALTOSE PERMEASE.//1.20E-10//197aa//23%//Q45632

50 TRACH20034840//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//5.90E-14//342aa//28%//P17437

TRACH20037360

TRACH20041830//Acdcs triseriatus putative disulfide-isomerase mRNA, partial cds.//3.10E-29//134aa//47%//AF306866

TRACH20042920//Human C3f mRNA, complete cds.//7.80E-195//381aa//89%//U72515

55 TRACH20048450//PROTEIN K4 (PROTEIN K3).//4.70E-57//431aa//32%//P18377

TRACH20050040//PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR (C210RF3).//8.50E-74//177aa//74%//P53801

TRACH20056980

EP 1 347 046 A1

TRACH20057690//RAC-BETA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-BETA) (AKT2 KINASE)//
8.80E-22//48aa//100%//P31751
TRACH20060150
5 TRACH20067620//N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC
2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)//8.20E-76//145aa//
92%//Q06430
TRACH20068660//Mouse 19.5 mRNA, complete cds//1.00E-55//263aa//41%//M32486
TRACH20068700//Homo sapiens adaptor protein CIKS mRNA, complete cds//1.50E-232//572aa//79%//
AF272151
10 TRACH20069180//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
hinge. isolate Lib-A2//1.00E-213//377aa//100%//AJ390247
TRACH20076740//FOLATE-LIKE TRANSPORTER DJ206D15.1 ON CHROMOSOME 1 (FRAGMENT)//1.00E-
61//276aa//46%//060779
TRACH20076760
15 TRACH20077540//DXS8237E PROTEIN (FRAGMENT)//6.00E-96//189aa//95%//P98175
TRACH20079690//ZINC FINGER PROTEIN 136//1.50E-113//368aa//58%//P52737
TRACH20082780
TRACH20084720//METHIONYL-TRNA SYNTHETASE, MITOCHONDRIAL (EC 6.1.1.10) (METHIONINE-- TRNA
LIGASE) (METRS) //8.50E-90//525aa//38%//074634
20 TRACH20085400//Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds//1.30E-89//
384aa//47%//AF302046
TRACH20085830//CYTOCHROME P450 4A8 (EC 1.14.14.1) (CYP1A8) (P450-KP1) (P450-PP1)//3.70E-247//
508aa//87%//P24464
TRACH20091230
25 TRACH20092680
TRACH20096610//LAMIN A (70 KDA LAMIN)//1.70E-77//164aa//93%//P02545
TRACH20099340
TRACH20105870//EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF- 4G)
(EIF4G) (P220) //9.20E-95//204aa//92%//Q04637
30 TRACH20107710
TRACH20109650
TRACH20111130
TRACH20115740
TRACH20118940
35 TRACH20121380//REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) (FRAGMENT)//7.60E-144//308aa//
92%//043566
TRACH20123110//Rattus norvegicus TM6P1 (TM6P1) mRNA. complete cds//2.10E-87//187aa//88%//AF186469
TRACH20123230//Homo sapiens IGHG3 gene for immunoglobulin heavy chain gamma 3 constant region, 4-exon
hinge. isolate Lib-A2//9.60E-213//377aa//99%//AJ390247
40 TRACH20134950
TRACH20135520
TRACH20136710//IG LAMBDA CHAIN V-II REGION NIG-84//2.20E-43//112aa//75%//P04209
TRACH20139820//SIGNAL RECOGNITION PARTICLE 68 KDA PROTEIN (SRP68)//3.70E-48//107aa//92%//
Q00004
45 TRACH20140820
TRACH20141240//Mus musculus G21 protein mRNA, complete cds//6.10E-26//60aa//93%//AF131207
TRACH20145440
TRACH20147250
50 TRACH20149970//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds//2.30E-
205//512aa//74%//U16802
TRACH20153810
TRACH20154860//RETINOIC ACID RECEPTOR ALPHA (RAR-ALPHA)//8.90E-221//443aa//92%//P10276
TRACH20162860//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3)
(COMPLEX I-B14.5B) (CI-B14. 5B). //1.80E-39//80aa//98%//095298
55 TRACH20163170//HOMEBOX PROTEIN MEIS1//1.50E-131//238aa//100%//000470
TRACH20164980//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.50E-163//488aa//56%//Q99676
TRACH20167220
TRACH20168350

EP 1 347 046 A1

TRACH20169800
 TRACH20180840
 TRACH20183170//Rattus norvegicus Sprague-Dawley SM-20 mRNA, complete cds.//1.60E-75//215aa//61%//
 U06713
 5 TRACH20184490//Homo sapiens mRNA for zinc finger protein (ZNF304 gene). //3.20E-111//477aa//46%//
 AJ276316
 TRACH20187180
 TRACH20190240//Homo sapiens mRNA for fibulin-4.//1.00E-98//179aa//97%//AJ132819
 TSTOM10001860
 10 TSTOM20001390
 TSTOM20003150
 TSTOM20005690//kelch- (Drosophila)-like 3 [Homo sapiens]//5.60E-211//399aa//98%//NP_059111
 TUTER20002830//Homo sapiens transformer-2-beta (SFRS10) gene, alternatively spliced products, complete
 cds.//4.70E-122//253aa//90%//AF057159
 15 UMVEN10001560//Anthocidaris crassispina mRNA for outer arm dynein light chain 1, complete cds.//1.90E-24//
 119aa//47%//AB010055
 UMVEN10001860//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//5.90E-25//
 180aa//33%//P30337
 UMVEN20000690
 20 UMVEN20003540
 UTERU20000740//Human fusion protein mRNA, complete cds.//4.90E-47//97aa//100%//M82829
 UTERU20004240//CGI-96 protein//2.10E-39//108aa//81%//NP_056518
 UTERU20006290
 UTERU20006960//endoplasmic reticulum resident protein 58//5.90E-51//150aa//63%//NP_076994
 25 UTERU20020010
 UTERU20022940//Human (p23) mRNA, complete cds.//2.80E-80//147aa//99%//L24804
 UTERU20030570//CHLORIDE CHANNEL PROTEIN CLC-KB (CLC-K2).//3.00E-252//469aa//99%//P51801
 UTERU20040610
 UTERU20046640//Mus musculus 1dlBp (LDLB) mRNA, complete cds.//0//839aa//83%//AF109377
 30 UTERU20046980//Mus musculus mRNA for thrombospondin type 1 domain, complete cds.//7.30E-117//232aa//
 67%//AB016768
 UTERU20050690
 UTERU20054460
 UTERU20055330
 35 UTERU20055480
 UTERU20055930
 UTERU20056010
 UTERU20059050
 UTERU20061030
 40 UTERU20064000
 UTERU20064860//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.50E-29//595aa//28%//P08640
 UTERU20065930//GTP-RHO BINDING PROTEIN 1 (RHOPHILIN).//6.10E-131//489aa//48%//Q61085
 UTERU20067050
 45 UTERU20068990
 UTERU20070040
 UTERU20070810
 UTERU20076390
 UTERU20081300
 50 UTERU20084260
 UTERU20094350
 UTERU20095380
 UTERU20095400
 UTERU20097760//OVCA2=candidate tumor suppressor [human, fetal brain, Peptide, 120 aa]//6.00E-30//66aa//
 95%//AAB36422
 55 UTERU20099720//Homo sapiens mRNA for SPIN protein.//6.50E-72//186aa//79%//Y14946
 UTERU20101240
 UTERU20114100

EP 1 347 046 A1

UTERU20115740//Human PMS2 related (hPMSR3) gene, complete cds.//1.00E-43//84aa//98%//U38979
 UTERU20116570//Homo sapiens actin-binding double-zinc-finger protein (abLIM) mRNA, complete cds.//4.80E-
 163//468aa//71%//AF005654
 UTERU20118110
 5 UTERU20118970
 UTERU20119060
 UTERU20119680
 UTERU20120310//Rattus norvegicus rexo70 mRNA, complete cds.//1.50E-65//178aa//78%//AF032667
 UTERU20124070
 10 UTERU20126880
 UTERU20134910
 UTERU20135860
 UTERU20143980
 UTERU20144640//ACID CERAMIDASE PRECURSOR (EC 3.5.1.23) (ACYLSPHINGOSINE DEACYLASE)
 15 (N-ACYLSPHINGOSINE AMIDOHYDROLASE) (AC) (PUTATIVE 32 KDA HEART PROTEIN) (PHP32).//1.90E-
 166//243aa//100%//Q13510
 UTERU20145480//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//4.40E-213//
 673aa//57%//AB011414
 UTERU20146310//DIACYLGLYCEROL KINASE ETA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK- ETA) (DAG
 20 KINASE ETA).//4.50E-242//485aa//92%//Q64398
 UTERU20146680
 UTERU20150870
 UTERU20151980//DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
 CIFICITY PROTEIN PHOSPHATASE HVH-5).//5.20E-15//248aa//31%//Q13202
 25 UTERU20158300
 UTERU20158800//P-SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND)
 (CD162 ANTIGEN).//2.20E-185//384aa//95%//Q14242
 UTERU20161570//PROBABLE G PROTEIN-COUPLED RECEPTOR RTA.//2.70E-141//303aa//85%//P23749
 UTERU20164260
 30 UTERU20168220//AIG1 PROTEIN.//7.70E-16//145aa//35%//P54120
 UTERU20176130//Mus musculus zinc finger protein 289 (Zip289) mRNA, complete cds.//4.00E-143//297aa//
 94%//AF229439
 UTERU20176320//DNA REPAIR PROTEIN RAD18.//1.10E-40//333aa//32%//P53692
 UTERU20178100
 35 UTERU20179880
 UTERU20183640//SEMAPHORIN 3B PRECURSOR (SEMAPHORIN V) (SEMA V).//1.20E-69//135aa//100%//
 Q13214
 UTERU20185230//Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, com-
 plete cds.//1.90E-255//571aa//80%//U95825
 40 UTERU20186740
 UTERU20188110//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//4.10E-
 157//315aa//97%//AF076183
 UTERU20188810

Claims

1. A polynucleotide selected from the group consisting of the following (a) to (g):

- (a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443;
- (b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 2444 to 4886;
- (c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 2444 to 4886, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
- (d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ

ID NOs: 1 to 2443, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;

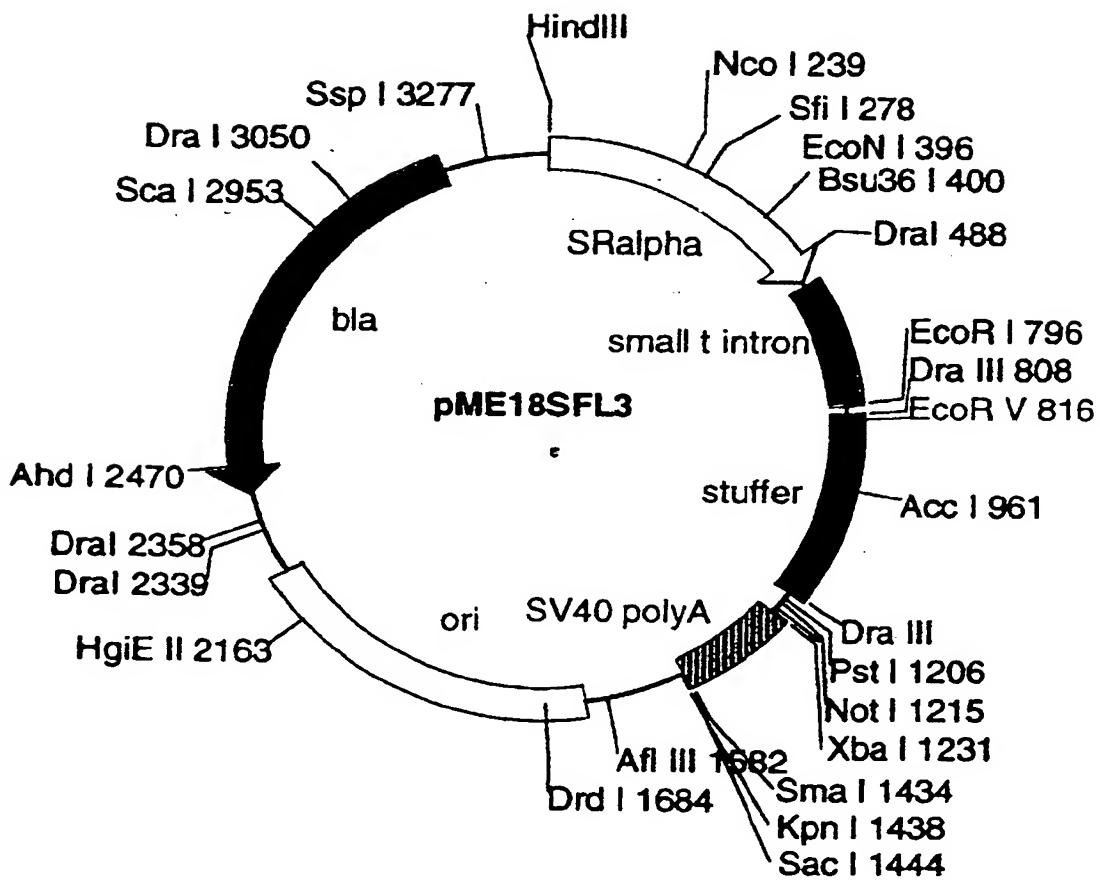
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443; and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443.

2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.
3. An antibody binding to the polypeptide or the peptide of claim 2.
4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.
5. A vector comprising the polynucleotide of claim 1.
6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.
7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.
8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.
9. An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 2443 or to a complementary strand thereof.
10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.
11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.
12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.
13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:
 - a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
 - b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.
14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 2443 and/or on at least one of the amino acid sequences of SEQ ID NOs: 2444 to 4886.

Figure 1





European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 02 00 8400

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	WO 01 53312 A (CHEN RUI HONG ;GOODRICH RYLE (US); HYSEQ INC (US); WANG DUNRUI (US) 26 July 2001 (2001-07-26) claims 1,6,8,10,12,13,17,19 and SEQ ID N 1016 and 2802 ---	1-14	C12N15/00 C07K14/00
X	DATABASE GENSEQ 'Online! DERWENT26 July 2001 (2001-07-26) TANG YT ET AL.: "Human polynucleotide SEQ ID N 1016" Database accession no. AAI58813 XP002206834 This sequence shows 99.9% identity with SEQ ID N 1 in 1726 nucleotide overlap. * the whole document *	1,14	
X	DATABASE GENESEQ PAT 'Online! Derwent26 July 2001 (2001-07-26) TANG YT: "Human polypeptide SEQ ID N 2802" Database accession no. AAM39657 XP002206835 This sequence shows 99.4% identity with SEQ ID N 2444 in 543 aa overlap * the whole document *	2,14	
X	DATABASE EMBL 'Online! 17 January 1998 (1998-01-17) MIKI Y. ET AL.: "Human (J. Swensen) cDNA clone 91-13, mRNA sequence" Database accession no. AF039235 XP002206836 Sequence shows 99.4% identity with SEQ ID N 1 in 1716 nt overlap * the whole document *	1,14	
			TECHNICAL FIELDS SEARCHED (Int.Cl.7) C12N C07K
The present search report has been drawn up for all claims			
Place of search MUNICH		Date of completion of the search 19 July 2002	Examiner Vix, O
CATEGORY OF CITED DOCUMENTS X: particularly relevant if taken alone Y: particularly relevant if combined with another document of the same category A: technological background O: non-written disclosure P: intermediate document T: theory or principle underlying the invention E: earlier patent document, but published on, or after the filing date D: document cited in the application L: document cited for other reasons & : member of the same patent family, corresponding document			

EPO FORM 1503 (03.02) (P/C/C1)



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 02 00 8400

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (InCL1.7)
X	WO 01 57182 A (HUMAN GENOME SCIENCES INC ; ROSEN CRAIG A (US); BARASH STEVEN C (US) 9 August 2001 (2001-08-09) claims 1, 7, 8, 9, 11, 13-15 and SEQ ID N 10300 ---	1-14	
X	DATABASE GENESEQ 'Online! Derwent7 November 2001 (2001-11-07) ROSEN CA ET AL.: "Human immune/hematopoietic antigen SEQ ID N 10300" Database accession no. AAM82707 XP002206837 This sequence shows 98.5% identity with SEQ ID N 2444 in 527 amino acid overlap * the whole document *	2,14	
X	DATABASE SWISSPROT 'Online! 1 July 2001 (2001-07-01) STRAUSBERG R ET AL.: "Hypothetical 58.8 kDa human protein" Database accession no. Q9BTE6 XP002206838 This sequence shows 100% identity with SEQ ID N 2444 in 527 aa overlap. * the whole document *	2,14	
A	US 6 265 165 B1 (GRUENERT DIETER C ET AL) 24 July 2001 (2001-07-24) * the whole document *	1-14	
A	GILL ROBERT W ET AL: "A new dynamic tool to perform assembly of Expressed Sequence Tags (ESTs)." CABIOS, vol. 13, no. 4, 1997, pages 453-457, XP001083718 * the whole document *	1-14	
The present search report has been drawn up for all claims			
Place of search MUNICH		Date of completion of the search 19 July 2002	Examiner Vix, O
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X: particularly relevant if taken alone Y: particularly relevant if combined with another document of the same category A: technological background O: non-written disclosure P: intermediate document</p> <p>T: theory or principle underlying the invention E: earlier patent document, but published on, or after the filing date D: document cited in the application L: document cited for other reasons &: member of the same patent family, corresponding document</p>			

EPO/CA/1503 02 02 (P04C01)



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 02 00 8400

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (InCL.7)
A	O'BRIEN KEVIN P ET AL: "Characterization of five novel human genes in the 11q13-q22 region." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 273, no. 1, 24 June 2000 (2000-06-24), pages 90-94, XP002206833 ISSN: 0006-291X * the whole document *	1-14	
A	SUZUKI Y ET AL: "CONSTRUCTION AND CHARACTERIZATION OF A FULL LENGTH-ENRICHED AND A 5'-END-ENRICHED CDNA LIBRARY" GENE, ELSEVIER, AMSTERDAM, NL, vol. 200, no. 1/2, 19 November 1997 (1997-11-19), pages 149-156, XP002917609 ISSN: 0378-1119 * the whole document *	1-14	
A	BODIAN D L: "IBLAST, a fully automated method for cDNA cloning in silico." FASEB JOURNAL, vol. 13, no. 7, 23 April 1999 (1999-04-23), page A1382 XP001056180 Annual Meeting of the American Societies for Experimental Biology on Biochemistry and Molecular Biology 99: San Francisco, California, USA; May 16-20, 1999 ISSN: 0892-6638 * the whole document *	1-14	
TECHNICAL FIELDS SEARCHED (InCL.7)			
The present search report has been drawn up for all claims			
Place of search		Date of completion of the search	Examiner
MUNICH		19 July 2002	Vix, O
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

EPO FORM 1503 03/87 (P4/C01)



European Patent
Office

Application Number

EP 02 00 8400

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

- ☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):
- ☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

- ☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.
- ☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.
- ☐ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:
- ☒ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

1-14 (partially)



European Patent
Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 02 00 8400

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. Claims: Invention 1: claims 1-14 (partially)

Polynucleotide of SEQ ID N 1 and its encoding polypeptide of
SEQ ID N 2444

2. Claims: Inventions 2-2442 : claims 1-14 (partially)

Polynucleotides of SEQ ID N 2-2442 and their encoding
polypeptides of SEQ ID N 2445-4885

3. Claims: Invention-2443 : claims 1-14 (partially)

Polynucleotide of SEQ ID N 2443 and its encoding polypeptide
of SEQ ID N 4886

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 02 00 8400

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

19-07-2002

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0153312 A	26-07-2001	AU 2292401 A	31-07-2001
		AU 2591801 A	31-07-2001
		AU 2593601 A	31-07-2001
		AU 2595501 A	31-07-2001
		AU 2596501 A	31-07-2001
		AU 2598301 A	31-07-2001
		AU 2728401 A	31-07-2001
		AU 2734401 A	31-07-2001
		AU 2734801 A	31-07-2001
		AU 2738501 A	31-07-2001
		AU 3265701 A	31-07-2001
		EP 1242596 A	25-09-2002
		EP 1240178 A	18-09-2002
		EP 1242580 A	25-09-2002
		EP 1242443 A	25-09-2002
		EP 1250346 A	23-10-2002
		EP 1254256 A	06-11-2002
		EP 1248848 A	16-10-2002
		WO 0153453 A	26-07-2001
		WO 0153326 A	26-07-2001
		WO 0153454 A	26-07-2001
		WO 0153455 A	26-07-2001
		WO 0153456 A	26-07-2001
		WO 0153466 A	26-07-2001
		WO 0152616 A	26-07-2001
		WO 0153500 A	26-07-2001
		WO 0153515 A	26-07-2001
		WO 0153485 A	26-07-2001
		US 6465620 B	15-10-2002
		US 2002146692 A	10-10-2002
		AU 5362001 A	30-10-2001
		WO 0179446 A	25-10-2001
		US 2002142953 A	03-10-2002
WO 0157182 A	09-08-2001	AU 2950801 A	07-08-2001
		AU 3095801 A	07-08-2001
		AU 3645901 A	07-08-2001
		AU 3646001 A	07-08-2001
		AU 3646101 A	07-08-2001
		AU 3646201 A	07-08-2001
		AU 3646301 A	07-08-2001
		AU 3646401 A	07-08-2001
		AU 3646501 A	07-08-2001
		AU 3646601 A	07-08-2001
		AU 3794301 A	07-08-2001
		AU 3794401 A	07-08-2001

EPO FORM P/0159

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 02 00 8400

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

19-07-2002

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 0157182 A		AU 3794701 A	07-08-2001
		AU 3794901 A	07-08-2001
		AU 3795001 A	07-08-2001
		AU 3795101 A	07-08-2001
		AU 3795201 A	07-08-2001
		AU 3795301 A	07-08-2001
		AU 3795401 A	07-08-2001
		AU 3795501 A	07-08-2001
		AU 3795701 A	07-08-2001
		AU 3795801 A	07-08-2001
		AU 3972601 A	07-08-2001
		AU 3972701 A	07-08-2001
		AU 3972801 A	07-08-2001
		AU 4140201 A	07-08-2001
		AU 4140301 A	07-08-2001
		AU 4140401 A	07-08-2001
		AU 4140501 A	07-08-2001
		AU 4140601 A	07-08-2001
		AU 4140701 A	07-08-2001
		AU 4140801 A	07-08-2001
		AU 4140901 A	07-08-2001
		AU 4141001 A	07-08-2001
		AU 4141101 A	20-08-2001
		AU 4141201 A	07-08-2001
		AU 4141301 A	07-08-2001
		AU 4141401 A	07-08-2001
		AU 4141501 A	07-08-2001
		AU 4141601 A	07-08-2001
		AU 4141701 A	07-08-2001
		AU 4141801 A	07-08-2001
		AU 4141901 A	07-08-2001
		AU 4313401 A	07-08-2001
		AU 4313501 A	07-08-2001
		AU 4313601 A	07-08-2001
		AU 4313701 A	14-08-2001
		AU 4526201 A	07-08-2001
		AU 4719001 A	07-08-2001
		AU 4719101 A	07-08-2001
US 6265165 B	24-07-2001	NONE	

THIS PAGE BLANK (USPTO)